



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 175930

TO: Manjunath N Rao
Location: REM-2A01/2C70
Art Unit: 1652
Friday, January 13, 2006
Case Serial Number: 10/618252

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine. Hensle@uspto.gov

Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

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STIC-Biotech/ChemLib

From: Rao, Manjunath N.
Sent: Saturday, January 07, 2006 11:44 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request for 10618252

From: Manjunath N. Rao
Art Unit 1652, Room 2A01
Mail Box in Room 2C70
Phone: 272-0939

Date: 1-7-06

Please search the following as soon as possible for application with serial number
10/618252

1. SEQ ID NO: 14 against all commercial nucleic acid sequence databases, issued patents/published applications nucleic acid sequence database and pending application nucleic acid sequence database. Please provide a print of results
2. SEQ ID NO: 15 against all commercial amino acid sequence databases, issued patents/published applications amino acid sequence database and pending application amino acid sequence database. Please provide a print of results.

If you have any questions please call me at the above phone number.

Thanks

1/9/2006

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or contact:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:

Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 02:08:14 ; Search time 17761 Seconds
(without alignments)
11540.875 Million cell updates/sec

Title: US-10-618-252-14

Perfect score: 3606
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBankl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
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12: gb_un:*
13: gb_vl:*
14: gb_hcg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3606	100.0	3606	6	AX009206	AX009206 Sequence
2	3463.8	96.1	7747	9	AY360383	AY360383 Mus muscu
3	3078.8	85.4	3373	9	AF110507	AF110507 Mus muscu
4	3064	85.0	7618	6	AX105862	AX105862 Sequence
5	3050.4	84.6	7581	6	AX105861	AX105861 Sequence
6	2912.4	80.8	3427	6	E60027	E60027 Novel phosp
7	2912.4	80.8	3427	6	AB027155	AB027155 Rattus no
8	2610.6	72.4	3219	6	AX687065	AX687065 Sequence
9	2167	60.1	3080	6	E60028	E60028 Novel phosp
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ALIGNMENTS

RESULT 1
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DEFINITION Sequence 14 from Patent EP0967284.
ACCESSION AX009206
VERSION AX009206.1 GI:9996571
KEYWORDS
SOURCE
MUS SP.
MUS SP.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 Lanfear, J. and Robas, N.M.
AUTHORS
TITLE Phosphodiesterases
JOURNAL Patent: EP 0967284-A 14 29-DEC-1999;
PRIZER LTD (GB), PRIZER (US)
FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 ACCCGTCGGTCTCTCATCTGCTTCCACCTCCCGGCGCTCCCGAGAGAGGCGC 60
DB 1 ACCCGTCGGTCTCTCATCTGCTTCCACCTCCCGGCGCTCCCGAGAGAGGCGC 60
QY 1 ACCCGTCGGTCTCTCATCTGCTTCCACCTCCCGGCGCTCCCGAGAGAGGCGC 120
1 ACCCGTCGGTCTCTCATCTGCTTCCACCTCCCGGCGCTCCCGAGAGAGGCGC 120
DB 1 ACCCGTCGGTCTCTCATCTGCTTCCACCTCCCGGCGCTCCCGAGAGAGGCGC 120
QY 121 AGGACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
121 AGGACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 AGGACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
121 AGGACAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 CAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCTT 240
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 ACCESSION AY360383
 VERSION AY360383.1 GI:38155284
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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 REFERENCE 1 (bases 1 to 7747)
 AUTHORS Hebb, A.L., Robertson, H.A. and Denovan-Wright, E.M.
 TITLE Striatal phosphodiesterase mRNA and protein levels are reduced in
 Huntington's disease transgenic mice prior to the onset of motor
 symptoms
 JOURNAL Neuroscience 123 (4), 967-981 (2004)
 PUBMED 14751289
 REFERENCE 2 (bases 1 to 7747)
 AUTHORS Hu, H., McCaw, E.A., Hebb, A.L., Gomez, G.T. and Denovan-Wright, E.M.
 TITLE Mutant huntingtin affects the rate of transcription of
 striatum-specific isoforms of phosphodiesterase 10A
 JOURNAL Eur. J. Neurosci. 20 (12), 3351-3363 (2004)
 PUBMED 15610167
 REFERENCE 3 (bases 1 to 7747)
 AUTHORS Hu, H., McCaw, E.A., Hebb, A.L.O., Gomez, G.T. and Denovan-Wright, E.M.
 TITLE Direct Substitution
 JOURNAL Submitted (01-AUG-2003) Department of Pharmacology, Dalhousie
 University, 5859 University Avenue, Trupper Medical Building, Rm15D,
 Halifax, NS B3H 4H7, Canada
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ACCESSION AF110507
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ORGANISM
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 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 1 (bases 1 to 3373)
 Soderling, S.H., Bayuga, S.J. and Beavo, J.A.
 Isolation and characterization of a dual-substrate
 phosphodiesterase gene family: PDE10A
 Proc. Natl. Acad. Sci. U.S.A. 96 (12), 7071-7076 (1999)

JOURNAL
 PUBMED
 10359840
 2 (bases 1 to 3373)
 Soderling, S.H., Bayuga, S.J. and Beavo, J.A.
 Direct Submission
 Submitted (02-DEC-1998) Pharmacology, Univ. of Washington, Seattle,
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 VERSION AX105862.1 GI:13921870
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 ORGANISM Mus sp.
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1
 AUTHORS Robertson, H.A. and Denovan-Wright, E.M.
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 for modulating same
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VERSION	AX105861.1	GI:13921869			
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ORGANISM	unidentified				
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AUTHORS	1				
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 LOCUS
 DEFINITION Novel phosphodiesterase and gene thereof.
 ACCESSION E60027
 VERSION E60027.1 GI:18630000
 KEYWORDS JP 2000224992-A/15.
 SOURCE
 ORGANISM Rattus sp.
 Rattus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Rattus.
 REFERENCE
 1 (bases 1 to 3427)
 OMORI K., KODERA A., FUJISHIGE K., MICHIHATA H. and YUASA K.
 Novel phosphodiesterase and gene thereof
 Patent: JP 200224992-A 15 AUG-2000;
 TANYABE SEIYAKU CO LTD
 OS Rattus sp. (rat)
 PN JP 2000224992-A/15
 PD 15-AUG-2000
 PF 11-MAY-1999 JP 1999129343
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 PI KENJI OMORI, ATSUSHI KODERA, KOTOMI FUJISHIGE, HIDEO MICHIHATA,
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C12N5/10, C12N6/16,
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ORIGIN

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Matches 3153; Conservative 0; Mismatches 226; Indels 35; Gaps 7;
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LOCUS Rattus norvegicus mRNA for PDE10A2, complete cds.
DEFINITION AB027155
ACCESSION AB027155.1 GI:6683032
VERSION AB027155.1
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 Fujishige, K., Kotera, J. and Omori, K.
Striatum- and testis-specific phosphodiesterase PDE10A isolation
and characterization of a rat PDE10A
Eur. J. Biochem. 266 (3), 1118-1127 (1999)
JOURNAL
PUBMED
10583409
2 (bases 1 to 3427)
REFERENCE
Omori, K., Fujishige, K. and Kotera, J.
Direct Submission
Submitted (12-MAY-1999) Kenji Omori, TANABE Seiyaku Co. Ltd.,
Discovery Research Laboratory, 2-50 Kawagishi-2-chome, Toda,
Saitama 335-8505, Japan (E-mail: k-omori@ctanabe.co.jp,
Tel:81-48-433-8041, Fax:81-48-433-8157)
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ORIGIN

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Beet Local Similarity	92.4%	Pred. No. 0		
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DB	132	ACCGCGCGCGCT	191	
QY	369	GCTCTGCGCGCGCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	428	
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DB	1632	GCACTCCAGAGGTGCAAGGCTCATGAGCACTTCAACTTGCAGGACGATCTGCGG	1691	
QY	1869	ACATCAGATATTCATTTGACATTTGCTCTTTCAGAACATGTGAGCTGAGATCTTTG	1928	
DB	1692	ACATCAGATATTCATTTGACATTTGCTCTTTCAGAACATGTGAGCTGAGATCTTTG	1751	
QY	1929	TCTACATGATCATCGGTCTTGTGAGCACTCTGTTTGAACCTTGAATAATTTGTGCGTT	1988	
DB	1752	TCTACATGATCATCGGTCTTGTGAGCACTCTGTTTGAACCTTGAATAATTTGTGCGTT	1811	
QY	1989	TTATCATGCTGTGAGAAAGAACTATCGGCGGCTCTTACCACTGAGACATGACAG	2048	
DB	1812	TTATCATGCTGTGAGAAAGAACTATGAGGCGGCTCTTACCACTGAGACATGACAG	1871	
QY	2049	TCAAGGTGCGACATGATATGCAATCTTCAAAACAAATGAGCTCTTCAAGACC	2108	
DB	1872	TCAAGGTGCGACATGATATGCAATCTTCAAAACAAATGAGCTCTTCAAGACC	1931	

QY	2109	TCGAGCGCAAAAGGCGCTGCTAATTTGGGTGTCGTGTGCAAGCACTGGACCAACAGGGGCTTCA	2168
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Db	1992	GTAAACAGCTACCTGCGAGAAATTTCAGACCAACCCCTTGCGCGCGCTGTACTCCACTCCACA	2051
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Db	2052	TGGAGCAACACCACTTCTCCAGACCGGTGTCCATCTTCACTGGAAAGGCAACAACATCT	2111
QY	2289	TCTCCACCCCTGAGCTCCAGCGAGTACGAGCGTGTGGAGATCATCCGCAAAAGCATCA	2348
Db	2112	TCTCCACCCCTGAGCTCCAGCGAGTACGAGCGTGTGGAGATCATCCGCAAAAGCATCA	2171
QY	2349	TCGCCACCGACCTCGCCCTATATCTTGGGAAACAGGAAACAATTGGAGAGATGTACAGA	2408
Db	2172	TCGCCACCTGACCTCGCACTGTACTTTGGGAAACGGAACAATTGGAGAGATGTACAGA	2231
QY	2409	CAGGGTCGCTGAACCTTCACAACAACAGTCCATCGAGACCGTGTCACTGGCTTGAATGTA	2468
Db	2232	CAGGGTCGCTGAACCTTCACAACAACAGTCCATCGAGACCGGTCATCGGCTTGAATGTA	2291
QY	2469	CTGCGCTGTGATCTTTTGTCTGTGTGACCAACATATGGCCGATTACAAAATTGACACGAA	2528
Db	2292	CTGCGCTGTGATCTTTTGTCTGTGTGACCAACATATGGCCGATTACAAAATTGACACGAA	2351
QY	2529	ATTATATATGACAAATTTCTGGGCTGAGGGTGTATGAGATGAAGAAGTGGGCTATACAGCC	2588
Db	2352	ATTATATATGACAAAGTTCTGGGCTGAGGGGATGAGATGAAGAAGTGGGATACAGCC	2411
QY	2589	TTCTCTATGATGACAGAGACAAGCGAGATGAAGTCCCTCAAAGGCAAGCTCGAATTTTACA	2648
Db	2412	TTCCCTATGATGACAGAGACAAGCGAGATGAAGTCCCTCAAAGGCAAGCTTGAATTTACA	2471
QY	2649	ATGCTGTGTGCCATTTCCCTGTATACACACTTGAACGACATCTCCACCCACAAGCTCT	2708
Db	2472	ATGCTGTGTGCCATCCCCCTGTATACACACTTGAACGACATCTCCACCCACAAGCTCT	2531
QY	2709	TGCTGAAGGCGCTGACGGGATTAACCTCATCATGTGGGAGAAAGGTAAATTGCGCGGGAGAGA	2768
Db	2532	TGCTGAAGGCGCTGACGGGATTAACCTCATCATGTGGGAGAAAGGTAAATTGAGGGAGAGA	2591
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QY	2829	ACGTGAAGGTTGAAGACTGATCTCTGAAGTGAAGTCACTGTATGTCTGCCACGACAACCGACT	2888
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QY	2889	AACCGCTCTCTGTGACTGTTCTTTTT-----TGTTTTCAAGGGGTGAACCCCT	2940
Db	2698	AACCGCTCTCTGTGACTGTTCTTTTTTTTATTTTATTTTAAACGGGGTGAACCCCT	2757
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QY	3061	CCTGACCTCGAATGTCTATTTGTCTCCACGGCGACGACCTGTCTGTGGAAGGGGCGAG	3120
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QY	3121	ACCAACAGAGAGGTTCTTGTCTGTGACTCTCCCATAGAGGTTGG---CAATTTCCCTGT	3177
Db	2931	ACGACAGAGAGGGGTTCTTACTGTGACTCTTTCATGAGAGGTTGTGTCTGTCTTCACTC	2990
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DEFINITION	Sequence 1 from Patent EP1281771.		
ACCESSION	AX687065		
VERSION	AX687065.1	GI:29409561	
KEYWORDS			
SOURCE			
ORGANISM	Mus musculus (house mouse)		
REFERENCE			
AUTHORS	1 James, L.C., Lebel, L.A., Menniti, P.S. and Strick, C.A.		
TITLE	Phosphodiesterase 10a cell-based assay and sequences		
JOURNAL	Patent: EP 1281771-A 1 05-FEB-2003;		
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Qy	585	TTGTTTCTGAAAGGTGTTAGTGCAGAGACTGTGAAAAGTGGCTGAAAGGAAACCAACA	644
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Qy	645	AAGCAAAAGATGAACCATCTCCCAAGAGTGCAGAGTACAGAGATACGAATATGTCAGG	704
Db	243	AAGCAAAAGATGAACCATCTCTTAAGAGTGCAGAGTACAGAGATACGAATATGTCAGG	302
Qy	705	GAGTCGTGTACGAGCTGAACGCTACATAGACGACGCTTGAACACGCGGCGGGACAAC	764
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Qy	765	ACGTGCTCTCTATGAGCTCAGACGATCATCAGAGATAGCAAAAACCGACGAGATTGG	824

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QY 3037 GACGTGCGTACTCCGTGGCTCCACCTGACCTCGAATGCTATTGTTCTCCAGGCCAGCA 3096
DB 2622 GACATCGGTATTTCATGGCTCCGGCTGACCCCGAATGCAATTGGCTACAGGCCAGAA 2681
QY 3097 CTGCACTGTCTGGAGGGGGCAGAGACACAGAGAGAGTTCTTGCTGCTACCTCCATCA 3156
DB 2682 CTGCGCTGCTGGAGGGGGCAGAGACAGAGAGGGGTTCTTACCTGACCTTCATCA 2741
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QY 3214 AATGGAGACACGCCCCCTTGTGTGAGTTTACATGTGACCTTCTTATAGTTAACTGAG 3273
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RESULT 9
E60028 3080 bp DNA linear PAT 31-JAN-2002
LOCUS Novel phosphodiesterase and gene thereof.
DEFINITION E60028
ACCESSION E60028.1 GI:18630001
VERSION JP 2000224992-A/16.
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3080)
Omoti.K., Kodera,A., Fujishige,K., Michihata,H. and Yuasa,K.
Novel phosphodiesterase and gene thereof
Patent: JP 2000224992-A 16 15-AUG-2000;
TANABE SEIYAKU CO LTD
OS Rattus sp. (rat)
PN JP 2000224992-A/16
PD 15-AUG-2000
PF 11-MAY-1999 JP 1999129343
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PI KEIZO YUASA
PC C12N15/09,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,PC
C12N5/10,C12N5/16,
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G01N33/573//
PC (C12N9/16,C12R1:91),C12N15/00,C12N5/00,C12N5/10,C12N15/00 CC
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS (634). (3000).
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Best Local Similarity 94.6%; Pred. No. 0;
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 ACCESSION AY462095
 VERSION AY462095.1 GI:42600940
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus

REFERENCE
 AUTHORS O'Connor, V., Genin, A., Davis, S., Karishma, K. K., Doyere, V., De Zeeuw, C. I., Sanger, G., Hunt, S. P., Richter-Levin, G., Mallet, J., Laroche, S., Blise, T. V. P. and French, P. J.
 1 (bases 1 to 3353)
 Differential Amplification of Intron-containing Transcripts Reveals Long Term Potentiation-associated Up-regulation of Specific Pde10a Phosphodiesterase Splice Variants

JOURNAL J. Biol. Chem. 279 (16), 15841-15849 (2004)
 PUBMED 14752115
 REFERENCE French, P. J., O'Connor, V., Genin, A., Davis, S., Karishma, K. K., Doyere, V., de Zeeuw, C., Sanger, G., Hunt, S. P., Richter-Levin, G., Mallet, J., Laroche, S. and Blise, T. V. P.
 Direct Substitution
 Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre, POBox 1738, Rotterdam 3000DR, The Netherlands

TITLE JOURNAL
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DB 595 GTTTGACGATGAAAAAGGTGAAGGCTTATCTTCTCTCCATCCCGAGTATTAGAG 654  
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 ACCESSION AY462092
 VERSION AY462092.1 GI:42600934
 KEYWORDS
 SOURCE
 ORGANISM
 Rattus norvegicus (Norway rat)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.
 REFERENCE
 1 (bases 1 to 3015)
 O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V., De
 Zeeuw C.I., Sanger G., Hunt S.P., Richter-Levin G., Mallet J.,
 Laroche S., Blies T.V.P. and French P.U.
 Differential Amplification of Intron-containing Transcripts Reveals
 Long Term Potentiation-associated Up-regulation of Specific Pde10A
 Phosphodiesterase Splice Variants
 J. Biol. Chem. 279 (16), 15841-15849 (2004)
 JOURNAL 14752115
 PUBMED 2 (bases 1 to 3015)
 REFERENCE
 French P.U., O'Connor V., Genin A., Davis S., Karishma K.K.,
 Doyere V., de Zeeuw C., Sanger G., Hunt S.P., Richter-Levin G.,
 Mallet J., Laroche S. and Blies T.V.P.
 Direct Submission
 TITLE Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre,
 Journal Pobox 1738, Rotterdam 3000DR, The Netherlands
 JOURNAL Location/Qualifiers
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ORIGIN

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LOCUS Rattus norvegicus mRNA for PDE10A3, complete cds.
DEFINITION AB027156
ACCESSION AB027156.1 GI:6683034
VERSION
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ORGANISM Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE
1 Fujishige, K., Kotera, J. and Omori, K.
Striatum- and testis-specific phosphodiesterase PDE10A isolation
and characterization of a rat PDE10A
Eur. J. Biochem. 266 (3), 1118-1127 (1999)
JOURNAL
PUBMED 10583409
REFERENCES
Omori, K., Fujishige, K. and Kotera, J.
Direct Submission
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Tel: 81-48-433-8041, Fax: 81-48-433-8157)
Location/Qualifiers
1..3030
/organism="Rattus norvegicus"

QY	5205	CGGCGCTGTA	CTCA	CTCCACCA	TGAGCA	CA	CCACTTCT	CCAGAC	GGTGTCCATCC	2264
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QY	2265	TTCACTGGA	AGGGCA	CAATATCTT	CTCA	CCCTGAG	CTCCAG	AGTACAG	CAAGTGTGC	2324
DB	2162	TCCACTGGA	AGGAC	CAATCTTCT	CCACCTG	AGCTC	AGCGAG	TACAG	AGAGTGC	2221
QY	2325	TGGAGATCA	TCCGCA	AAAGCCAT	CATGCG	CA	CCCTG	CTATCTT	TGGAAACAGA	2384
DB	2222	TGGAGATCA	TCCGCA	AAAGCCAT	CATGCG	CA	CCCTG	CTATCTT	TGGAAACAGA	2281
QY	2385	AGCAGTTGA	AGGAGAT	GTACCA	GACAG	GGGTG	CGCTGA	AACTCC	CAACCAAGTCCATCGAG	2444
DB	2282	AGCAGTTGA	AGGAGAT	GTACCA	GACAG	GGGTG	CGCTGA	AACTCC	CAACCAAGTCCATCGAG	2341
QY	2445	ACCGTGTCA	TGCGCTT	GATGAT	GA	CTGCTGT	GATTTT	GTCTGT	GACCAAACTATGCGC	2504
DB	2342	ACCGGTGTCA	TGCGCTT	GATGAT	GA	CTGCTGT	GATTTT	GTCTGT	GACCAAACTATGCGC	2401
QY	2505	CAGTTACAA	AAATTTGA	CAGCGA	ATGATAT	TATG	CA	GAATTTCT	GGGCTGAGGGTGA	2564
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QY	2565	TGAAGAAG	CTGGGCA	TACAG	CCCATTTCT	TATG	ATG	ATG	ATG	2624
DB	2462	TGAAGAAG	CTGGGCA	TACAG	CCCATTTCT	TATG	ATG	ATG	ATG	2521
QY	2625	CTCAAGGG	CAGCTCG	GAATTTCA	ATGCTGT	GGCCAT	TTCCTG	CTATAC	CACTTGA	2684
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DB	2582	AGATCTCTC	CAACCA	CAGAGCCT	CTGTGA	AGCCCTG	CAAGGATTA	ACCTCA	TACATG	2641
QY	2745	AGAAAGTA	ATTTGCG	GGGGA	AGAGAC	AGCA	ATGTGA	TTTCA	GGCCAGGCGGCGCTTA	2804
DB	2642	AGAAAGTA	ATTTGCG	GGGGA	AGAGAC	AGCA	ATGTGA	TTTCA	GGCCAGGCGGCGCTTA	2695
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OY	1185	CAATCACCGAGTGCAGGTTGTGTAGAGGTCGCGCAACAAGACCGAACTGAATGACTTCC	1244
Db	1343	CAATCACCGAGTGCAGGTTGTGTAGAGGTCGCGCAACGAACTGAATGACTTCC	1402
OY	1245	TACTGACGTATCAAAGAATCACTCTTGTATACATAGTTCATTAAGCTCTTACTTGTAAC	1304
Db	1403	TGCTGATGTATCAABAGCATACTTGTATTACATATGTGCGCATAGACTCTTACTTGAAC	1462
OY	1305	AACATCATATATATGCAAAAAATCTAGTGAAGCCGACCGCTGGCGCTCTTCCAGGTGG	1364
Db	1463	AACATCATATATATGCAAAAAATCTAGTGAAGCCGACCGCTGGCGCTCTTCCAGGTGG	1522
OY	1365	ACCACAAACAAAGAGCTGTACTCCGACCGTGTGACATTTGGGAGAGAACAGAGGGGA	1424
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OY	1425	AGCCCATCTTCAAGAAAGACCAAGAGATCAGATTTTCCATTGAAGAAAGGAATTCGTGTC	1484
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Db	1763	TGAGCGCAGGCGAGCTGTATGGCGTGTGTGACATGAGTGAACAGATCAAGCGGACGCGCT	1822
OY	1665	TCTCCAAAGCAGACGAGAACCACTTCAAGATGTTGTCGTCTTCTGCGCACTGCGCTTGGC	1724
Db	1823	TCTCCAAAGCAGATGAGAACCACTTCAAGATGTTGTCGTCTTCTGCGCCTCTGCGCCCTGC	1882
OY	1725	ACTGTGCTTAACATGTACACAGGATCCGCGACTGAGATNGCATCTACAGGGGTACATGG	1784
Db	1883	ACTGTGCTTAACATGTACACAGGATCCGCGACTGAGATNGCATCTACAGGGGTACATGG	1942
OY	1785	AGAAAGCTTTCCTACACAGCATCTGCACTCCGAGAGTGGCAGAGCCTCATGCGCTTCA	1844
Db	1943	AGAAAGCTTTCCTACACAGCATCTGCACTCCGAGAGTGGCAGAGCCTCATGCACTTCA	2002
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OY	1905	AGAACATGTGGCTGGGATCTTTGTCTACATGATCATGCGGCTGTGGGGACATCTGTG	1964
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OY	1965	TTGAACCTTGA AAAAATTTGTGCGCTTTTATCATGTCTGTGAAGAACTATCGCGGGTTC	2024
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OY	2085	ACAAACAATGGCCTCTTCAAGACCTTGAACGCGAAGGCGCTGCTAATTTGGGTGTCGTGC	2144
Db	2243	ACAAACAATGGCCTCTTCAAGACCTTGAACGCGAAGGCGCTGCTAATTTGGGTGTCGTGC	2302
OY	2145	ATGACCTTGACCAAGAGGCTTCAAGTACAGCTACCTGCAAGATTTGACCAACCCCTTGG	2204
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QY	2265	TTTCACTGTGAAGGGGCACAATATCTTCTCCACCTGAGCTCCAGGAGTACGACGGTGC	2324
Db	2423	TTCCAGCTGTGAAGGACACAAATCTTCTCCACCTGAGCTCCAGGAGTACGACGGTGC	2482
QY	2335	TGAGATTCATCCGAAAGCCATCATTCGCGACCGACCTCGCCCTATCTTTGGGAACAGGA	2384
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QY	2385	AGCAGTTGGAGAAATGTACACAGACAGGGTCCGAAACCTCCAAACAGTCCCATGAG	2444
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Db	2603	ACCGTGCATCGGCTTGATGTATGATCTGCTCGTGTATCTTTGCTGTGACCAACTATAGC	2662
QY	2505	CAGTTTACAAATTTGACACGCGAATGATATATATGACAAATTTCTGGGCTGAGGGTATGGA	2564
Db	2663	CAGTTTACAAATTTGACACGCGAATGATATATATGACAGTTTCTGGGCTGAGGGGATAGA	2722
QY	2565	TGAAGAGCTGGGCAATACAGCCCATTCCTATGATGACAGACAAACGAGATGAGTCC	2624
Db	2723	TGAAGAGCTGGGCAATACAGCCCATTCCTATGATGACAGACAAACGAGATGAGTCC	2782
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QY	2745	AGAGGTATATTCGCGGGGAGAGAGACGATATGTGATTTTCAGGGCCAGCCCGGGGCTTA	2804
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QY	2805	GCAAGAGCAACCTCGAAGAGCTGAAACGTGAAGTTGAAGACTGATTCCTGAAGTACGTC	2863
Db	2957	GCAAGAGCAACCTCGAAGAGCTGAAACGTGAAAGCTGATGATCTGAGGTATGTC	3015

RESULT 14

LOCUS AY462093 3553 bp mRNA linear ROD 12-APR-2004

DEFINITION Rattus norvegicus PDE10A13 (Pde10a) mRNA, complete cds, alternatively spliced.

ACCESSION AY462093

VERSION AY462093.1 GI:46200936

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

TAXONOMY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 3553)

AUTHORS O'Connor,V., Genin,A., Davis,S., Karishma,K.K., Doyere,V., De Zeeuw,C.I., Sanger,G., Hunt,S.P., Richter-Levin,G., Mallet,J., Laroche,S., Bliss,T.V.P. and French,P.J.

TITLE Differential Amplification of Intronic-Containing Transcripts Reveals Long Term Potentiation-associated Up-regulation of Specific Pde10A Phosphodiesterase Splice Variants

JOURNAL J. Biol. Chem. 279 (16), 15841-15849 (2004)

PUBMED 14752115

REFERENCES 2 (bases 1 to 3553)

AUTHORS Doyere,V., O'Connor,V., Genin,A., Davis,S., Karishma,K.K., French,P.J., De Zeeuw,C., Sanger,G., Hunt,S.P., Richter-Levin,G., Mallet,J., Laroche,S. and Bliss,T.V.P.

TITLE Direct Submission

Submitted (10-NOV-2003) Neuro-Oncology, Erasmus Medical Centre,

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Qy	1725	ACTGTGTAATGATACACAGATCCGCACTCGAATGATCTACAGGGTTACATG	1784
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 QY 1902 TCGAGAACATGTGGCTGTGGATCTTGTCTACATGATCCATCGATCTTGTGGACATCTT 1961
 DB 1501 TTGAAACATGTGGCTGTGGATTTTGTCTACATGATCGATCGTGTGGACATCTT 1560
 QY 1962 GTTTTGAATTGAAAAATTTGTGCGCTTTTATCATGTCTGTGAAGAAACTATCGCGGCG 2021
 DB 1561 GCTTTGAGCTTGAAAAAGTTGTGCTTTTATATGTCTGTGAAGAAACTATCGCGGCGG 1620

QY 2022 TTCTTACCAACTGGAAGATGCAAGTCAAGTGTGACCACTGTAGATGTATCCATCTTC 2081
 DB 1621 TTCTTATACAACTGGAAGATGCGGTCACTGTAGACCACTGTAGATGTATCCATCTTC 1680
 QY 2082 AAAACAAATGCGCTCTTCAACAGACTCGAGCGCAAAAGCCTGTATTTGCGTCTGT 2141
 DB 1681 AGAACAAATCAACGCTTTTCAACAGACTCGAGCGCAAAAGCCTGTATTTGCGTCTGT 1740
 QY 2142 GCATGACCTTGACCAAGGCGCTTCAATTAAGCTACCTGACAGAGTTGACCAACCCCTC 2201
 DB 1741 GTCATGACCTTGACCAAGGCGCTTCAATTAAGCTACCTGACAGAGTTGACCAACCCCTC 1800
 QY 2202 TGGCGGCGCTGTACTCCACTTCAACATGAGCAACCACTTCTCCAGACGCTGTCCA 2261
 DB 1801 TGGCGGCGCTGTACTCCACTTCAACATGAGCAACCACTTCTCCAGACGCTGTCCA 1860
 QY 2262 TCTTCACTGGAAGGCGCAATATCTTCTCAACCTTGAAGCTTCCAGCGATTAACAGCAGG 2321
 DB 1861 TCTTCACTGGAAGGCGCAATATCTTCTCAACCTTGAAGCTTCCAGCGATTAATGAGCAGG 1920
 QY 2322 TGTGGAATGATCCGCAAAAGCATCATGCGCACCGACCTGCGCTATATCTTGGGAACA 2381
 DB 1921 TGTGGAATGATCCGCAAAAGCATCATGCGCACCGACCTTGTATATCTTGGAAACA 1980
 QY 2382 GGAAGCACTTGGAGAGATGTATACCAAGAGGCTGCTGAACCTTCCACAAAGTCCATC 2441
 DB 1981 GGAAGCACTTGGAGAGATGTATACCAAGAGGCTGCTGAACCTTAACTTAATCAATCACATA 2040
 QY 2442 GAGACCGTGTATGCGCTTGAATGATGACTGCTGTGATCTTTGCTGTGTACCAAACTAT 2501
 DB 2041 GAGACCGTGTATGCTTGTATGATGACTGCTGTGATCTTTGCTGTGTACCAAACTGT 2100
 QY 2502 GGGCAGTTACAAAATTTGACAGCGATGATATATATGACAAATTTGAGGCTGAGGCTGATG 2561
 DB 2101 GGGCAGTTACAAAATTTGACAGCGCAATGATATATATGACAAATTTGAGGCTGAGGCTGATG 2160
 QY 2562 AGATGAAGAACTGGGCAATACAGCCATTTCTATGATGACAGAGCAAGGAGATGAAG 2621
 DB 2161 AATGAAGAAATTTGGGAATACAGGCTTATTTCTATGATGACAGAGCAAGGAGATGAAG 2220
 QY 2622 TCCCTCAAGGCGAGCTCGGATTTCTAACATGCTGTGGCAATTTCCCTGCTATACCACTTGA 2681
 DB 2221 TCCCTCAAGGCGAGCTTGGGTTCTAACATGCGGTGCGCAATTTCCCTGCTATACCACTTGA 2280
 QY 2682 CGCAGATCTTCCCAACCAAGAGCCTGCTGAAGGCGCTGAGGGAATTAACCTCAATCAGT 2741
 DB 2281 CCGAGATCTTCCCTCCACGAGGCGCTTCTGAAAGCATGCAAGGATTAATCTCACTCAGT 2340
 QY 2742 GGGAGAAAGTAAATTCGCGGGGAAAGACAGCAATGTGATTTCAAGGCCAGGCCCGGCGC 2801
 DB 2341 GGGAGAAAGTAAATTCGAGGGGAGGAGACTGCAACCTGSAATTTCAATCCCATCCGCGGCTC 2400

Search completed: January 12, 2006, 08:50:41
 Job time : 17779 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 11, 2006, 19:49:54 ; Search time 2023 Seconds
(without alignments)
11879.823 Million cell updates/sec

Title: US-10-618-252-14
Perfect score: 3606
Sequence: 1 acgcgcgcgcctccatctg.....aattcaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues
Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: genesegn1980a:*
- 2: genesegn1990a:*
- 3: genesegn2000a:*
- 4: genesegn2001a:*
- 5: genesegn2001b:*
- 6: genesegn2002a:*
- 7: genesegn2002b:*
- 8: genesegn2003a:*
- 9: genesegn2003b:*
- 10: genesegn2003c:*
- 11: genesegn2003d:*
- 12: genesegn2004a:*
- 13: genesegn2004b:*
- 14: genesegn2005a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3606	100.0	3606	AAZ36971	Aaz36971 cDNA enco
2	3064	85.0	7618	AAAF85097	AAf85097 Nucleotid
3	3050.4	84.6	7581	AAAF85096	AAf85096 Nucleotid
4	2912.4	80.8	3427	AAA09591	Aaa09591 Human pho
5	2610.6	72.4	3219	ACC48919	Acc48919 Rat phosp
6	2498	69.3	4076	AAZ47000	Aaz47000 Rat phosp
7	2344.8	65.0	2497	ADT92216	Adt92216 Murine ph
8	2167	60.1	2560	ADT92218	Adt92218 Rat phosp
9	2167	60.1	3080	AAA09592	Aaa09592 Human pho
10	1871.8	51.9	4388	ADm34017	Adm34017 DNA enco
11	1871.8	51.9	4389	AAK36711	Aak36711 Human pho
12	1871.8	51.9	4389	AAAC63696	Aac63696 Human pho
13	1871.8	51.9	4389	AAAD59989	Aad59989 Human pho
14	1864.2	51.7	2406	AAA09590	Aaa09590 Human pho
15	1864.2	51.5	2554	AAZ36963	Aaz36963 DNA enco
16	1792.2	49.7	4576	AAA09589	Aaa09589 Human pho
17	1792.2	49.7	4576	AD036625	Ado36625 Human pho
18	1792.2	49.7	4576	AE869162	Aeb69162 Human mod
19	1790.2	49.6	2798	AAZ36964	Aaz36964 DNA enco

20	1787.4	49.6	2340	13	ADR46242	Adr46242 Human pho
21	1787.4	49.6	3195	2	AAK36712	Aak36712 Human pho
22	1787.4	49.6	3195	4	AAAC63697	Aac63697 Human pho
23	1787.4	49.6	3195	10	AAAD59990	Aad59990 Human pho
24	1787.4	49.6	3195	12	ADm34019	Adm34019 DNA enco
25	1787.4	49.6	4381	4	AAAF84500	AAf84500 Human cyc
26	1786.6	49.5	3631	4	ABA03665	Abao3665 Human pde
27	1785	49.5	2298	4	AAK36710	Aak36710 Human pho
28	1785	49.5	2298	4	AAAC63695	Aac63695 Human pho
29	1785	49.5	2298	10	AAAD59988	Aad59988 Human pho
30	1785	49.5	2298	12	ADm34015	Adm34015 DNA enco
31	900.2	25.0	1068	3	AAZ36970	Aaz36970 DNA enco
32	787.8	21.8	1017	13	ADR46244	Adr46244 Human pho
33	781.4	21.7	981	13	ADR46246	Adr46246 Human pho
34	528.4	14.7	782	4	AAH04188	Aah04188 Human cdn
35	528	14.6	1519	4	AAH15486	Aah15486 Human cdn
36	497.2	13.8	540	3	AAZ36973	Aaz36973 DNA enco
37	484.2	13.4	4446	5	AAAS87492	Aas87492 DNA enco
38	469.2	13.0	477	2	AAK36739	Aak36739 Human pho
39	469.2	13.0	477	4	AAAC66715	Aac66715 AA386789
40	469.2	13.0	477	10	AAAD60021	Aad60021 Mouse exp
41	469.2	13.0	477	12	ADm34052	Adm34052 Human pho
42	441.4	12.2	487	3	AAZ36972	Aaz36972 DNA enco
43	333.8	9.3	404	2	AAK36738	Aak36738 Human pho
44	333.8	9.3	404	4	AAAC66711	Aac66711 H32734 ES
45	333.8	9.3	404	10	AAAD60016	Aad60016 Rat expre

ALIGNMENTS

RESULT 1
AAZ36971
ID AAZ36971 standard; cDNA; 3606 BP.

AAZ36971.

13-MAR-2000 (first entry)

cDNA encoding a murine phosphodiesterase enzyme designated PDE11.

XX Phosphodiesterase enzyme; PDE11; cGMP; GMP; male erectile process;

KW sexual dysfunction; PDE11 imbalance; ss.

XX Mus sp.

XX Key Location/Qualifiers

FT CDS 458..2848

FT /*tag= a /product= "phosphodiesterase enzyme"

BP67284-A1.

29-DEC-1999.

XX 21-MAY-1999; 99EP-00303985.

XX 28-MAY-1998; 98GB-00011500.

PR 30-OCT-1998; 98GB-00023882.

PR 04-DEC-1998; 98GB-00026777.

PR 09-APR-1999; 99GB-00008247.

PR 10-MAY-1999; 99GB-00010801.

XX (PF12) PFIZER LTD.

XX (PF12) PFIZER INC.

XX Lanfear J, Robas NM;

XX WPI; 2000-064614/06.

XX P-PSDB; AAY53940.

XX Novel polypeptides and polynucleotides used to identify agents which

PT modulate phosphodiesterase11 activity.

XX Claim 4; Page 68-70; 158pp; English.

XX The present sequence encodes a murine phosphodiesterase enzyme, CC designated PDE11. PDE11 sequences from human and rat are also disclosed. CC PDE11 is found in the striatum and corpus cavernosum. PDE11 is believed CC to catalyze the conversion of cGMP to GMP. As cGMP is the messenger in CC the male erectile process, inhibiting the activity of PDE11 is likely to CC increase the concentration of cGMP and so enhance the male erectile CC process. The PDE11 enzymes are used in assays for identifying agents CC which can affect PDE11 activity or expression. They are also used to CC screen for agents useful in the treatment of sexual dysfunction. The CC identified agent can be used in a pharmaceutical compositions to treat a CC disease or condition associated with PDE11. A PDE11 gene or expression CC product can be used to prepare a medicament for the treatment or CC modulation of disturbances associated with a PDE11 imbalance. The gene or CC expression product can also be used to screen for modulators of PDE11 CC activity or expression

XX Sequence 3606 BP; 861 A; 1013 C; 962 G; 770 T; 0 U; 0 Other;

Query Match 100.0%; Score 3606; DB 3; Length 3606;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCGCTCCGCTCTCATCTGCTCTTCCACCTCCCGCGCGCTCTCCGAGAAAGGAGGCGCC 60

DB 1 AGCGCTCCGCTCTCATCTGCTCTTCCACCTCCCGCGCGCTCTCCGAGAAAGGAGGCGCC 60

QY 61 AGCGCGCGCTGAG 120

DB 61 AGCGCGCGCTGAG 120

QY 121 AGGACAAAG 180

DB 121 AGGACAAAG 180

QY 121 AGGACAAAG 180

DB 121 AGGACAAAG 180

QY 181 CAGAGCGGCTGAG 240

DB 181 CAGAGCGGCTGAG 240

QY 181 CAGAGCGGCTGAG 240

DB 181 CAGAGCGGCTGAG 240

QY 241 GCTGCTCTCTGCG 300

DB 241 GCTGCTCTCTGCG 300

QY 301 GGGTGCACGCT 360

DB 301 GGGTGCACGCT 360

QY 361 CGGCGCGCGCGCTGCG 420

DB 361 CGGCGCGCGCGCTGCG 420

QY 421 CTTTGCACGCGCTTGGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 480

DB 421 CTTTGCACGCGCTTGGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCT 480

QY 481 TCGCGAGTCTTCCGAGAGCTGACCGAGTCTTCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

DB 481 TCGCGAGTCTTCCGAGAGCTGACCGAGTCTTCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 540

QY 541 GGTGAAGGCTTAATCTTCTCTCATCTCCGAGGATTTAGATGAAATTTGTTCTGAAAGGTGT 600

DB 541 GGTGAAGGCTTAATCTTCTCTCATCTCCGAGGATTTAGATGAAATTTGTTCTGAAAGGTGT 600

QY 601 TAGTCAGAGACTGTGAGAAAGTGGCTGAGAGAGAAACCAACAAAGCAAGAGATGAAC 660

DB 601 TAGTCAGAGACTGTGAGAAAGTGGCTGAGAGAGAAACCAACAAAGCAAGAGATGAAC 660

QY 661 ATCTCCCAAGAGAGTCAAGAGGTACCAAGATACGAATATGCAAGGAGTGTGTACAGAGT 720

DB 661 ATCTCCCAAGAGAGTCAAGAGGTACCAAGATACGAATATGCAAGGAGTGTGTACAGAGT 720

QY 720 ATCTCCCAAGAGAGTCAAGAGGTACCAAGATACGAATATGCAAGGAGTGTGTACAGAGT 720

DB 720 ATCTCCCAAGAGAGTCAAGAGGTACCAAGATACGAATATGCAAGGAGTGTGTACAGAGT 720

QY 721 GAACAGCTACATAGAGAGAGCGCTTGACACAGCGCGCGGAGCAACACACTGCTCTCTATAGA 780

DB 721 GAACAGCTACATAGAGAGAGCGCTTGACACAGCGCGCGGAGCAACACACTGCTCTCTATAGA 780

QY 781 GCTCAGCAGCATCATCAGAGATAGCCACAAACCGACGAGATTTGCACTGTACTTCTTTGG 840

DB 781 GCTCAGCAGCATCATCAGAGATAGCCACAAACCGACGAGATTTGCACTGTACTTCTTTGG 840

QY 841 AGAGTGCATTAATAGCTGTGTGTGTGTATATACACCCCGGATGAAAGAGCCCAACCCCG 900

DB 841 AGAGTGCATTAATAGCTGTGTGTGTGTATATACACCCCGGATGAAAGAGCCCAACCCCG 900

QY 901 GCTCATCCCTCAGAGGCGCCATCACCCAGAGTACACATCTCTGCTACTGTGCGCAATTC 960

DB 901 GCTCATCCCTCAGAGGCGCCATCACCCAGAGTACACATCTCTGCTACTGTGCGCAATTC 960

QY 961 TAGGAAAGCGTTGT 1020

DB 961 TAGGAAAGCGTTGT 1020

QY 1021 CCTGGAATCAGAGAACCCGCAATCCAGTCTGTCTTTGCTTGGCCCATGTGCACTGCAATTGG 1080

DB 1021 CCTGGAATCAGAGAACCCGCAATCCAGTCTGTCTTTGCTTGGCCCATGTGCACTGCAATTGG 1080

QY 1081 AGACTTGAATTTGAGTCTTGAACCTGTACAGGCACTGGGCGCAAGAGGCGCTTCTGCGCTCAG 1140

DB 1081 AGACTTGAATTTGAGTCTTGAACCTGTGTACAGGCACTGGGCGCAAGAGGCGCTTCTGCGCTCAG 1140

QY 1141 CCATCAGAGAGTTGGCAACGCAATCTTGTGGGCTTCCGTAGCAATATACACAGGTGCA 1200

DB 1141 CCATCAGAGAGTTGGCAACGCAATCTTGTGGGCTTCCGTAGCAATATACACAGGTGCA 1200

QY 1201 GGTGTGTAGAGTCTCGCCAAACAGACCGAACTGAATATCTTCTTCACTGACAGTATCAA 1260

DB 1201 GGTGTGTAGAGTCTCGCCAAACAGACCGAACTGAATATCTTCTTCACTGACAGTATCAA 1260

QY 1261 GACATCTTGTATATACATAGTTGGCATATGACTCTCTCTTGTAAACATCATGATATATGC 1320

DB 1261 GACATCTTGTATATACATAGTTGGCATATGACTCTCTCTTGTAAACATCATGATATATGC 1320

QY 1321 AAAAAATCTAGTGAACGCGGACCGGTGCGCGCTTCCAGGTGAGCAACAAAGAA 1380

DB 1321 AAAAAATCTAGTGAACGCGGACCGGTGCGCGCTTCCAGGTGAGCAACAAAGAA 1380

QY 1381 GCTGTATCTCGACCTGTGTGAATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

DB 1381 GCTGTATCTCGACCTGTGTGAATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440

QY 1441 GACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTCTGATCAAGTGCAGAGAAACAGG 1500

DB 1441 GACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTCTGATCAAGTGCAGAGAAACAGG 1500

QY 1501 CGAAGTCTTGAACAATTCGCGATGCTACGCGGACCTTCTTAAACAGAGAGTGGACCT 1560

DB 1501 CGAAGTCTTGAACAATTCGCGATGCTACGCGGACCTTCTTAAACAGAGAGTGGACCT 1560

QY 1561 GTACACAGGCTTACACACAGAGAAATTTCTGTGTATGCGCTTGTATGAGCCAGAGCAGGCT 1620

DB 1561 GTACACAGGCTTACACACAGAGAAATTTCTGTGTATGCGCTTGTATGAGCCAGAGCAGGCT 1620

QY 1621 GATTGGCGGTGTGAGAGATGAGTGAACAAGATGAGGAGTGTGAGCGCTTCTCAGAGACAGAGA 1680

DB 1621 GATTGGCGGTGTGAGAGATGAGTGAACAAGATGAGGAGTGTGAGCGCTTCTCAGAGACAGAGA 1680

QY 1681 GAACAACTTCAAGATGTTGTGCTTCTTGTGCGCACTGGCTTGTGCACTGTGTCTTAAACATGTA 1740

DB 1681 GAACAACTTCAAGATGTTGTGCTTCTTGTGCGCACTGGCTTGTGCACTGTGTCTTAAACATGTA 1740

QY 1741 CCAAGAGATCCGCGCATCTCAAGATGATATTAAGGTTTACATGAGAAAGCTTTCTTACCA 1800

DB 1741 CCAAGAGATCCGCGCATCTCAAGATGATATTAAGGTTTACATGAGAAAGCTTTCTTACCA 1800

QY 1801 CAGCATCTGACCTTCCAGAGAGTGGCAAGGCTCTATGCGCTTCAACCTAACAGACGCGAT 1860

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Db      ||||| 1801 CAGCATCTGCACTCGAGAGTGGCAGAGCCCTCAGCGCTTCAACCTACAGCAGCAT 1860
Qy      ||||| 1861 CTGCGGGGACATCGAGCTATTCCACTTTGACATTGGTCCCTTTCAGAGACATGTGGCTGG 1920
Db      ||||| 1861 CTGCGGGGACATCGAGCTATTCCACTTTGACATTGGTCCCTTTCAGAGACATGTGGCTGG 1920
Qy      ||||| 1921 GATCTTGTCTACATGATCATCGGCTTGTGGGACATCTGTGTTTGAACCTGAAAAATT 1980
Db      ||||| 1921 GATCTTGTCTACATGATCATCGGCTTGTGGGACATCTGTGTTTGAACCTGAAAAATT 1980
Qy      ||||| 1981 GTGGCTTTTATCATGTCTGTGAAGAAAGAACTATCGCGGGGTCCCTTACACAACTGGAA 2040
Db      ||||| 1981 GTGGCTTTTATCATGTCTGTGAAGAAAGAACTATCGCGGGGTCCCTTACACAACTGGAA 2040
Qy      ||||| 2041 GGATGAGTCAAGGTTGACACTGACATGATGCGCATCTTCAAAAACAATGGCTCTT 2100
Db      ||||| 2041 GGATGAGTCAAGGTTGACACTGACATGATGCGCATCTTCAAAAACAATGGCTCTT 2100
Qy      ||||| 2101 CACAGACTCGAGCGCAAGGCTGCTAAATGCGTGTGTGTCATGACCTGGACCAAG 2160
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Qy      ||||| 2161 GGGCTTCAGTAACTGCTGACAAAGTTGACACACCCCTGCGCGCTGTATCTCAC 2220
Db      ||||| 2161 GGGCTTCAGTAACTGCTGACAAAGTTGACACACCCCTGCGCGCTGTATCTCAC 2220
Qy      ||||| 2221 CTCACATGAGAACACACACTTCTCCAGAGGTTGCTCATGCTGAGTGAAGGCA 2280
Db      ||||| 2221 CTCACATGAGAACACACACTTCTCCAGAGGTTGCTCATGCTGAGTGAAGGCA 2280
Qy      ||||| 2281 CAATATCTTCTCCAGCTGAGTCCAGAGTACAGAGAGTCTGAGATCATCCGCA 2340
Db      ||||| 2281 CAATATCTTCTCCAGCTGAGTCCAGAGTACAGAGAGTCTGAGATCATCCGCA 2340
Qy      ||||| 2341 AGCCATCATGCGACCGGCTGCTGATCTTGGGAAACAGAGAGTGTGAGAGAT 2400
Db      ||||| 2341 AGCCATCATGCGACCGGCTGCTGATCTTGGGAAACAGAGAGTGTGAGAGAT 2400
Qy      ||||| 2401 GTACCAAGAGGGTGTGTAACCTCAACACAGTCCATCGAGACCGTGTCACTGGCTT 2460
Db      ||||| 2401 GTACCAAGAGGGTGTGTAACCTCAACACAGTCCATCGAGACCGTGTCACTGGCTT 2460
Qy      ||||| 2461 GATGATGATGCTGTGATCTTGTCTGTGACCAACTATGGCCAGTTTCAAAATTGAC 2520
Db      ||||| 2461 GATGATGATGCTGTGATCTTGTCTGTGACCAACTATGGCCAGTTTCAAAATTGAC 2520
Qy      ||||| 2521 AGCGAATGATATATATGCAAAATCTGGGCTGAGGGTGAATGAAAGTGGGCAT 2580
Db      ||||| 2521 AGCGAATGATATATATGCAAAATCTGGGCTGAGGGTGAATGAAAGTGGGCAT 2580
Qy      ||||| 2581 ACAGCCCATTCCTATGATGACAGAGACAGCGAGATGAAGTCCCTCAAGGGGAGCTCGG 2640
Db      ||||| 2581 ACAGCCCATTCCTATGATGACAGAGACAGCGAGATGAAGTCCCTCAAGGGGAGCTCGG 2640
Qy      ||||| 2641 ATTCTACAAATGCTGTGCAATCCCTCTATACCACTTGAACGAGATCTCCACCCAC 2700
Db      ||||| 2641 ATTCTACAAATGCTGTGCAATCCCTCTATACCACTTGAACGAGATCTCCACCCAC 2700
Qy      ||||| 2701 AGAGCTCTGTGTAAGGCTGACAGGATTAACCTCAATCAGTGGGAGAAATTTCCCGG 2760
Db      ||||| 2701 AGAGCTCTGTGTAAGGCTGACAGGATTAACCTCAATCAGTGGGAGAAATTTCCCGG 2760
Qy      ||||| 2761 GGAAGAGACAGCAATGAGATTTGAGGCGCAGGCGCGCTGACAAAGACACACTGA 2820
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Qy      ||||| 2821 GAAGCTGAACGTGAAGTTGAAGACTGATCTGAAAGTGAAGTCTGTGCTGCGCAGCA 2880
Db      ||||| 2821 GAAGCTGAACGTGAAGTTGAAGACTGATCTGAAAGTGAAGTCTGTGCTGCGCAGCA 2880
Qy      ||||| 2881 ACCGACTCAACTGCTTGTGACTGCTTGTGTTTGTGTTTCAAGGGGTGAACCCCTT 2940
Db      ||||| 2881 ACCGACTCAACTGCTTGTGACTGCTTGTGTTTGTGTTTCAAGGGGTGAACCCCTT 2940

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Db      ||||| 2881 ACCGACTCAACTGCTTGTGACTGCTTGTGTTTGTGTTTCAAGGGGTGAACCCCTT 2940
Qy      ||||| 2941 GTCAAGAGTACCGTTCGATATCCATGTGAAGACAGACGATCCCTGTCGGCAGACAC 3000
Db      ||||| 2941 GTCAAGAGTACCGTTCGATATCCATGTGAAGACAGACGATCCCTGTCGGCAGACAC 3000
Qy      ||||| 3001 CTGCGACAGTGAAGAACCGAGCTGACGTTGACAGTGTGAGAGTCTGCTGCTCCA 3060
Db      ||||| 3001 CTGCGACAGTGAAGAACCGAGCTGACGTTGACAGTGTGAGAGTCTGCTGCTCCA 3060
Qy      ||||| 3061 CCTGACCTCCGAATGCTATTTGCTCCAGGCGACGACCTGCTGTGAGGGGGCAGAG 3120
Db      ||||| 3061 CCTGACCTCCGAATGCTATTTGCTCCAGGCGACGACCTGCTGTGAGGGGGCAGAG 3120
Qy      ||||| 3121 ACCAAGAGAGGTTCTTGGCTGCAATCTCTCCATAGAGGTGTGGCAGTTCCCTGGTCT 3180
Db      ||||| 3121 ACCAAGAGAGGTTCTTGGCTGCAATCTCTCCATAGAGGTGTGGCAGTTCCCTGGTCT 3180
Qy      ||||| 3181 GTGGCATGCTGCTGTGGTGGCATTTGTTAGAAATGGGACACAGCCCTTGTGTGA 3240
Db      ||||| 3181 GTGGCATGCTGCTGTGGTGGCATTTGTTAGAAATGGGACACAGCCCTTGTGTGA 3240
Qy      ||||| 3241 GTTACATGTGACTTCTTATAGTTTAACTGAGTTTGTGCTGGACATGTAATGAA 3300
Db      ||||| 3241 GTTACATGTGACTTCTTATAGTTTAACTGAGTTTGTGCTGGACATGTAATGAA 3300
Qy      ||||| 3301 GGTCAAGTCCACAGGTGACAGAAATCAAATCTGTGATTAACAGTGTGACATGAGTAA 3360
Db      ||||| 3301 GGTCAAGTCCACAGGTGACAGAAATCAAATCTGTGATTAACAGTGTGACATGAGTAA 3360
Qy      ||||| 3361 TGTCTTTTGAAGTCTATCTGGGGGACATAGTGAATGCTGCTCAGACAGAAAGCATTA 3420
Db      ||||| 3361 TGTCTTTTGAAGTCTATCTGGGGGACATAGTGAATGCTGCTCAGACAGAAAGCATTA 3420
Qy      ||||| 3421 CCTGCGCTCATCCAGGGGACACAGGTTATCCAGGCAATCGGGAACTGAAGCTTTC 3480
Db      ||||| 3421 CCTGCGCTCATCCAGGGGACACAGGTTATCCAGGCAATCGGGAACTGAAGCTTTC 3480
Qy      ||||| 3481 ACTTCAACCATGTCAAAGATTAAACCTTCCCTCCCTCATAGTAACTTGGGCA 3540
Db      ||||| 3481 ACTTCAACCATGTCAAAGATTAAACCTTCCCTCCCTCATAGTAACTTGGGCA 3540
Qy      ||||| 3541 ACTGCGCCCAATCCCTTATACAAAGAAATTAAGTAAGCATATAATTTAAAAAAA 3600
Db      ||||| 3541 ACTGCGCCCAATCCCTTATACAAAGAAATTAAGTAAGCATATAATTTAAAAAAA 3600
Qy      ||||| 3601 AAAAAA 3606
Db      ||||| 3601 AAAAAA 3606

RESULT 2
AAF85097
ID AAF85097 standard; cDNA; 7618 BP.
XX
AC AAF85097;
XX
DT 09-JUL-2001 (first entry)
XX
DE Nucleotide sequence of murine PDE10A gene cDNA clone.
XX
KW PDE10A gene; striatum; CAG repeat disorder; Huntington's disease;
XX Schizophrenia; Alzheimer's disease; Parkinson's disease; stroke; trauma;
XX de.
XX
OS Mus sp.
XX
PN W0200124781-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000MC-CA001188.
XX

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PR 07-OCT-1999; 99CA-02285690.
 PR 07-OCT-1999; 99US-0158043P.
 PR 12-JUL-2000; 2000US-0217765P.
 XX
 PA (NOVA-) NOVANEURON INC.
 PI Robertson HA, Denovan-Wright EM;
 XX
 XX WPI; 2001-308190/32.
 DR
 PT Novel composition for treating CAG repeat disorder such as Huntington's
 XX disease, comprises a compound which modulates PDE10A expression.
 XX
 PS Example 5; Fig 19; 143pp; English.
 CC The present sequence represents a cloned PDE10A polynucleotide. PDE10A is
 CC a gene that is normally highly expressed in mammalian striatum.
 CC Expression of this gene decreases during development of CAG repeat
 CC disorders. Quantification of expression of the PDE10A gene is useful for
 CC detecting the presence of or predisposition for a CAG repeat disorder.
 CC Compounds which modulate PDE10A expression are used for treating a CAG
 CC repeat disorder, e.g. Huntington's disease, Schizophrenia, Alzheimer's
 CC disease, Parkinson's disease, stroke and trauma
 CC
 SQ Sequence 7618 BP; 2062 A; 1802 C; 1764 G; 1986 T; 0 U; 4 Other;
 Query Match 85.0%; Score 3064; DB 4; Length 7618;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 3070; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 525 GTTTGACGATGAAAAGTGAAGGCTATCTTCTCTCCATCCCGAGTATTAGAT 584
 DB 273 GTTTACCGATGAAAAGTGAAGGCTATCTTCTCTCCATCCCGAGTATTAGAT 332
 QY 585 TTGTTTCTGAAAAGTGTAGTGAAGACTGTGTGAAAAGTGTGTGAAGAAAACCA 644
 DB 333 TTGTTTCTGAAAAGTGTAGTGAAGACTGTGTGAAAAGTGTGTGAAGAAAACCA 392
 QY 645 AAGCAAAAGATGAACATCTCCCAAGGAAGTGAAGCAAGTGAACGAATATATGCA 704
 DB 393 AAGCAAAAGATGAACATCTCCCAAGGAAGTGAAGCAAGTGAACGAATATATGCA 452
 QY 705 GAGTGCTGACAGCTGAACAGCTACATAGACAGCGCTGTGACACGCGGGGACAAC 764
 DB 453 GAGTGCTGACAGCTGAACAGCTACATAGACAGCGCTGTGACACGCGGGGACAAC 512
 QY 765 ACTTGCTCTCTATAGACTCAGACGATCATAGATAGCCCAAAAAGCCGACGATTTG 824
 DB 513 ACTTGCTCTCTATAGACTCAGACGATCATAGATAGCCCAAAAAGCCGACGATTTG 572
 QY 825 CACTGTACTCTCTGAGAGTGAATATAGCTGTGTGTTCAATACACCGGGATGA 884
 DB 573 CACTGTACTCTCTGAGAGTGAATATAGCTGTGTGTTCAATACACCGGGATGA 632
 QY 885 AGGAAGGCCAACCCCGCTCATCTCTGACGCGCCATCAACGAGGTACCAACATCTTG 944
 DB 633 AGGAAGGCCAACCCCGCTCATCTCTGACGCGCCATCAACGAGGTACCAACATCTTG 692
 QY 945 CCTACGTGCGCAAGTCTAGAGAGAGCTGTGTGTAGAGATATCTTGGGATGAGCAT 1004
 DB 693 CCTACGTGCGCAAGTCTAGAGAGAGCTGTGTGTAGAGATATCTTGGGATGAGCAT 752
 QY 1005 TTTCCTGAGATCTGGCTTGGATCAGAAACCCGATCCAGTCTTCTTTGCTTGCCCA 1064
 DB 753 TTTCCTGAGATCTGGCTTGGATCAGAAACCCGATCCAGTCTTCTTTGCTTGCCCA 812
 QY 1065 TTGTACTGCGCATTTGAGACTTGTGATCTTGAATGTACAGGCACTGGGCAAA 1124
 DB 813 TTGTACTGCGCATTTGAGACTTGTGATCTTGAATGTACAGGCACTGGGCAAA 872
 QY 1125 AAGCCTTCTGCTCAGCCATCAGAGGTTGCAACGCCAATCTTGGGCTTCGTAG 1184
 DB 873 AAGCCTTCTGCTCAGCCATCAGAGGTTGCAACGCCAATCTTGGGCTTCGTAG 932

QY 1185 CATATACACAGGTGAGGTGTGTAGAGGTCTGCGCAACAGACGAACTGATGACTTCC 1244
 DB 933 CATATACACAGGTGAGGTGTGTAGAGGTCTGCGCAACAGACGAACTGATGACTTCC 992
 QY 1245 TACTGACGTATCAAAAGACATCTTTGATTAACATATGTTGCCATATAGACTCTTGAAC 1304
 DB 993 TACTGACGTATCAAAAGACATCTTTGATTAACATATGTTGCCATATAGACTCTTGAAC 1052
 QY 1305 ACATATATATATGCAAAAAATCTAGTAACGCGCAACGCGCGGCTTCCAGTGG 1364
 DB 1053 ACATATATATATGCAAAAAATCTAGTAACGCGCAACGCGCGGCTTCCAGTGG 1112
 QY 1365 ACCAAGAAGCAAGAGCTGTACTCGACCTGTTTGAATTTGGGAGGAGAAAGAGGGA 1424
 DB 1113 ACCAAGAAGCAAGAGCTGTACTCGACCTGTTTGAATTTGGGAGGAGAAAGAGGGA 1172
 QY 1425 AGCCATCTTCAAGAAACCAAGAGATCAATTTTCCATTGAGAAAGGATTTGCTGTC 1484
 DB 1173 AGCCATCTTCAAGAAACCAAGAGATCAATTTTCCATTGAGAAAGGATTTGCTGTC 1232
 QY 1485 AAGTGCAGAAACAGGCGAAGTCTTGAACATTTCCGATGCGCTAAGCGGACCTGCTTA 1544
 DB 1233 AAGTGCAGAAACAGGCGAAGTCTTGAACATTTCCGATGCGCTAAGCGGACCTGCTTA 1292
 QY 1545 ACAAGGAGTGGACCTGTACACAGGCTACACCAAGAGAACTTGTGTATGCCATAG 1604
 DB 1293 ACAAGGAGTGGACCTGTGTACACAGGCTACACCAAGAGAACTTGTGTATGCCATAG 1352
 QY 1605 TGAAGCGAGGACGCTGATTTGGCGTGTGACAGATGTGAACAGATACGCGTACGCT 1664
 DB 1353 TGAAGCGAGGACGCTGATTTGGCGTGTGACAGATGTGAACAGATACGCGTACGCT 1412
 QY 1665 TCTCCAAACAGACGAGAAACAATTCAGATTTGCTGTCTTCTGCGCACCTGCTGC 1724
 DB 1413 TCTCCAAACAGACGAGAAACAATTCAGATTTGCTGTCTTCTGCGCACCTGCTGC 1472
 QY 1725 ACTGTCTAATGATGACACAGATCCGCACTCGAATGATCTACAGGGTTACATAG 1784
 DB 1473 ACTGTCTAATGATGACACAGATCCGCACTCGAATGATCTACAGGGTTACATAG 1532
 QY 1785 AGAAGCTTCTTACACAGATCTTGACCTTCGAGAGTGCAGAGGCTCATGCGCTTCA 1844
 DB 1533 AGAAGCTTCTTACACAGATCTTGACCTTCGAGAGTGCAGAGGCTCATGCGCTTCA 1592
 QY 1845 ACCTACAGACAGATCTGCGCGGACATCGAGCTTATTCACCTTGAACATTTGCTTTCG 1904
 DB 1593 ACCTACAGACAGATCTGCGCGGACATCGAGCTTATTCACCTTGAACATTTGCTTTCG 1652
 QY 1905 AGAATGATGGCTGGAGATCTTTGTCTACATGATCATCGGCTTGTGGACATCTGTT 1964
 DB 1653 AGAATGATGGCTGGAGATCTTTGTCTACATGATCATCGGCTTGTGGACATCTGTT 1712
 QY 1965 TTGAACCTTGAATAATTTGCGCGTTTATCATGTCTGTGAAGAAACATATCGCGGTTTC 2024
 DB 1713 TTGAACCTTGAATAATTTGCGCGTTTATCATGTCTGTGAAGAAACATATCGCGGTTTC 1772
 QY 2025 CTTACCAAACTGGAAGATGACATGATGATGATGATGATGATGATGATGATGATGAT 2084
 DB 1773 CTTACCAAACTGGAAGATGACATGATGATGATGATGATGATGATGATGATGATGAT 1832
 QY 2085 ACAACATGAGCTCTTACAGACCTGAGCGCAAAAGGCTCTAAATTGCGTGTGCTGCC 2144
 DB 1833 ACAACATGAGCTCTTACAGACCTGAGCGCAAAAGGCTCTCTAATTGCGTGTGCTGCC 1892
 QY 2145 ATGACCTGGAACACAGGCGCTTCAATTAACAGCTACCTGAGAGTTGCAACACCCCTG 2204
 DB 1893 ATGACCTGGAACACAGGCGCTTCAATTAACAGCTACCTGAGAGTTGCAACACCCCTG 1952
 QY 2205 CGGCGCTTACTCCACCTTCCACATGAGCAACACATTTCTCCAGACGCTGTCATCC 2264
 DB 1953 CGGCGCTTACTCCACCTTCCACATGAGCAACACATTTCTCCAGACGCTGTCATCC 2012

QY 2265 TTACGCTGGAGGGGCAATATCTTCTCCACCTTGAGCTCCAGCGAGTACAGCAGGTCC 2324
 DB 2013 TTCACTGGAGAGGGGCAATATCTTCTCCACCTTGAGCTCCAGCGAGTACAGCAGGTCC 2072
 QY 2335 TGGAGATCATCCGCAAGGCAATCATTCGCCACCGACCTCGCCCTTATCTTTGGGAAACAGGA 2384
 DB 2073 TGGAGATCATCCGCAAGGCAATCATTCGCCACCGACCTCGCCCTTATCTTTGGGAAACAGGA 2132
 QY 2385 AGCAGTTGAGGAGATGTACAGAGCAGAGGTGCTGACCTGACCAACACAGTCCATCGAG 2444
 DB 2133 AGCAGTTGAGGAGATGTACAGAGCAGAGGTGCTGACCTGACCAACACAGTCCATCGAG 2192
 QY 2445 ACCGTGTCACTCGCTTGTATGATGATGCTGCTGTGATCTTTTGTGTGACCAACATATGCGC 2504
 DB 2193 ACCGTGTCACTCGCTTGTATGATGATGCTGCTGTGATCTTTTGTGTGACCAACATATGCGC 2252
 QY 2505 CAGTTACAAATTTGACAGGCAATGATATATATGCAAAATTTGGGGGTGAGGGGTGAGAGA 2564
 DB 2253 CAGTTACAAATTTGACAGGCAATGATATATATGCAAAATTTGGGGGTGAGGGGTGAGAGA 2312
 QY 2565 TGAAGAAGCTGGGATACAGCCCAATCTATGATGACAGAGCAAGAGAGATGAATGCC 2624
 DB 2313 TGAAGAAGCTGGGATACAGCCCAATCTATGATGACAGAGCAAGAGAGATGAATGCC 2372
 QY 2625 CTCAGAGGAGCTCGGATTTCTCAATGCTGTGSCCATTCCTGCTATACCACTTGAACGC 2684
 DB 2373 CTCAGAGGAGCTCGGATTTCTCAATGCTGTGSCCATTCCTGCTATACCACTTGAACGC 2432
 QY 2685 AGATCTCTCCACCAAGAGCCTCTGTGAGAGCCTGACAGGGATTAACCTCAACACAGTGGG 2744
 DB 2433 AGATCTCTCCACCAAGAGCCTCTGTGAGAGCCTGACAGGGATTAACCTCAACACAGTGGG 2492
 QY 2745 AGAAGGTAATTTGCGGGGGAAGAGACAGCAATGTGAATTTGAGGCCAGGCCCGGCGCCTTA 2804
 DB 2493 AGAAGGTAATTTGCGGGGGAAGAGACAGCAATGTGAATTTGAGGCCAGGCCCGGCGCCTTA 2552
 QY 2805 GCAAGAGCACACCTGAGAGAGCTGAAAGGTGGAAGCTGATCTGAAATGAGCTCC 2864
 DB 2553 GCAAGAGCACACCTGAGAGAGCTGAAAGGTGGAAGCTGATCTGAAATGAGCTCC 2612
 QY 2865 TGAATGCTGCCAGCAACCACTGCAACCTGCTTGTGATGATCTGCTTTTGTGTTTCA 2924
 DB 2613 TGAATGCTGCCAGCAACCACTGCAACCTGCTTGTGATGATCTGCTTTTGTGTTTCA 2672
 QY 2925 GGGGTGAACCCCTGTGAGAGGTACCGTGGCATATTCATGTAAGAGAGAGAGCTCC 2984
 DB 2673 GGGGTGAACCCCTGTGAGAGGTACCGTGGCATATTCATGTAAGAGAGAGAGCTCC 2732
 QY 2985 TGCCTGCGGACACACCTCGGACAGTGAAGCAACCAAGCTCTGCGGTTCAGACGTCCG 3044
 DB 2733 TGCCTGCGGACACACCTCGGACAGTGAAGCAACCAAGCTCTGCGGTTCAGACGTCCG 2792
 QY 3045 CTACTCGTGGCTTCACCTGACCTCCGAAATGCTATTTGCTCCAGGGCAGAGCTGACCTG 3104
 DB 2793 CTACTCGTGGCTTCACCTGACCTCCGAAATGCTATTTGCTCCAGGGCAGAGCTGACCTG 2852
 QY 3105 TCTGGAAGGGGAGAGAGCCAGAGAGAGTCTTGCCTGACATCTCCCATGAGGGGTGAG 3164
 DB 2853 TCTGGAAGGGGAGAGAGCCAGAGAGAGTCTTGCCTGACATCTCCCATGAGGGGTGAG 2912
 QY 3165 CCAAGTTCCTGCTTCTGTGCAATGCTGCTGCTGGTGGCATTTGTTAGAAATGGAACACA 3224
 DB 2913 CCAAGTTCCTGCTTCTGTGCAATGCTGCTGCTGGTGGCATTTGTTAGAAATGGAACACA 2972
 QY 3225 CGCCCTTGTGTGAAGTTTACATGTAACCTTTCTTATAGTTTAACTGAGTTTGGGCTG 3284
 DB 2973 CGCCCTTGTGTGAAGTTTACATGTAACCTTTCTTATAGTTTAACTGAGTTTGGGCTG 3032
 QY 3285 GGAACATGTATAGAGGTACAGGTCCAGGTGACAGAGAAATCCAAATCTGTGATTAAC 3344
 DB 3033 GGAACATGTATAGAGGTACAGGTCCAGGTGACAGAGAAATCCAAATCTGTGATTAAC 3092
 QY 3345 AGGTGACATAAGGTATGCTCTTTCAGTCTATCTGGGGGCAATAGGTGAGTCTGCTCA 3404

DB 3093 AGGTGACATAAGGTATGCTCTTTCAGTCTATCTGGGGGACATATGAGTCTGCTCA 3152
 QY 3405 CTGAGAGAGAGCATATCTTGCCTCTATTCAGGGGACACAGGGTACATCCAGGACATCG 3464
 DB 3153 CTGAGAGAGAGCATATCTTGCCTCTATTCAGGGGACACAGGGTACATCCAGGACATCG 3212
 QY 3465 GGGAACTGAAGCTTCATCTTGAACCATGTCAAGAAATTAACACCTCCCTCCCTC 3524
 DB 3213 GGGAACTGAAGCTTCATCTTGAACCATGTCAAGAAATTAACACCTCCCTCCCTC 3272
 QY 3525 ACTGAGCCTTGGGCACTGCGCCATATCCCTTATACAAAGAAATTAAGGACATA 3584
 DB 3273 ACTGAGCCTTGGGCACTGCGCCATATCCCTTATACAAAGAAATTAAGGACATA 3332
 QY 3585 TAAATTTAAAAA 3606
 DB 3333 TAAATTTCTCCAGCAGCAAA 3354
 RESULT 3
 AAF85096
 ID AAF85096 standard; cDNA; 7581 BP.
 AC AAF85096;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DB Nucleotide sequence of murine PDE10A gene cDNA clone cPDE10A.
 XX
 KW PDE10A gene; striatum; CAG repeat disorder; Huntington's disease;
 KW Schizophrenia; Alzheimer's disease; Parkinson's disease; stroke; trauma;
 ds.
 OS Mus sp.
 XX
 PN MO200124781-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 06-OCT-2000; 2000WC-CA001188.
 XX
 PR 07-OCT-1999; 99CA-02286690.
 PR 07-OCT-1999; 99US-0158043P.
 PR 12-JUL-2000; 2000US-0217765P.
 XX
 PA (NOVA-) NOVANEURON INC.
 XX
 PI Robertson HA, Denovan-Wright BW;
 PT WPI; 2001-308190/32.
 XX
 DR Novel composition for treating CAG repeat disorder such as Huntington's
 PT disease, comprises a compound which modulates PDE10A expression.
 XX
 PS Example 5; Fig 15; 143bp; English.
 XX
 CC The present sequence represents a cloned PDE10A polynucleotide. PDE10A is
 CC a gene that is normally highly expressed in mammalian striatum.
 CC Expression of this gene decreases during development of CAG repeat
 CC disorder. Quantification of expression of the PDE10A gene is useful for
 CC detecting the presence of or predisposition for a CAG repeat disorder.
 CC Compounds which modulate PDE10A expression are used for treating a CAG
 CC repeat disorder, e.g. Huntington's disease, Schizophrenia, Alzheimer's
 CC disease, Parkinson's disease, stroke and trauma
 XX
 SQ Sequence 7581 BP; 2038 A; 1796 C; 1759 G; 1969 T; 0 U; 19 Other;
 Query Match 84.6%; Score 3050.4; DB 4; Length 7581;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 3068; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
 QY 525 GTTTAGCAGATGAAGAGGCTTATCTTCTCTCCATCCCAAGTATTAAGTAAAT 584

Db 273 GTTGAAGATGAAAGTGGAAGGCTATCTTCTCCATCCCGATTAATGAAAT 332
Qy 585 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAAGTGCTGAAAGAGAAAAACAAC 644
Db 333 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAAGTGCTGAAAGAGAAAAACAAC 392
Qy 645 AAGCAAAAGATGAACCATCTCCCAAGAAAGTGAGAGGATACAGAGATACGAATATGACAG 704
Db 393 AAGCAAAAGATGAACCATCTCCCAAGAAAGTGAGAGGATACAGAGATACGAATATGACAG 452
Qy 705 GAGTGTGTACGAGCTGAAACAGCTACATAGAGAGCGCTGGAACAGCGCGGGACAAAC 764
Db 453 GAGTGTGTACGAGCTGAAACAGCTACATAGAGAGCGCTGGAACAGCGCGGGACAAAC 512
Qy 765 ACCTGCTCTTATAGACTCAGAGCATCATCAGATAGCCACAAAAGCCGAGATTGG 824
Db 513 ACCTGCTCTTATAGACTCAGAGCATCATCAGATAGCCACAAAAGCCGAGATTGG 572
Qy 825 CACTGACTTCTTGAGAGTGCAATATAGCTGTGTGTTCATACGACCGGGATGA 884
Db 573 CACTGACTTCTTGAGAGTGCAATATAGCTGTGTGTTCATACGACCGGGATGA 632
Qy 885 AAGAAAGCCAAACCCGGCTCATCCCTGAGAGGCCATCACCGAGGATACCATCTCG 944
Db 633 AAGAAAGCCAAACCCGGCTCATCCCTGAGAGGCCATCACCGAGGATACCATCTCG 692
Qy 945 CCTAGTGCCCAAGTCTAGAGAAAGCTTTGTGTAGAGATATCTTGGGGATGAGCAT 1004
Db 693 CCTAGTGCCCAAGTCTAGAGAAAGCTTTGTGTGTAGAGATATCTTGGGGATGAGCAT 752
Qy 1005 TTCCTGAGAGTCTGGCTGGATCAGAAACCGGATCCAGTCTGTCTTTCCTGGCCA 1064
Db 753 TTCCTGAGAGTCTGGCTGGATCAGAAACCGGATCCAGTCTGTCTTTCCTGGCCA 812
Qy 1065 TTGTCACTGCCATTGAGAGCTTGAATTTGGATCTTGAACGTGTACAGGCCCTGGGCAAG 1124
Db 813 TTGTCACTGCCATTGAGAGCTTGAATTTGGATCTTGAACGTGTACAGGCCCTGGGCAAG 872
Qy 1125 AGGCTTTGCTCCTCAGCCATCAGAGAGTTGCAACAGCCCATCTTGGGCTTCCGTAG 1184
Db 873 AGGCTTTGCTCCTCAGCCATCAGAGAGTTGCAACAGCCCATCTTGGGCTTCCGTAG 932
Qy 1185 CAATACACAGAGTGAGGTGTAGAGGTCTGGCCAAAGAGACCGAATCGAATGACTTC 1244
Db 933 CAATACACAGAGTGAGGTGTAGAGGTCTGGCCAAAGAGACCGAATCGAATGACTTC 992
Qy 1245 TACTGACGTATCAAGACATATCTTGTATACATAGTTGCCATAGACTCTTACTTGAAC 1304
Db 993 TACTGACGTATCAAGACATATCTTGTATACATAGTTGCCATAGACTCTTACTTGAAC 1052
Qy 1305 ACATCATGATATATGCAAAAAATCTTAGTGAACGCCGACCGCTGCGGCTTCCAGGTGG 1364
Db 1053 ACATCATGATATATGCAAAAAATCTTAGTGAACGCCGACCGCTGCGGCTTCCAGGTGG 1112
Qy 1365 ACCAAGAAGCAAGAGCTGTACTGGAACCTGTTTGAACATTTGGGAGAGAGAGGGGA 1424
Db 1113 ACCAAGAAGCAAGAGCTGTACTGGAACCTGTTTGAACATTTGGGAGAGAGAGGGGA 1172
Qy 1425 AGCCCATCTTCAAGAGACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTGCTGTC 1484
Db 1173 AGCCCATCTTCAAGAGACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTGCTGTC 1232
Qy 1485 AAGTGGCAAGAACAGCGGAAGTCTTGAAACATTTCCGATGCTTACGCGGACCTCGCTTTA 1544
Db 1233 AAGTGGCAAGAACAGCGGAAGTCTTGAAACATTTCCGATGCTTACGCGGACCTCGCTTTA 1292
Qy 1545 ACAAGGAGGTGACCTGTATACAGAGTACACAGAGAGAACATTTCTGTGTATGCCCATAG 1604
Db 1293 ACAAGGAGGTGACCTGTATACAGAGTACACAGAGAGAACATTTCTGTGTATGCCCATAG 1352
Qy 1605 TGAGCCGAGGACGCTGATTTGGCTGTGTCAGATGGTGAACAAGATCAGCGGTAGCGCT 1664

Db 1353 TGAGCCGAGGACGCTGATTTGGCTGTGTCAGATGTGTAAACAAGATCAGCGGTAGCGCT 1412
Qy 1665 TTCTCAAGACAGACGAGAACAACTTCAAGATTTGTGCTTTCGCCACATCGGCTTGC 1724
Db 1413 TTCTCAAGACAGACGAGAACAACTTCAAGATTTGTGCTTTCGCCACATCGGCTTGC 1472
Qy 1725 ACTGTGTAACTGTATACACAGATCCGCCACTCAGAAATGCATCTACAGGGTTACATAG 1784
Db 1473 ACTGTGTAACTGTATACACAGATCCGCCACTCAGAAATGCATCTACAGGGTTACATAG 1532
Qy 1785 AGAAGCTTTCTTCAACACAGCATCTGCACCTCCGAGAGGTGGCAGGCTCATGCGCTTCA 1844
Db 1533 AGAAGCTTTCTTCAACACAGCATCTGCACCTCCGAGAGGTGGCAGGCTCATGCGCTTCA 1592
Qy 1845 ACCTACGAGACGCAATCTGCGGGGACATCGAGCTATTCACATTGACATTTGGCTCTTGC 1904
Db 1593 ACCTACGAGACGCAATCTGCGGGGACATCGAGCTATTCACATTGACATTTGGCTCTTGC 1652
Qy 1905 AGAATGTGGCTGGGATCTTTGTCTACATGATCATCGGCTTGTGGGACATCTGTT 1964
Db 1653 AGAATGTGGCTGGGATCTTTGTCTACATGATCATCGGCTTGTGGGACATCTGTT 1712
Qy 1965 TTGAACTTGAAAAATTTGTGCCGTTTATCATGTCTGTGAAGAGAACTATCGCGGTTTC 2024
Db 1713 TTGAACTTGAAAAATTTGTGCCGTTTATCATGTCTGTGAAGAGAACTATCGCGGTTTC 1772
Qy 2025 CTTACCAACATGGAAGCATGTCAGCTGAGTGGGACATCTGCATGTATTCCTTCAAA 2084
Db 1773 CTTACCAACATGGAAGCATGTCAGCTGAGTGGGACATCTGCATGTATTCCTTCAAA 1832
Qy 2085 ACAACATGGGCTCTTTCACAGACCTCGAGCCAAAGGCTCTAATTTGCTGTGTGCC 2144
Db 1833 ACAACATGGGCTCTTTCACAGACCTCGAGCCAAAGGCTCTAATTTGCTGTGTGCC 1892
Qy 2145 ATGACCTTGAGACCAAGGGGCTTTCAGTAAACAGCTACCTGCAAGAGTTGACCAACCCCTGG 2204
Db 1893 ATGACCTTGAGACCAAGGGGCTTTCAGTAAACAGCTACCTGCAAGAGTTGACCAACCCCTGG 1952
Qy 2205 CGGCGCTGTATCTCCACCTCCACATGAGAACACCACTTCTCCAGACGGTGTCCATCC 2264
Db 1953 CGGCGCTGTATCTCCACCTCCACATGAGAACACCACTTCTCCAGACGGTGTCCATCC 2012
Qy 2265 TTCAGCTGGAAGGGCAATATCTTCTCCACCTGAGCTCAGAGGATACAGAGAGGTGC 2324
Db 2013 TTCAGCTGGAAGGGCAATATCTTCTCCACCTGAGCTCAGAGGATACAGAGAGGTGC 2072
Qy 2325 TGAAGATCATCCGAAAGCCATCATGCGCACCGACTGCGCTTATCTTTGGGAAACAGGA 2384
Db 2073 TGAAGATCATCCGAAAGCCATCATGCGCACCGACTGCGCTTATCTTTGGGAAACAGGA 2132
Qy 2385 AGCAGTTGGAAGATGTATCCAGACAGGAGTGGCTGAAACCTCCACAAACGATCCCATGAG 2444
Db 2133 AGCAGTTGGAAGATGTATCCAGACAGGAGTGGCTGAAACCTCCACAAACGATCCCATGAG 2192
Qy 2445 ACCGTGTATCGGCTGTATGATGACTGCTGTGATCTTTGCTGTGACAAACTATGGC 2504
Db 2193 ACCGTGTATCGGCTGTATGATGACTGCTGTGATCTTTGCTGTGACAAACTATGGC 2252
Qy 2505 CAGTTACAAAATTGACAGCGAATATATATGCAAAATTTGCGGCTGAGGGGTGATGGA 2564
Db 2253 CAGTTACAAAATTGACAGCGAATATATATGCAAAATTTGCGGCTGAGGGGTGATGGA 2312
Qy 2565 TGAAGAGCTGGGCAATACAGCCCATTTCTTATGATGACAGAGACAGAGGATGAAATGCC 2624
Db 2313 TGAAGAGCTGGGCAATACAGCCCATTTCTTATGATGACAGAGACAGAGGATGAAATGCC 2372
Qy 2625 CTAAGGGCAGCTGGGATTTTCAATGTGTGTCATTTCCCTGCTATPACACTTGAAGC 2684
Db 2373 CTAAGGGCAGCTGGGATTTTCAATGTGTGTCATTTCCCTGCTATPACACTTGAAGC 2432
Qy 2685 AGATCTTCCCAACCAAGAGCTCTGTGAAGGCTGAGAGGATACCTCAATCAGTGGG 2744
Db 2433 AGATCTTCCCAACCAAGAGCTCTGTGAAGGCTGAGAGGATACCTCAATCAGTGGG 2492

QY 789 GCATCATCAGATAGAGCAAAAGCCGACGATTTGCACTGTACTTCTTGGAGAGTGA 848
| | | | |
Db 612 GATATCATCAGATAGACCAAAAGCCGATTTGCACTGTACTTCTTGGAGAGTGA 671
| | | | |
QY 849 AATAATAGCTGTGTGTGTTCAATACCACTGGGATGAGAGGCCAACCCCGCTCATCC 908
| | | | |
Db 672 AATAATAGTGTGTGTGTTCAACCACTGGGATGAGAGGCCAACCCCGCTCATCC 731
| | | | |
QY 909 CTGCAAGGCCCCATCACCCAGGGTACCACTCTGTGCTTAAGTGTGCAAGTCTAAGAA 968
| | | | |
Db 732 CGCAGGGGCCATCACCCAGGGCAACCACTCTGTGCTTAAGTGTGCAAGTCTAAGAA 791
| | | | |
QY 969 CGTTGTGTAGAGGATATCTTGGGGATGAGGATTTCTCGAGGTATCTGGCTTGAAT 1028
| | | | |
Db 792 CCTGTGTGTAGAGGATATCTTGGGGATGAGGATTTCTCGAGGTATCTGGCTTGAAT 851
| | | | |
QY 1039 CAGGAACCCGATCCAGTGTGTTCTTGTGCCATTTGCACTGCACTTGAAGACTTGA 1088
| | | | |
Db 852 CAGGAACCCGATCCAGTGTGTTCTTGTGCCATTTGCACTGCACTTGAAGACTTGA 911
| | | | |
QY 1089 TTGGCATCTTTGAATCTGTAACAGGCACTGGGGCAAAAGGCCCTTGTGCTCAAGCTCAG 1148
| | | | |
Db 912 TTGGCATCTTTGAATCTGTAACAGGCACTGGGGCAAAAGGCCCTTGTGCTCAAGCTCAG 971
| | | | |
QY 1149 AGTTGCAACAGCCATCTTGTGGGCTTCCGTAGCAATACACAGGTGCAAGTGTGA 1208
| | | | |
Db 972 AGTTGCAACAGCCATCTTGTGGGCTTCCGTAGCAATACACAGGTGCAAGTGTGA 1031
| | | | |
QY 1209 GAGGTCGCGCAACAGACCGAATGATGACTTCTGACTGACGTATCAAAAGACTT 1268
| | | | |
Db 1032 GAGGTCGCGCAACAGACCGAATGATGACTTCTGACTGACGTATCAAAAGACTT 1091
| | | | |
QY 1269 TTGATTAATAGTGTGCAATAGACTCTCTACTTGAACATCATGATATGCAAAAAATC 1328
| | | | |
Db 1092 TTGATTAATAGTGTGCAATAGACTCTCTACTTGAACATCATGATATGCAAAAAATC 1151
| | | | |
QY 1339 TAGTGAACGCGACCGCTGCGGCTCTTCAAGTGAACCAAGAACAGGCTGTACT 1388
| | | | |
Db 1152 TAGTGAACGCGACCGCTGCGGCTCTTCAAGTGAACCAAGAACAGGCTGTACT 1211
| | | | |
QY 1389 CGGACTGTGTTGCAATGGGAGAGAAAGAGGGAGGCCCATCTTCAAGAAACCAAG 1448
| | | | |
Db 1212 CGGACTGTGTTGCAATGGGAGAGAAAGAGGGAGGCCCATCTTCAAGAAACCAAG 1271
| | | | |
QY 1449 AGATCAGATTTTCCATTGAGAAAGGATTTGCTGTCAATGTGCAAGAACAGGCAAGTCT 1508
| | | | |
Db 1272 AGATCAGATTTTCCATTGAGAAAGGATTTGCTGTCAATGTGCAAGAACAGGCAAGTCT 1331
| | | | |
QY 1509 TGAACATTTCCGATGCTACGCGGACCCGCTTTAAAGGGAGGTGACCTGTACAG 1568
| | | | |
Db 1332 TGAACATTTCCGATGCTACGCGGACCCGCTTTAAAGGGAGGTGACCTGTACAG 1391
| | | | |
QY 1569 GCTACACCAAGAGAACATTTGTGTATGCCCATAGTGAAGCGAGCAGCTGTATGCG 1628
| | | | |
Db 1392 GCTACACCAAGAGAACATTTGTGTATGCCCATAGTGAAGCGAGCAGCTGTATGCG 1451
| | | | |
QY 1629 TGTGTGAGATGTTGAACAAGATCAGCGGTAGCGCTTCTTCAAGACAGAGAACAACT 1688
| | | | |
Db 1452 TGTGTGAGATGTTGAACAAGATCAGCGGTAGCGCTTCTTCAAGACAGAGAACAACT 1511
| | | | |
QY 1689 TCAAGATGTTGCTGTCTGTGCGACTGTGCGCTGTGCACTGTGCAATGTACACAGA 1748
| | | | |
Db 1512 TCAAGATGTTGCTGTCTGTGCGACTGTGCGCTGTGCACTGTGCAATGTACACAGA 1571
| | | | |
QY 1749 TCCGCACTCAGAAATCATCTACAGGTTACCATGAGAGAGCTTTCTTCAACAGACTCT 1808
| | | | |
Db 1572 TCCGCACTCAGAAATCATCTACAGGTTACCATGAGAGAGCTTTCTTCAACAGACTCT 1631
| | | | |
QY 1809 GCACTCTCGAGAGTGTGCAAGGCTCTATGCGCTTCACTTACAGACGCACTGTGCGGG 1868
| | | | |
Db 1632 GCACTCTCGAGAGTGTGCAAGGCTCTATGCGCTTCACTTACAGACGCACTGTGCGGG 1691
| | | | |

QY 1869 ACATGAGACTATTCACATTTGACATTTGTCCTTTGAGAAACATGAGCCCTGGGATCTTTG 1928
| | | | |
Db 1692 ACATGAGACTATTCACATTTGACATTTGTCCTTTGAGAAACATGAGCCCTGGGATCTTTG 1751
| | | | |
QY 1929 TCTACATGATCCATGTGCTTTGTGGGACATCTCTGTTTGAACCTTGAATAATGTCCGTT 1988
| | | | |
Db 1752 TCTACATGATCCATGTGCTTTGTGGGACATCTCTGTTTGAACCTTGAATAATGTCCGTT 1811
| | | | |
QY 1989 TTATCATGCTGTGAAGAAACATATCGGCGGCTTCTTACCAACAAGTGAAGCATGACG 2048
| | | | |
Db 1812 TTATCATGCTGTGAAGAAACATATCGGCGGCTTCTTACCAACAAGTGAAGCATGACG 1871
| | | | |
QY 2049 TCACGAGTGGCACTGCAATGTATGCAATCTTCAAAACAACAATGAGCTTCAAGAAC 2108
| | | | |
Db 1872 TCACGAGTGGCACTGCAATGTATGCAATCTTCAAAACAACAATGAGCTTCAAGAAC 1931
| | | | |
QY 2109 TCGAGCGCAAGGCTGCTAATTTGCTGTCTGTGTCATGACCTTGAACCAAGGGCTTCA 2168
| | | | |
Db 1932 TCGAGCGCAAGGCTGCTAATTTGCTGTCTGTGTCATGACCTTGAACCAAGGGCTTCA 1991
| | | | |
QY 2169 GTTACAGCTACCTGAGAAAGTTGACCAACCCCTGGCGGCTGTACTTCACTTCAACCA 2228
| | | | |
Db 1992 GTTACAGCTACCTGAGAAAGTTGACCAACCCCTGGCGGCTGTACTTCACTTCAACCA 2051
| | | | |
QY 2239 TGGACCAACCACTTCTTCCAGACGATGTCCATCTTCAAGTGAAGGGCAAAATATCT 2288
| | | | |
Db 2052 TGGACCAACCACTTCTTCCAGACGATGTCCATCTTCAAGTGAAGGGCAAAATATCT 2111
| | | | |
QY 2289 TTTCCACCTGAGCTTCCAGCGATGACAGAGTGTCTGAGATCATCCGCAAAAGCATCA 2348
| | | | |
Db 2112 TTTCCACCTGAGCTTCCAGCGATGACAGAGTGTCTGAGATCATCCGCAAAAGCATCA 2171
| | | | |
QY 2349 TCGCACCGACCTGCGCTTATCTTTGGGAAACAGAAACAGTTGAGAGAGATGTACAGA 2408
| | | | |
Db 2172 TCGCACCGACCTGCGCTTATCTTTGGGAAACAGAAACAGTTGAGAGAGATGTACAGA 2231
| | | | |
QY 2409 CAGGTCGCTGAACTTCCACAACCAAGTCCATTCAGACCGTGTCACTCGACTGTATGATGA 2468
| | | | |
Db 2232 CAGGTCGCTGAACTTCCACAACCAAGTCCATTCAGACCGGCTGTATGATGATGA 2291
| | | | |
QY 2469 CTGCTGTGATCTTTGCTGTGACCAAACTATGCGCGATTACAAATTTGACAGGAAATG 2528
| | | | |
Db 2232 CTGCTGTGATCTTTGCTGTGACCAAACTATGCGCGATTACAAATTTGACAGGAAATG 2351
| | | | |
QY 2529 AATATATGCAGAATCTTGGGCTGAGGGTATGATGAAGAAAGCTGGGATATACGCCCA 2588
| | | | |
Db 2352 AATATATGCAGAATCTTGGGCTGAGGGTATGATGAAGAAAGTGGGATATACGCCCA 2411
| | | | |
QY 2589 TTCTATGATGAGACAGACCAAGCAGATGAAGTCCCTCAAGGGCAGCTCGGATTTTACA 2648
| | | | |
Db 2412 TTCTATGATGAGACAGACCAAGCAGATGAAGTCCCTCAAGGACAGCTTGGATTTTACA 2471
| | | | |
QY 2649 ATGCTGTGCAATTTCTGTATATACCACTTGAACGCAATCTTCCACCAAGAGCTTC 2708
| | | | |
Db 2472 ATGCTGTGCAATTTCTGTATATACCACTTGAACGCAATCTTCCACCAAGAGCTTC 2531
| | | | |
QY 2709 TGTCTGAAGGCTGCGAGGATTAACCTCAATCAGTGGGAGAAAGGTAATTTGCGGGGAAAGA 2768
| | | | |
Db 2532 TGTCTGAAGGCTGCGAGGATTAACCTCAATCAGTGGGAGAAAGGTAATTTGAGGGGAAAGA 2591
| | | | |
QY 2769 CAGCAATGTGATTTTCAAGGCCAGGCCCGGCGCTTGAAGAGACCACTGAGAGTGA 2828
| | | | |
Db 2592 CAGCAATGTGATTTTCAAGGCCAGGCCCGGCGCTTGAAGAGACCACTGAGAGTGA 2645
| | | | |
QY 2829 ACGTGAAGTGAAGACTGTATCTTGAAGTGAAGCTTGAATGTCTTCCAGACCAAGACTC 2888
| | | | |
Db 2646 CAGCAAGTGTGATGATGATCTGAGG-----TATGTCTGCTTGAAGAGCCGCA 2697
| | | | |
QY 2889 AACCTGCTTGTGACTTGTCTTTT-----TGTTTCAAGGGGTAAGAACCCCT 2940
| | | | |
Db 2698 AACCTGCTTGTGACTTGTCTTTTATTTTATTTTATTTTATTTTAAAGGGGTGAAGAACTCT 2757
| | | | |
QY 2941 GTCAAGAGTACCGTGCATATCATGTGAAGACAGACTCCCTTGTGCGGACAGAC 3000
| | | | |

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Db      2758 CTCAGAGGATACCGTGCATATCCATGTAGAGATGACTCTCT-----GCGCACAC 2810
Qy      3001 CTCGACATGAGCAACCCAGGCTCGCGGTTCAGAGCTCGGCTACTCCGTGCTCCA 3060
Db      2811 CTCGACCTGAGCAACCCGGGCTCCACCGTGTTCAGAGCTGGCTATTCATGCTCCG 2870
Qy      3061 CCTGACCTCCGAATGCTATTGTCTCCAGGCGACGACTGCTGTGAGGGGGCAAG 3120
Db      2871 CCGACCCCGGAATGCAATTTGTCTACAGGCGAGAACTGGCTGGAGGGGGCAGAG 2930
Qy      3121 ACCACGAGAGAGTTTGTGCTGCTCATCTCCCACTGAGGGGTGG---CCAGTCCCTGGT 3177
Db      2931 ACACACGAGAGGGGTCTTCTTACCTGCAATCTTCATGAGGGGTGTCTGTGTTCATCTC 2990
Qy      3178 TCTGTGCATGCTGCTGTGTGTGATGTGTAGGAATGGACACACGCCCTGTGTGT 3237
Db      2991 TTAACAGAGATGCTACTGCTGTGTGTGCGCTTTGTAGAAATGGACACATGCCCC-TGTCTGT 3049
Qy      3238 GAAATTACATGTGACCTTCTTAAAGGTTAACTGAGTTGTGGCTTGGACACATGTAAT 3297
Db      3050 GAAATTACATGTGACCTTCTTAAAGGTTAACTGAGTTGTGGCTTGGACACATGTAAT 3109
Qy      3298 GAAAGTCAAGTCCACAGGTGACAGAGAAATCCAACTGTATTAACAGTGTGACTACAG 3357
Db      3110 GAAAGTTCAGTCCACAGGTGATAGAAATTCAGCTGTAAAGTTACAGGTGACTACAA 3169
Qy      3358 GTATGCTCTTTCAGTCTATCTGGGGGACATAGGTGCTGTGCTCACTCAGAGGAAGC 3417
Db      3170 GTGTGTTCATTGATTTTACTGGGGGGCATAGAGTGAAGTCCACAGAGGAAGAGC 3229
Qy      3418 ATACCTCTGCGCTCATCCAGGGGACACAGGGTACATCCAGGCACTGGGAACTGAAGCT 3477
Db      3230 ATACCTCTGCGCTCATCCAGGGGACACAGGGTACATCCAGGCACTGAAG-- 3287
Qy      3478 CTGACTTCAAAACATGTCAAAAGAAATTAACACTCCCTCCCTCCCTCACTGTAGCTTGG 3537
Db      3288 CTCACCTCAAAACATGTCAAAAGAAATTAACACACCCCTCCCTCACTGTAGCTTGG 3547
Qy      3538 GCAACTGCGGCAATCCCTTATATCAAAAGAAATTAAGTAAGCAATTAATTT 3591
Db      3348 GCAACTTCCGCAACCTTCAACAAAGAAATTAAGTAAGCGCTTAATTT 3401

RESULT 5
ACC48919 standard; cDNA; 3219 BP.
XX      ACC48919;
AC      ACC48919;
XX      11-AUG-2003 (first entry)
DT      XX
XX      Rat phosphodiesterase 10A cDNA.
DE      Rat; phosphodiesterase 10A; PDE10A; enzyme; tranquilizer; neuroleptic;
KW      nootropic; antiaddictive; gene; ss.
XX      Rattus sp.
OS
XX      Key      Location/Qualifiers
XX      FH      CDS      116..2440
XX      FT      /*tag= a
XX      FT      /product= "PDE10A"
XX      FT      /transl_except= (pos:272..280,aa:Val-Arg)
XX      FT      /transl_except= (pos:1249..1249,aa:Gln-Val)
XX      FT      /transl_except= (pos:1904..1912,aa:Ser-Tyr)
XX      FT      /transl_except= (pos:2435..2437,aa:DVD)
XX      PN      EP1281771-A2.
XX      PD      05-FEB-2003.
XX      PF      16-JUL-2002; 2002EP-00254973.

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XX      31-JUL-2001; 2001US-0308978P.
PR      (PF12) PFIZER PROD INC.
XX      James LC, Lebel LA, Menneti FS, Strick CA;
XX      WPI, 2003-335006/32.
XX      P-PSDB; ABR42040.
XX      Screening for agents that inhibit intracellular phosphodiesterase 10A
XX      PT activity for use in treating disorders of movement of mood and anxiety,
XX      PT by using striatal medium spiny neurons to identify inhibitors at cellular
XX      PT level.
XX      Claim 10; Fig 1A; 27pp; English.
XX      The present sequence is that of cDNA encoding rat phosphodiesterase 10A
XX      CC (PDE10A). Human PDE10A was used to screen an expressed sequence tag (EST)
XX      CC database, and a rat EST having homology to an internal portion of the
XX      CC human protein was identified. EST and RACE information identified the 5'
XX      CC and 3' ends of the sequence from rat brain RNA, and the present full-
XX      CC length rat PDE10A cDNA was obtained by PCR amplification. The invention
XX      CC provides a cell-based assay using striatal medium spiny neurons to
XX      CC identify agents that inhibit PDE10A activity at the cellular level. The
XX      CC inhibitors are useful e.g. for treating disorders of movement or mood,
XX      CC anxiety, psychosis, drug addiction, and disorders of symptom deficient
XX      CC cognition
XX      Sequence 3219 BP; 849 A; 836 C; 829 G; 705 T; 0 U; 0 Other;

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Query Match      72.4%; Score 2610.6; DB 10; Length 3219;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 2844; Conservative 0; Mismatches 214; Indels 35; Gaps 7;

Qy      525 GTTGAAGGATGAAAGGTGAAGGCTTATCTTCTCCATCCCAAGTATTAGTAAT 584
Db      123 GTTGAAGGATGAAAGGTGAAGGCTTATCTTCTCCATCCCAAGTATTAGTAAT 182
Qy      585 TTGTTCTGAAAGTGTAAAGTGTGACAGACTGTGGAAGGTGCTGAAGAGAAACCAAC 644
Db      183 TTGTTCTGAAAGTGTAAAGTGTGACAGACTGTGGAAGGTGCTGAAGAGAAACCAAC 242
Qy      645 AAGCAAAAGTGAACCATCTCCCAAGAGTCAAGAGTTCAGAGTATGAATATGCAAG 704
Db      243 AAGCAAAAGTGAACCATCTCTTAAGAAAGTCAAGAGTTCAGAGTATGAATATGCAAG 302
Qy      705 GAGTGTATACGAGTGAACAGTACATAGAGAGGCTTGACACAGGCGGGGACAAC 764
Db      303 GAGTGTATACGAGTGAACAGTACATAGAGAGGCTTGACACAGGCGGGGACAAC 362
Qy      765 ACCTGCTCTATATGAGCTCAGACAGCATCATAGATAGCCACAAAGCCGACGATTTG 824
Db      363 ACCTGCTCTATATGAGCTCAGACAGCATCATAGATAGCCACAAAGCCGACGATTTG 422
Qy      825 CACTGACTTCTTGAAGAGTGAATATATGCTGTGTGTGTTCAATACACCCGGGATGA 884
Db      423 CACTGACTTCTTGAAGAGTGAATATATGCTGTGTGTGTTCAATACACCCGGGATGA 482
Qy      885 AGGAAGGCAACCCCGGCTCATCCCTGACAGGCGCCATCAACCCAGGTTACCAACCATCTGT 944
Db      483 AGGAAGGCAACCCCGGCTCATCCCTGACAGGCGCCATCAACCCAGGTTACCAACCATCTGT 542
Qy      945 CTTAGCTGGCAAGTCTAGAGAACGTTGTGTAGAGATATCTTGGAGTAGCGAT 1004
Db      543 CTTATGTGGCAAGTCTAGAGAACCTGTGTGTAGAGATATCTTGGAGTAGCGAT 602
Qy      1005 TTCTTGAGGTATCTGCTGCGATTCAGAACCCGCAATCCAGTCTGTCTTGTGTTGCCA 1064
Db      603 TTCCAGAGGCACTGTGTGAGATCAGAACCCGCAATCCAGTCTGTCTTGTGTTGCCA 662
Qy      1065 TTGTCACTGCAATGAGACTTGAATGGCATCTTGAACCTGTACAGGACTGAGGCAAG 1124

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D6 663 TTGTGACTGCGCATTTGGAGACTTGATTTGGACTTCCTGAACTGTACAGAGCATGCGGGGAAAG 722

QY 1125 AGGCTTCTGCTTCAAGCCATCAAGAGTTTGAAACAGCCAAATCTTGTGGCTTCCGTAG 1184

D6 723 AGGCTTCTGCTTCAAGCCATCAAGAGTTTGAAACAGCCAAATCTTGTGGCTTCCGTAG 782

QY 1185 CAATACACAGGTTGAGGTTGATAGAGGCTGCGCCAAACAGACCGAACTGAATGACTTCC 1244

D6 783 CAATACACAGGTTGAGGTTGATAGAGGCTGCGCCAAACAGACCGAACTGAATGACTTCC 842

QY 1245 TACTGACGTATCAAGAATATCTTGTATATACATAGTTGCGCATAGACTCTCTACTTGAAC 1304

D6 843 TGCTGATGATATCAAGAATATCTTGTATATACATAGTTGCGCATAGACTCTCTACTTGAAC 902

QY 1305 ACATCATGATATATGCAAAAAATCTTAGTGAACCGGACCGCTGCGGCTCTTCCAGGTGG 1364

D6 903 ACATCATGATATATGCAAAAAATCTTAGTGAACCGGACCGCTGCGGCTCTTCCAGGTGG 962

QY 1365 ACCAAGAAGCAAGGAGCTGTCTGGAACCTGTTTGAACATTTGGGGAGAGAGAGGGGA 1424

D6 963 ACCAAGAAGCAAGGAGCTGTCTGGAACCTGTTTGAACATTTGGGGAGAGAGAGGGGA 1022

QY 1425 AGCCCATCTTCAAGAAGCAAGAGATCAGATTTTCCATTGAGAAAGGGAATGCTGTGTC 1484

D6 1023 AGCCCATCTTCAAGAAGCAAGAGATCAGATTTTCCATTGAGAAAGGGAATGCTGTGTC 1082

QY 1485 AAGTGGCAAGAACAGGCGGAAGTCTTGAAATTCCTCGATGCTTACCGGACCTCGCTTTA 1544

D6 1083 AAGTGGCAAGAACAGGCGGAAGTCTTGAAATTCCTCGATGCTTACCGGACCTCGCTTTA 1142

QY 1545 ACAGGAGGTGGACCTGTATCAAGGCTACACACAGAGAAACATTTGTTATGCCCATAG 1604

D6 1143 ACAGGAGGTGGACCTGTATCAAGGCTATACACACAGGAAACATTTGTTATGCCCATAG 1202

QY 1605 TGAGCCGAGCGAGCTGTATGAGCTGTGTGTCAGATGCTGAAACAAGATCAGCGGTAGCGCT 1664

D6 1203 TGAGCCGAGCGAGCTGTATGAGCTGTGTGTCAGATGCTGAAACAAGATCAGCGGTAGCGCT 1262

QY 1665 TCTCCAAAGACAGAGAAACATTTCAAGATGTTTGTCTCTTCTGCGGACCTGCGCTTGC 1724

D6 1263 TCTCCAAAGACAGATAGAAACAATTCAGATGTTTGTCTCTTCTGCGGCTGCGCTTGC 1322

QY 1725 ACTGTGCTATCAAGTATACACAGAGATCCGCACTCAGAAATGATCTTACAGGGTTACATAG 1784

D6 1323 ACTGTGCTATCAAGTATACACAGAGATCCGCACTCAGAGTGCATCTACAGGGTTACATAG 1382

QY 1785 AGAAGCTTCTTACACAGCATCTGCACTTCAGAGAGTGGCAAGGCTCATGCGCTTCA 1844

D6 1383 AGAAGCTGCTTACACAGCATCTGCACTTCAGAGAGTGGCAAGGCTCATGCACTTCA 1442

QY 1845 ACCTACAGAGAGCATCTGCGCGGAGCATGAGCTATTCACATTTGACATTTGGTCTTTTCG 1904

D6 1443 ACTTCCAGAGCATCTGCGCGGAGCATGAGCTATTCACATTTGACATTTGGTCTTTTCG 1502

QY 1905 AGAATGATGGCTGAGGATCTTGTCTATCATGATGCATGCTTGTGGGACATCTGTT 1964

D6 1503 AGAATGATGGCTGAGGATCTTGTCTATCATGATGCATGCTTGTGGGACATCTGTT 1562

QY 1965 TTGAACTTGAATAATTTGTGCGCTTTTATCATGCTGTGAAAGAAACTATTCGCGGGTTTC 2024

D6 1563 TTGAACTTGAATAATTTGTGCGCTTTTATCATGCTGTGAAAGAAACTATTCGCGGGTTTC 1622

QY 2025 CTTACCAACAATGGAAGCATGCACTGCGGTGGCACATGCACTGATATGCTTCAATTTCAAA 2084

D6 1623 CTTACCAACAATGGAAGCATGCACTGCGGTGGCACATGCACTGATATGCTTCAATTTCAAA 1682

QY 2085 ACAACAATGGGCTCTTCAAGACCTCGAGCGCAAGGCTGCTATTTGGGTGTCTGTGTC 2144

D6 1683 ACAACAATGGGCTCTTCAAGACCTTGAAGCGCAAAAGGCTGCTATTTGCTGTGTC 1742

QY 2145 ATGACTGTGACCAAGGGCTTCAAGTAAACAGCTACCTGCAAGAGTTTCAACACCCCTTGG 2204

D6 1743 ATGACTGTGACCAAGGGCTTCAAGTAAACAGCTACCTGCAAGAGAGTTTCAACACCCCTTGG 1802

QY 2205 CGGCGCTGTACTCCACTCCACCATGAGAGCAACACACTTTCGCCGAGCGGTGTCATCC 2264

D6 1803 CTGCGTGTACTCCACTCCACCATGAGAGCAACACACTTTCGCCGAGCGGTGTCATCC 1862

QY 2265 TTCACTGGAAGGAGCAATATCTTCTCACCTGAGCTCCAGCGAGTACAGAGAGTGC 2324

D6 1863 TTCACTGGAAGGAGCAACATCTTCTCACCTGAGCTCCAGCGAGTACAGAGAGTGC 1922

QY 2325 TGGAGATCATCCGCAAGACCATCATGCGCACAGACTGCGCTTATCTTTGGGAACAGGA 2384

D6 1923 TGGAGATCATCCGCAAGACCATCATGCGCACAGACTGCGCTTATCTTTGGGAACAGGA 1982

QY 2385 AGCAGTTGAGAGAGATGTAACCAAGCAGGGGTGCTGAACCTCCACAAACAGTCCCATCGAG 2444

D6 1983 AGCAGTTGAGAGAGATGTAACCAAGCAGGGGTGCTGAACCTCCACAAACAGTCCCATCGAG 2042

QY 2445 ACCGTGATCGGCTTGTATGATGATGCTGCTGTGATCTTTGCTGTGACCAAACTATGGC 2504

D6 2043 ACCGTGATCGGCTTGTATGATGATGCTGCTGTGATCTTTGCTGTGACCAAACTATGGC 2102

QY 2505 CAGTTACAAAATTGACAGCGAATGATATATGCAAAATTTGCGGCTGAGGCTATGAGA 2564

D6 2103 CAGTTACAAAATTGACAGCAATGATATATGACAGAGTTCGGGCTGAGGGGAGTGAAGA 2162

QY 2565 TGAAGAAGCTGGGCAATACAGCCCATTCCTATGATGAGACAGAGCAAGGAGATGAAGTCC 2624

D6 2163 TGAAGAAGCTGGGCAATACAGCCCATTCCTATGATGAGACAGAGCAAGGAGATGAAGTCC 2222

QY 2625 CTCAAGGAGCTCGGATTTCAATATGCTGTGCGCATTCCTGCTATACCATTTGAGCGC 2684

D6 2223 CTCAAGGAGCTCGGATTTCAATATGCTGTGCGCATTCCTGCTATACCATTTGAGCGC 2282

QY 2685 AGATCTTCCACCCACAGAGCTCTGCTGAAGGCTCGAAGGATTAACCTCAATCATGTGG 2744

D6 2283 AGATCTTCCACCCACAGAGCTCTGCTGAAGGCTCGAAGGATTAACCTCAATCATGTGG 2342

QY 2745 AGAAGTAAATTCGCGGGGAGAGACAGCAATGTGAAATTTCAAGGCCAGGCGCGGCTTA 2804

D6 2343 AGAAGTAAATTCGAGGGAGAGAGACAGCAATGTGAAATTTCAAGGCCAGGCGCGGCTTA 2396

QY 2805 GCAAGAGACACCTGAGAGAGTGAACGTGAAGTTGAAGATGATCTGAAGTGAAGTCC 2864

D6 2397 GCAAGAGACACCTGAGAGAGTGAACGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTCC 2448

QY 2865 TGAATGCTGCGCAGAGAACCGACTCAACCTGCTCTGTGATCTTCTTTTGG----- 2917

D6 2449 TGAATGCTGCGCAGAGAACCTGCAACCTGCTCTGTGATCTTCTTTTATTTTAT 2508

QY 2918 -TTTTCAAGGGGTGAACCCCTGTGAGAAAGTACCGTGCATATCCATGTAAGACAGA 2976

D6 2509 TTTTTCATCGGGGTGAACCTCTCTCAAGAGTACCGTGCATATCCATGTAAGACAGA 2568

QY 2977 GCACTCCCTGTGCTGCGGACACACTCGGACAGTGAAGCAACCAAGGCTTGTGCGGTTC 3036

D6 2569 TGACTCCCT-----GGGACACCTGGACCGTGAAGCAACCGGGCTTCAACCGGTTC 2621

QY 3037 GACGTGCGCTACTCGGTGCTCACCTTGAACCTCGGAATGCTATTTTGTCTCCAGGCGACGA 3096

D6 2622 GACATCGGCTATTTCTATGCTGCTCGCTGAACCCCGAAATGCAATTTGCTACCAAGGCAAGA 2681

QY 3097 CTGCACTGTCTGGAAGGGGAGAGACACAGAGAGGTTCTTGGCTGTGATCTCCCATGA 3156

D6 2662 CTGCGCTGTGAGAGGGGAGAGACAGAGAGGGGTTCTTACCTGATCTTTCATGA 2741

QY 3157 GGGTGTGG---CAATTCCTGTGTTCTGTGCAATGCTGCTGTGGTGGCAATTTGTTAGG 3213

D6 2742 GGGTGTGTGTTCTGTGTTCTTCACTCTTCAACAGAGATGCTACTGTGTGGCTTTGTGA 2801

QY 3214 AATGGAGACACGCGCTTGTGTAAGTTTACATGTAACCTTCTTATAGTTAACTGAG 3273

D6 2802 AATGGAGACACGCGCC--TGTGTGAAGTTTACATGTAACCTTCTTATAGTTAACTGAG 2860

QY 3274 TTTGTGGCTGGAGACATGTAATGAAGTCAAGTCCACAGGTGACAGAAATCCAAA 3333
DB 2861 TTCGTAGCTGGGACCCCTGTATGAAAGGTACAGTCCACAGGTGATGAGAAATTCAG 2920
QY 3334 CTGTGATTAACAGGTGACTACAGATAGCTTTTCAAGTCTATCTGGGGGACATAGGATG 3393
DB 2921 CTGTAGTTACAGGTGACTATTAAGTGTATTCATGTTACCTGGGGGACATGAGGTG 2980
QY 3394 AGTGTGCTCACTCAGAAAGAACATACCTGTGCTCCATCCAGGGGACACAGGTACAT 3453
DB 2981 AGTCAAGCTCAGAGAGAGAAAGCATCTCTGCTCATCAAGGGGACACAGGTACAT 3040
QY 3454 CCCAGGCATCGGGGACCTGAGCTCTCACTTCAACCATGTCAAGATTTAAACACCTC 3513
DB 3041 CCAGGCATCAGAGAACTGAG--CTCACCTCAACCATGTCAAGAAATTTAAACACACC 3098
QY 3514 CCTCCCTCTCACTGTAGCTTCTGGCACTGGCCCAATCCCTTTTACAAAGAAATTA 3573
DB 3099 CCTATCCCTCACTGTAGCTTCTGGCACTGGCCCAACCTTTCACAAAGAAATTA 3158
QY 3574 AGTAAGCATATTAATTTAAAAA 3606
DB 3159 AGTAAGCGTATTAATTTCTCTCAGCAGCAAA 3191
RESULT 6
AA247000
ID AA247000 standard; DNA: 4076 BP.
XX AA247000;
AC 05-JUN-2000 (first entry)
DT
XX
XX Rat phosphodiesterase encoding genomic DNA.
XX Phosphodiesterase; rat; brain; cellular response; hormone;
XX neurotransmitter; ds.
XX
XX Rattus sp.
OS
XX
XX Key Location/Qualifiers
XX FH 955..3319
XX FT /*tag= a
XX FT /product= "phosphodiesterase"
XX
XX EP980911-A2.
XX PD 23-FEB-2000.
XX PF 04-JUN-1998; 98BP-00110192.
XX PR 04-JUN-1998; 98BP-00110192.
XX PA (FARB) BAYER AG.
XX PI Munder F;
XX DR WPI; 2000-258589/23.
XX DR P-PSDB; AAY57306.
XX PT New rat brain phosphodiesterase, potentially useful as regulator of
XX PT cellular response to hormones and neurotransmitters.
XX PS Claim 1; Fig 1; 13pp; English.
XX CC This DNA encodes a phosphodiesterase, derived from rat brain.
XX CC Phosphodiesterases are regulators of the cellular response to e.g.
XX CC hormones and neurotransmitters
SQ Sequence 4076 BP; 1040 A; 1044 C; 1039 G; 953 T; 0 U; 0 Other;
Query Match 69.3%; Score 2498; DB 3; Length 4076;
Best Local Similarity 91.9%; Pred. No. 0;

	Matches 2726;	Conservative 0;	Mismatches 205;	Indels 35;	Gaps 7;
QY	652	AGATGACCATCTCCCAAGAAAGTACAGACGTACCAAGATACGAATATGACGGAGTGT			711
DB	1129	AGATGACCATCTCTTAAGAAAGTACAGACGTACCAAGACAGAACTACAGAGGTGT			1188
QY	712	GTAAGAGCTGAACAGCTCATATGAGCAGGCTTGAACACGGGCGGGGACAACTGT			771
DB	1189	GTACAGGCTGAACAGCTCATATGAGCAGGCTTGAACACGGGCGGGGACAACTGT			1248
QY	772	CCTATGAGCTCAGACATCATGAGATAGCCAAAGCCGACGGAATTTGACTGTA			831
DB	1249	CCTATGAGCTCAGACATCATGAGATAGCCAAAGCCGACGGAATTTGACTGTA			1308
QY	832	CTTCTTGAGAGTCAATATAGCTGTGTGTTCATACACCCGGGATGAAGAGG			891
DB	1309	CTTCTTGAGAGTCAATATAGCTGTGTGTTCATACACCCGGGATGAAGAGG			1368
QY	892	CCAAACCCGGCTCATCCCTGCAAGGCGCCATCACCCAGGGTACACCATCTGCTACGT			951
DB	1369	TCAACCCGGCTCATCCCTGCAAGGCGCCATCACCCAGGGTACACCATCTGCTACGT			1428
QY	952	GSCAAGTCTAGGAAGACGTTGTGTAGAGATATCTTGGGATGAGCGAATTTCTCG			1011
DB	1429	GSCAAGTCTAGGAAGACCTGTGTGTAGAGATATCTTGGGATGAGCGAATTTCTCG			1488
QY	1012	AGTACTGCTGGAATCAGAAACCGCATCCAGTCTGTTCTTTGCTTCCATTTCTAC			1071
DB	1489	AGGCACTGCTGGAATCAGAAACCGCATCCAGTCTGTTCTTTGCTTCCATTTCTAC			1548
QY	1072	TGCAATTGAGACTTGAATTTGGATCTTGAACCTGTAACGGGCACTGGGGCAAGAGGCTT			1131
DB	1549	TGCAATTGAGACTTGAATTTGGATCTTGAACCTGTAACGGGCACTGGGGCAAGAGGCTT			1608
QY	1132	CTGCTCAGCCATCAGAGAGTGTCAACAGCCCATCTTGTGGCTTCCGTGACATACA			1191
DB	1609	CTGCTCAGCCATCAGAGAGTGTCAACAGCCCATCTTGTGGCTTCCGTGACATACA			1668
QY	1192	CCAGGTGCAAGTGTGTAGAGTCTGGCCAAAGACCGAATGATGATCTTCTACTCA			1251
DB	1669	CCAGGTGCAAGTGTGTAGAGTCTGGCCAAAGACCGAATGATGATCTTCTACTCA			1728
QY	1252	CGTATCAAGACATCTTTGATTAACATGTTGCGATGACCTGCTCACTTGAACATCAT			1311
DB	1729	TGATCAAGACATCTTTGATTAACATGTTGCGATGACCTGCTCACTTGAACATCAT			1788
QY	1312	GATATATGCAAAAAATCTAGTACGCGACGCGCTGCGCTTTCAGGTGACCAAA			1371
DB	1789	GATATATGCAAAAAATCTAGTACGCGACGCGCTGCGCTTTCAGGTGACCAAA			1848
QY	1372	GAAACAAGAGCTGTACTCGGACCTGTTTGAATTTGGGAGAGAGAGGGAAGCCCAT			1431
DB	1849	GAAACAAGAGCTGTACTCGGACCTGTTTGAATTTGGGAGAGAGAGGGAAGCCCAT			1908
QY	1432	CTTCAAGAAAGACCAAGAGATCATTTTCCATTGGAAGAAAGGATTGCTGCAAGTGC			1491
DB	1909	CTTCAAGAAAGACCAAGAGATCATTTTCCATTGGAAGAAAGGATTGCTGCAAGTGC			1968
QY	1492	ANGAACAGGGAAGTCTTGAACATTTCCGATGCTACGGGACCTCGCTTTTAAACAGGA			1551
DB	1969	ANGAACAGGGAAGTCTTGAACATTTCCGATGCTACGGGACCTCGCTTTTAAACAGGA			2028
QY	1552	GCTGACCTGTACACAGGCTTACACAGAGAACTTTCTGTATGCTTATGAGCCG			1611
DB	2029	GCTGACCTGTACACAGGCTTATACACGCGGAACATTTCTGTATGCTTATGAGCCG			2088
QY	1612	AGCAGCGTATGCTGCTGTGTGATGAGTGAACAAGATCAGAGGATAGGCGCTTCCAA			1671
DB	2089	CGCAGCGTATGCTGCTGTGTGATGAGTGAACAAGATCAGAGGATAGGCGCTTCCAA			2148
QY	1672	GACAGACGAGAACATTTCAAGATTTTGTGCTTCTGCGCACTGCGCTTGTGACTGTG			1731
DB	2149	GACGATGAGAACATTTCAAGATTTTGTGCTTCTGCGCTTGTGACTGTGACTGTG			2208

1732 TAAACATGACCAAGAGATCCGACCTCAGAAATGATCTTACAGGGTTACCATGAGAGCT 1791
2209 TAAACATGATACCAAGAGATCCGACCTCAGAAATGATCTTACAGGGTTACCATGAGAGCT 2268
1792 TTCCCTACCAAGACATCTGACCTCCGAGAGTGGCAAGGCTCATGCGCTTCAACCTAAC 1851
2269 GTCTTACCAAGACATCTGACCTCCGAGAGTGGCAAGGCTCATGAGCTTCAACCTTGC 2328
1852 AGCAGCATCTGCGGAGACATGAGCTATTCACTTTGACATTGGTCTTTGAGAACAT 1911
2329 AGCAGCATCTGCGGAGACATGAGCTATTCACTTTGACATTGGTCTTTGAGAACAT 2388
1912 GTGGCTGTGGATCTTGTCTATATATATCATGATGCTGTGGGACATCTGTTTGAAT 1971
2389 GTGGCTGTGGATCTTGTCTATATATATCATGATGCTGTGGGACATCTGTTTGAAT 2448
1972 TGAATAATTTGTCGCTTTTATCATGATCTGTGAAGAACTATCGCGGGTCTTACCA 2031
2449 TGAATAATTTGTCGCTTTTATCATGATCTGTGAAGAACTATCGCGGGTCTTACCA 2508
2032 CAACCTGAAAGCATGACATGACGCTGACATGATGATGATGATGATGATGATGATGAT 2091
2509 CAACCTGAAAGCATGACATGACGCTGACATGATGATGATGATGATGATGATGATGAT 2568
2092 TGGGCTCTTCAAGACCTCGAGGCAAGGCGCTGAATTGGGTGTGTGTCATGACCT 2151
2569 TGGGCTCTTCAAGACCTCGAGGCAAGGCGCTGAATTGGGTGTGTGTCATGACCT 2628
2152 GGACCAACAGGGCTTCACTTAAAGCTTCACTGACAGAACTTGAACAACCCCTGCGCGCT 2211
2629 GGACCAACAGGGCTTCACTTAAAGCTTCACTGACAGAACTTGAACAACCCCTGCGCGCT 2688
2212 GTATCTCACTTCAACATGAGAGCAACAACCTTCTCCAGACGCTGTCTTCACTTCACT 2271
2689 GTATCTCACTTCAACATGAGAGCAACAACCTTCTCCAGACGCTGTCTTCACTTCACT 2748
2272 GGAAGGGGCAATATCTTCTCAACCTGAGCTTCAAGGCTGACAGGAGTACAGGAGTAC 2331
2749 GGAAGGGGCAATATCTTCTCAACCTGAGCTTCAAGGCTGACAGGAGTACAGGAGTAC 2808
2332 CATCGCAAGGCTCATCTGACCAAGGCTGCTGCTTATCTTGGGAAACAGAAACAGT 2391
2809 CATCGCAAGGCTCATCTGACCAAGGCTGCTGCTTATCTTGGGAAACAGAAACAGT 2868
2392 GAGAGAGATGATCAAGACAGGCTGCTGAACTTCAACAACAGTCCATGAGACGCTGT 2451
2869 GAGAGAGATGATCAAGACAGGCTGCTGAACTTCAACAACAGTCCATGAGACGCTGT 2928
2452 CATCGCTTGAATGATGATGCTGCTGATGCTTGTGCTGTGACCAAACTATGCGCAGTTAC 2511
2929 CATCGCTTGAATGATGATGCTGCTGATGCTTGTGCTGTGACCAAACTATGCGCAGTTAC 2988
2512 AAAATTGACAGGAGATGATATATATGAGAAATTTGAGGCTGAGGATGATGATGAGAA 2571
2989 AAAATTGACAGGAGATGATATATATGAGAAATTTGAGGCTGAGGAGATGATGAGAA 3048
2572 GCTGGGCAATACAGCCCATCTTATATGAGCAAGAACAGAGATGAAGTCCCTCAAG 2631
3049 GTTGGGGATACAGCCCATCTTATATGAGCAAGAACAGAGATGAAGTCCCTCAAG 3108
2632 GCAAGCTCGAATCTTCAATGCTGTGCGCAATCCCTGCTATATACCACTTGAACGAGATCCT 2691
3109 ACAGCTTGAATCTTCAATGCTGTGCGCAATCCCTGCTATATACCACTTGAACGAGATCCT 3168
2692 CCCACCCACAGAGCTTGTGCTGAAGGCTGACAGGATTAACCTCAATCAGTGGAGAAAGT 2751
3169 CCCACCCACAGAGCTTGTGCTGAAGGCTGACAGGATTAACCTCAATCAGTGGAGAAAGT 3228
2752 AATTGCGGGGAGAGACAGCAATGTGATTTCAAGCCCAAGGCTCGGCGCTTAGCAAGAG 2811
3229 AATTGAGGGGAGAGACAGCAATGTGATTTCAAGCCCA-----GCACATAGCAAAAG 3282

2812 CACACCTGAGAGAGCTGAACGTGAAGTTGAAGACTGATCTGAAAGTACGTCTGATGTC 2871
3283 CACATCTGAAGAGCGCGACAGAGAAAGTGTGATGATGATGATGATGATGATGATGATGAT 3334
2872 TGCCAGCAACCGACTCAACCTGCTTGTGATCTTGTGATCTTGTGATCTTGTGATCTTGTGAT 2923
3335 TGCCAGCAACCGACTCAACCTGCTTGTGATCTTGTGATCTTGTGATCTTGTGATCTTGTGAT 3394
2924 AGGGGTGAAGAACCCCTGTCAAGAGGTACCGTGTGATGATGATGATGATGATGATGATGATGAT 2983
3395 ACGGGGTGAAGAACCTGTCAAGAGGTACCGTGTGATGATGATGATGATGATGATGATGATGAT 3454
2984 CTGCTTGGCGACACACCTCGGACAGTGAAGCAACCGACTGTGCGCTTGTGATGATGATGATGAT 3043
3455 CT-----GCGCACCTTCCGACCGTGAAGCAACCGGCTTGTGATGATGATGATGATGATGATGAT 3507
3044 GCTACTCGGTGGCTTCAACCTGACCTTCCGATGATGATGATGATGATGATGATGATGATGATGAT 3103
3508 GCTATTTCATGGCTTCCGCTGACCCCGAATGCCATTGTGATGATGATGATGATGATGATGATGAT 3567
3104 GTCTGAGAGGGGAGAGACAGAGAGAGGTCTTGTGATGATGATGATGATGATGATGATGATGAT 3163
3568 GAGTGAAGGGGAGAGAGAGAGAGAGGTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 3627
3164 G---CAAGTCCCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3220
3628 GTTCTGTGCTTCACTTCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3687
3221 CACAGCCCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3280
3688 CACATGCCCC-TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3746
3281 CCGTGAAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3340
3747 CCGTGAAGCCCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3806
3341 TTACAGGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3400
3807 TTACAGGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3866
3401 TCCACTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3460
3867 TCCAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3926
3461 ATCGGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3520
3927 ATCGAGAGAGAGAG--CTCACCTCAACCATGATGATGATGATGATGATGATGATGATGATGATGAT 3984
3521 CCGTCACTGAT 3580
3985 CCGTCACTGAT 4044
3581 CATATTAATTTTAAAAA 3606
4045 CGTATTAATTTTCTTCAGCAAGCAAA 4070

RESULT 7
ADT92216
ID ADT92216 standard; cDNA; 2497 BP.
XX
XX
ADT92216;
XX
DT 13-JAN-2005 (first entry)
XX
XX Murine phosphodiesterase 10A7 (PDE10A7) encoding cDNA.
DE
XX
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
KM neuroprotective; gene therapy; transgenic; gene; 89; mouse.
OS Mus musculus.
XX
XX
FH Key Location/Qualifiers

QY 2048 GTCACGGTGGCAGCATGATGTCATCTTCAAAAACAACATATGAGCTCTTCAAGAC 2107
 Db 1670 GTCACGGTGGCAGCATGATGTCATCTTCAAAAACAACATATGAGCTCTTCAAGAC 1729
 QY 2108 CTCGAGCGGAAAGGCTGCTAAATTGCTGTCTGTGTCATGACCTGAGCCAGAGGGCTTC 2167
 Db 1730 CTCGAGCGGAAAGGCTGCTAAATTGCTGTCTGTGTCATGACCTGAGCCAGAGGGCTTC 1789
 QY 2168 AGTAAAGTACTCTGAGAAAGTTCCAGCCACCCCTGAGCGGCTGTACTCTCCACTCCACC 2227
 Db 1730 AGTAAAGTACTCTGAGAAAGTTCCAGCCACCCCTGAGCGGCTGTACTCTCCACTCCACC 1849
 QY 2228 ATGAGCAACACCATCTTCCAGAGCGGATGTCATCTTCACTGAGAAAGGCAATATC 2287
 Db 1850 ATGAGCAACACCATCTTCCAGAGCGGATGTCATCTTCACTGAGAAAGGCAATATC 1909
 QY 2288 TTCTCCACCTGAGCTCCAGAGGATACAGAGAGTGTGAGATCATCCGCAAAAGCCATC 2347
 Db 1910 TTCTCCACCTGAGCTCCAGAGGATACAGAGAGTGTGAGATCATCCGCAAAAGCCATC 1969
 QY 2348 ATGCCCAACGACCTGAGCTCTTATCTTGGGAAACAGAAAGCACTTGGAGAGATGTAACG 2407
 Db 1970 ATGCCCAACGACCTGAGCTCTTATCTTGGGAAACAGAAAGCACTTGGAGAGATGTAACG 2029
 QY 2408 ACAGGGGTGCTGAACCTCCACAACAGTCCCATCCGAGACCGTGTCACTGGCTTGTATGATG 2467
 Db 2030 ACAGGGGTGCTGAACCTCCACAACAGTCCCATCCGAGACCGTGTCACTGGCTTGTATGATG 2089
 QY 2468 ACTGCTGTGATCTTGTGCTCTGTGACCAAACTATGCGCAGTTACAAATTTGACAGCGAT 2527
 Db 2090 ACTGCTGTGATCTTGTGCTCTGTGACCAAACTATGCGCAGTTACAAATTTGACAGCGAT 2149
 QY 2528 GATATATATGCAAGATTTCTGGGCTGAGGGTGTAGATGAAGAAGCTGGGCATACAGCCC 2587
 Db 2150 GATATATATGCAAGATTTCTGGGCTGAGGGTGTAGATGAAGAAGCTGGGCATACAGCCC 2209
 QY 2588 ATTCCTATGATGAGACAGAGCAAGCGAGATGAAGTCCCTCAAGGGGAGCTCGGATTTCTAC 2647
 Db 2210 ATTCCTATGATGAGACAGAGCAAGCGAGATGAAGTCCCTCAAGGGGAGCTCGGATTTCTAC 2269
 QY 2648 AATGCTGTGAGCTTCCCTGTATACCAACTTGAAGCAGATCTCCACCAAGAGCCT 2707
 Db 2270 AATGCTGTGAGCTTCCCTGTATACCAACTTGAAGCAGATCTCCACCAAGAGCCT 2329
 QY 2708 CTGCTGAAGGCTCTGAGAGGATTAACCTCAATCACTGAGAGAAAGTAAATTGCGGGGAAAG 2767
 Db 2330 CTGCTGAAGGCTCTGAGAGGATTAACCTCAATCACTGAGAGAAAGTAAATTGCGGGGAAAG 2389
 QY 2768 ACAGCAATGTGATTTCAAGGCGCAGGCGCGGCGCTAGCAAGAGCAACCTGAGAAAGCTG 2827
 Db 2330 ACAGCAATGTGATTTCAAGGCGCAGGCGCGGCGCTAGCAAGAGCAACCTGAGAAAGCTG 2449
 QY 2828 AACGTGAAGGTGAAGACTGATCTTGAAGTGAAGTCTCTGATGTCTGCC 2875
 Db 2450 AACGTGAAGGTGAAGACTGATCTTGAAGTGAAGTCTCTGATGTCTGCC 2497
 RESULT 8
 ID ADT92218 standard; cDNA; 2560 BP.
 XX ADT92218;
 AC
 XX 13-JAN-2005 (first entry)
 DT
 XX Rat phosphodiesterase 10A7 (PDE10A7) encoding cDNA.
 DE
 XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
 KM neuroprotective; gene therapy; transgenic; gene; ss; rat.
 XX
 XX Rattus norvegicus.
 XX

FH Key Location/Qualifiers
 FT CDS 71..2458
 FT /tag=a
 FT /product="PDE10A7"
 FT /note=" phosphodiesterase 10A7"
 WO2004090126-A2.
 21-OCT-2004.
 30-MAR-2004; 2004WO-US009878.
 03-APR-2003; 2003US-0459603P.
 (MEMO-) MEMORY PHARM CORP.
 Wang D, Bugaj-Gaweda B;
 WPI; 2004-748763/73.
 DR P-PSDB; ADT92219.
 DR
 XX
 XX
 XX
 XX
 XX
 PT New isolated polynucleotide comprising a polynucleotide sequence coding
 PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for
 PT treating or preventing memory, psychiatric or cognitive disorders.
 XX
 XX
 XX
 PS Claim 3; SEQ ID NO 3; 93bp; English.
 CC The invention relates polynucleotide sequences coding for mammalian
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
 CC identifying an agent that modulates the expression or activity of a
 CC phosphodiesterase in transfected host cells is provided which involves
 CC measuring amounts of cAMP or GMP produced in the presence of the agent.
 CC The agent inhibits the expression or activity of the phosphodiesterase.
 CC The polynucleotides are useful in diagnostic assays and for screening
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for
 CC treating or preventing memory, psychiatric or cognitive disorders. The
 CC present sequence represents a cDNA encoding a rat PDE10A7 enzyme.
 SQ Sequence 2560 BP; 654 A; 675 C; 664 G; 567 T; 0 U; 0 Other;
 Query Match 60.1%; Score 2167; DB 13; Length 2560;
 Best Local Similarity 94.6%; Pred. No. 0;
 Matches 2270; Conservative 0; Mismatches 115; Indels 14; Gaps 2;
 QY 505 GTTTGGAGGAAAGGGAAGGCTTATCTTCTCCATCCCAAGGATTAAGTAAAT 584
 Db 141 GCTTACGATGAAGGTAAGGAGGCTTATCTTCTCCATCCCAAGGATTAAGTAAAT 200
 QY 585 TTGTTTCTGAAGTGTATGTCAGAGACTGTGAAAGTGTGCTGAAGAAACCAACA 644
 Db 201 TTGTTTCTGAAGTGTATGTCAGAGACTGTGAAAGTGTGCTGAAGAAACCAACA 260
 QY 645 AAGCAAAAGTGAACCATCTCCAGAAAGTCAAGAGTACAGAGTACGAATATGCAAG 704
 Db 261 AAGCAAAAGTGAACCATCTCTTAAAGAAAGTCAAGAGTACAGAGTACGAATATGCAAG 320
 QY 705 GAGGTGTATGAGGTGAAGAGCTTACATTAAGAGCAGCGCTGGAACAAGGCGGGAACAAC 764
 Db 321 GAGGTGTATGAGGTGAAGAGCTTACATTAAGAGCAGCGCTGGAACAAGGCGGGAACAAC 380
 QY 765 ACTGCTCTCTATAGCTCAGACGATCATCAGAGTATGCAACAAAGCCGACGATTTG 824
 Db 381 ACTGCTCTCTATAGCTCAGAGTATCAGAGTATCAGAGTATGCAACAAAGCCGACGATTTG 440
 QY 825 CACTGACTCTCTTGAAGTGAAGTAAATTAAGCTGTGTGTGTTCAATACACCCGGGATGA 884
 Db 441 CACTGACTCTCTTGAAGTGAAGTAAATTAAGCTGTGTGTGTTCAATACACCCGGGATGA 500
 QY 885 AGGAAGGCAACCCCGGCTATCCCTGAGAGGCGCATACCAAGGATACCAATCTCTG 944
 Db 501 AGGAAGGCAACCCCGGCTATCCCTGAGAGGCGCATACCAAGGATACCAATCTCTG 560
 QY 945 CTAAGTGGCAAGTCTAGAAAGCTTGTGTGAGAGATATCTTGGGAGTGAAGCAT 1004

Db	561	CCATATGTGGCCAAATCTTAGAAGACCCCTGTGTAAGACATCTTTGGGAATGAGCAT	620
Qy	1005	TTCTCTGAGGTACTGGCCCTGGAAATCAGAAACCCGCATCCAGTCTGTCTTTTGGCTTGGCCA	1064
Db	621	TTCCCAAGAGCACTGGTCTGGAAGTCAGAAACCCGAATCCAGTCTGTCTTTTGGCTTGGCTTA	680
Qy	1065	TTGTCACTGCACTTGAAGACTTGAATGGCATCTTGAACCTGTACAGGCACCTGGGGCAAG	1124
Db	681	TTGTCACTGCACTTGAAGACTTGAATGGCATCTTGAACCTGTACAGGCACCTGGGGCAAG	740
Qy	1125	AGGCTTCTGCTCAAGCATCAGAGAGTTGGAACAGCAATCTTGGGCTTCGGTAG	1184
Db	741	AGGCTTCTGCTCAAGCATCAGAGAGTTGGAACAGCAATCTTGGGCTTCGGTAG	800
Qy	1185	CAATACACCAAGTGCAGAGTGTGTAGAGTCTGCGCAAAACAGACCGAACTGAATGACTTCC	1244
Db	801	CAATACACCAAGTGCAGAGTGTGTAGAGTCTGCGCAAAACAGACCGAACTGAATGACTTCC	860
Qy	1245	TACTGACGTATCAAGAATATCTTGAATAATAGTTGCCATAGACTCTCTACTTGAAC	1304
Db	861	TGCTGAGATATCAAGAATATCTTGAATAATAGTTGCCATAGACTCTCTACTTGAAC	920
Qy	1305	ACATCATGATATATGCAAAAAATCTAGTGAAACGCCGACCGTGGCCCTCTTCCAGGTGG	1364
Db	921	ACATCATGATATATGCAAAAAATCTAGTGAAACGCCGACCGTGGCCCTCTTCCAGGTGG	980
Qy	1365	ACCAACAAGAACAAGAGCTGTAATCTCGACCTGTTGACATTTGGGAGAGAGAGAGGGGA	1424
Db	981	ACCAACAAGAACAAGAGCTGTAATCTCGACCTGTTGACATTTGGGAGAGAGAGAGGGGA	1040
Qy	1425	AGCCCATCTTCAAGAAAGACAAAGAGATCAGATTTTCCATTGAGAAAGGATTCGTGTC	1484
Db	1041	AGCCCATCTTCAAGAAAGACAAAGAGATCAGATTTTCCATTGAGAAAGGATTCGTGTC	1100
Qy	1485	AAATGGCAAGAACAGGCGAAGTCTTGAAATTTCCGATAGCTTACGCGAACCTGGCTTAA	1544
Db	1101	AAATGGCAAGAACAGGCGAAGTCTTGAAATTTCCGATAGCTTACGCGAACCTGGCTTAA	1160
Qy	1545	ACAGGAGAGTGAACCTGTACACAGGCTTCAACAAGAGAACTTCTGTATGCCCCATAG	1604
Db	1161	ACAGGAGAGTGAACCTGTACACAGGCTTCAACAAGAGAACTTCTGTATGCCCCATAG	1220
Qy	1605	TGAGCCGAGGCAAGCCTGATTTGGCGTGTGACAGATGTGAACAAGATCAGCGGTAAGCGCT	1664
Db	1221	TGAGCCGAGGCAAGCCTGATTTGGCGTGTGATGGAATGTGTTAAACAAGATCAGCGGCAAGCT	1280
Qy	1665	TTTCCAAAGCAGACGAGAACAACTTCAAGATTTTGTCTGTCTTCTGCGCACTGGCTTTGC	1724
Db	1281	TCTCCAAAGCAGATGAGAACAACTTCAAGATTTTGTCTGTCTTCTGCGCTCTGGCCCTGTC	1340
Qy	1725	ACTGTGCTTAAATGTATCCACAGAGATCCGCACTCAGAAATGCAATCAGAGGTTACATGG	1784
Db	1341	ACTGTGCTTAAATGTATCCACAGAGATCCGCACTCAGAGTGCATCTACAGGTTACATGG	1400
Qy	1785	AGAAGCTTCTCTACCAACAGCATCTGCACCTCCGAGAGTGGCAAGCCTCAATGCGCTTCA	1844
Db	1401	AGAAGCTGTCTTACCAACAGCATCTGCACCTCTGAGGAATGGCAAGCCTCAATGCACTTCA	1460
Qy	1845	ACCTTACAGACGCAATCTGCGGGAACATGAGCTATTCACCTTTGAACATTTGTCCTTTGG	1904
Db	1461	ACCTTGCACAGCAATCTGCGGGAACATGAGCTATTCACCTTTGAACATTTGTCCTTTGG	1520
Qy	1905	AAGAATGTGGGCTGGGATCTTTGTCTAATAGATCAATGAGCTTGTGGGACATCTGTT	1964
Db	1521	AAGAATGTGGGCTGGGATCTTTGTCTAATAGATCAATGAGCTTGTGGGACATCTGTT	1580
Qy	1965	TTGAATCTTGAATAATGTGCGGTTTATCATGTCTGTGAAGAAAGTATCGGCGGGTTTC	2024
Db	1581	TTGAATCTTGAATAATGTGCGGTTTATCATGTCTGTGAAGAAAGTATAGCGGGTTTC	1640
Qy	2025	CTTACCAACAATGGAAGATGCAATGACGGTGGCACTGTGATGTGCATCTTCAAA	2088

Db	1641	CTTACCAAACTGGAGCAATGCACTCACGGTGGCGACTGATGTACGCCATCTTCAA	1700
Qy	2085	ACAAACAATGGCTCTTTCACAGACCTCGAGCGCAAAAGGCTGTAAATTGGCTGTGGCC	2144
Db	1701	ACAAACAATGGCTCTTTCACAGACTTGAAGCGCAAAAGGCTGTAAATTGGCTGTGGCC	1760
Qy	2145	ATGACTTGGACCAAGAGGGCTTCAGTAAACAGTACCTGCAAGAAATGTGACCAACCCCTGG	2204
Db	1761	ATGACTTGGACCAAGAGGGCTTCAGTAAACAGTACCTGCAAGAAATGTGACCAACCCCTGG	1820
Qy	2205	CGGCGCTGTACTCCACCTCCACATGAGCAACCACTTCTCCAGACGGTGTCAATCC	2264
Db	1821	CTGGCTGTACTCCACCTCCACATGAGCAACCACTTCTCCAGACGGTGTCAATCC	1880
Qy	2265	TTCACTGTGAAGGGCAATATCTTCTTCCACCTGACCTCGAGGAAATGAGAGAGTGC	2324
Db	1881	TTCAGCTGGAAAGGCAACAACATCTTCTTCCACCTGACCTCGAGGAAATGAGAGAGTGC	1940
Qy	2325	TGGAGATCATCCGAAAGCCATCATTCGCGACCGACCTCGCCCTAATCTTTGGAAACAGA	2384
Db	1941	TGGAGATCATCCGAAAGCCATCATTCGCGACCTGACCTCGACCTAATCTTTGGAAACAGA	2000
Qy	2385	AGCAGTTGGAGAGATGTACCAAGACAGGGTGCCTGAACCTTCCACAACCATGCCATCGAG	2444
Db	2001	AGCAGTTGGAGAGATGTACCAAGACAGGGTGCCTGAACCTTCCACAACCATGCCATCGAG	2060
Qy	2445	ACCGTGTCAATGGCTTTGATGATGATCGTGCCTGATCTTTGCTGTGTGCAAACTAATGC	2504
Db	2061	ACCGGCTATCGGCTTGAATGATGATGCTGCGATCTTGTCTGTGTGCAAACTAATGC	2120
Qy	2505	CAGTTACAAAATTGACAGCGAATGATATATAATGCAGAAATTCGTGGCTGAGGGTGTATGA	2566
Db	2121	CAGTTACAAAATTGACAGCAATGATATATATATGACAGAAATTCGTGGCTGAGGGGTATGA	2180
Qy	2565	TGAAGAACGTGGGCTATACAGCCCATTTCTATGATGACAGAGACAAAGGAGATGAAATCC	2622
Db	2181	TGAAGAAATTTGGGGATACAGCCCATCTTATGATGACAGAGACAAAGGAGATGAAATCC	2244
Qy	2625	CTCAAGGGCAGCTCGAATTTCTTCAATATGCTGTGGCCATTCCTGTCTATACACTTGAAGC	2684
Db	2241	CTCAAGGACAGTTGGATTTCTTCAATATGCTGTGGCCATTCCTGTCTATACACTTGAAGC	2300
Qy	2685	AGATCTCTCCACCCACAGAGCTCTGTCTGAAAGGCTCGAGAGGATTAACCTCAATCATGTGG	2744
Db	2301	AGATCTCTCCACCCACAGAGCTCTGTCTGAAAGGCTCGAGAGGATTAACCTCAATCATGTGG	2366
Qy	2745	AGAAGGTAAATTCGCGGGGAAGAGACAGCAATGTGATTTCAAGGCCCAAGCCCGCGCCTA	2804
Db	2361	AGAAGGTAAATTCGAGGGAGAGACAGCAATGTGATTTCAAGGCCCA-----GCAACTA	2411
Qy	2805	GCAAGAGCAACTGTAGAAAGCTGAAAGTGAAGCTTGAAGACTGATCTGAAATGACATCC	2866
Db	2415	GCAAAAGCAACTGTAGAAAGCCGACAGGAAGGTGATGATGATCTGAGCTCGAGG-----	2466
Qy	2865	TGATGTCTGCCACGAGAACGATCAACATCGTCTGTGACTTGGTCTTTTGTATTTTCA	2923
Db	2467	TGATGTCTGCCACGAGAACTGACTCAACCTGTCTGTGACTTGGTCTTTTGTATTTTCA	2525

RESULT 9
 AAA09592
 ID AAA09592 standard; cDNA to mRNA; 3080 BP.
 XX
 AC AAA09592;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human phosphodiesterase 10 (PDE10) nucleotide sequence SEQ ID 4.
 XX
 KW Phosphodiesterase 10; PDE10; human; ss.
 XX
 OS Homo sapiens.
 XX

FN JP200224992-A.
XX 15-AUG-2000.
XX 11-MAY-1999; 99JP-00129343.
XX 30-NOV-1998; 98JP-0038861.
XX (TANA) TANABE SEIYAKU CO.
XX WPI, 2000-605129/58.
DR Novel phosphodiesterase and its gene for research on complex mechanism of
XX intracellular information transfer.
XX Claim 2, Page 24-27, 29pp; Japanese.
XX
XX Sequences AAA0589-A09592 encode human phosphodiesterase 10 (PDE10)
CC proteins AAB2683-B2685. Phosphodiesterase 10 and its gene are useful
CC for research on the complex mechanism of intracellular information
CC transfer. The invention includes a recombinant vector containing a PDE10
CC gene, and a cell transformed with the vector. Sequences AAA0593-A09606
CC represent PCR primers used in the isolation of the PDE10 polynucleotide
CC sequences of the invention
XX
SQ Sequence 3080 BP; 776 A; 826 C; 805 G; 673 T; 0 U; 0 Other;

Query Match 60.1%; Score 2167; DB 3; Length 3080;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 2270; Conservative 0; Mismatches 115; Indels 14; Gaps 2;

QY 525 GTTTACGGATGAAAGGTGAAGGCGCTATCTTCTCCATCCCGATTTAGATGAT 584
DB 663 GTTTACGGATGAAAGGTGAAGGCGCTATCTTCTCCATCCCGATTTAGATGAT 742
QY 585 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGCGTGAAGAGAAACCA 644
DB 743 TTGTTTCTGAAAGTGTAGTGCAGAGACTGTGAAAAGTGCGTGAAGAGAAACCA 802
QY 645 AAGCAAAAGATGAAACCATCTCTTAAGAAAGTGAAGAGATGCAAGATGCAATG 704
DB 803 AAGCAAAAGATGAAACCATCTCTTAAGAAAGTGAAGAGATGCAAGATGCAATG 862
QY 705 GAGTGTATGAGAGTGAACAGCTACATGAGACAGCGCTGGAACGCGCGGGGCAAC 764
DB 863 GAGTGTATGAGAGTGAACAGCTACATGAGACAGCGCTGGAACGCGCGGGGCAAC 922
QY 765 AACTGCTCTCTATGAGCTCAGACAGATCATCAGATAGCAAAAGCCGAGATTG 824
DB 923 AACTGCTCTCTATGAGCTCAGACAGATCATCAGATAGCAAAAGCCGAGATTG 982
QY 825 CACTGTACTCTCTGAGAGTGAATTAATAGCTGTGTGTTCATATACCAACCGGAT 884
DB 983 CACTGTACTCTCTGAGAGTGAATTAATAGCTGTGTGTTCATATACCAACCGGAT 1042
QY 885 AGGAAGGCAACCCGCGCTCATCCCTGACGCGCCATCAACCGAGGTACCAATCTCG 944
DB 1043 AGGAAGGCAACCCGCGCTCATCCCTGACGCGCCATCAACCGAGGTACCAATCTCG 1102
QY 945 CCTACGTGCGCAAGTCTAGAGAGAGCTGTGTGTGAGAGATATCTTGGGATGAGCAT 1004
DB 1103 CCTACGTGCGCAAGTCTAGAGAGAGCTGTGTGTGAGAGATATCTTGGGATGAGCAT 1162
QY 1005 TTCTCGAGAGTACTGCGCTGGAATGAGAACCCGCAATCCAGTCTGTCTTTGCTTCC 1064
DB 1163 TTCTCGAGAGTACTGCGCTGGAATGAGAACCCGCAATCCAGTCTGTCTTTGCTTCC 1222
QY 1065 TTGTACATGCGCATTTGGAATGATTTGGATCTTGAACGTGACAGGCACTGGGGCAAG 1124
DB 1223 TTGTACATGCGCATTTGGAATGATTTGGATCTTGAACGTGACAGGCACTGGGGCAAG 1282
QY 1125 AGGCTTTGCTGCGCATGAGAGTTGCAACGCCAATCTTCTTGGGCTTCCGTAG 1184
DB

DB 1283 AGGCTTTGCTGCGCATGAGAGTTGCAACGCCAATCTTCTTGGGCTTCCGTAG 1342
QY 1185 CAATACACAGGTGAGGTGTGTAGAGTCTCGCAACAGACCGAATGATGATCTCC 1244
DB 1343 CAATACACAGGTGAGGTGTGTAGAGTCTCGCAACAGACCGAATGATGATCTCC 1402
QY 1245 TACTGACGTATCAAAAGCATACTTTGATTAATATGTTGCCATAGACTCTACTTTGAAC 1304
DB 1403 TGCTGAGTATCAAAAGCATACTTTGATTAATATGTTGCCATAGACTCTACTTTGAAC 1462
QY 1305 ACATCATGATATATGCAAAAAAATCTAGTAAAGCCGACCGCTGCGCTCTTCCAGGTGG 1364
DB 1463 ACATCATGATATATGCAAAAAAATCTAGTAAAGCCGACCGCTGCGCTCTTCCAGGTGG 1522
QY 1365 ACCACAAAGACAGAGAGTGTACTCGACCTGTTGACATTTGGGAGAGAAAGAGGGGA 1424
DB 1523 ACCACAAAGACAGAGAGTGTACTCGACCTGTTGACATTTGGGAGAGAAAGAGGGGA 1582
QY 1425 AGCCATCTTCAAGAAAGACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTGCTGTC 1484
DB 1583 AGCCGCTTCAAGAAAGACCAAGAGATCAGATTTTTCATTGAGAAAGGATTTGCTGTC 1642
QY 1485 AAGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCGATGCTTACGCGGACCTGCTTTA 1544
DB 1643 AAGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCGATGCTTACGCGGACCTGCTTTA 1702
QY 1545 ACAGGAGATGAGACCTGTACACAGGCTACACAGAGAACATCTGTATGCGCATAG 1604
DB 1703 ACAGGAGATGAGACCTGTACACAGGCTATACACAGGAACTTCTGTATGCGCATAG 1762
QY 1605 TGAGCCGAGGAGCGGTGATTTGGCGTGTGAGATGATGTAACAGATCAGCGGTAGCGCT 1664
DB 1763 TGAGCCGCGGAGCGGTATGCGTGTGTGCAAAATGTTAACAATACGCGGACGCGCT 1822
QY 1665 TTCTCAAGACAGACGAGAACATTTCAAGATGTTCTGTCTTCTGCGCACTGCGCTTGC 1724
DB 1823 TTCTCAAGACGAGATGAGAACATTTCAAGATGTTCTGTCTTCTGCGCGCTTGC 1882
QY 1725 ACTGTGCTAAATGATACACAGAGATCCGCACTGAAATGATCTACAGGGTTACAGTGG 1784
DB 1883 ACTGTGCTAAATGATACACAGAGATCCGCACTGAGATGATCTACAGGGTTACAGTGG 1942
QY 1785 AGAAGCTTCTTACCAACAGATCTGACCTCCGAGAGTGGCAAGGCTCATGCGCTTCA 1844
DB 1943 AGAAGCTGTCTTACCAACAGATCTGACCTCTGAGAGATGSCAAGGCTCATGCACTTCA 2002
QY 1845 ACTTACCAACAGATCTGCGGAGCATGAGCTATTTCACTTTGACATTTGCTCTTTCG 1904
DB 2003 ACTTGCAGACAGCATCTGCGGAGCATGAGCTATTTCACTTTGACATTTGCTCTTTCG 2062
QY 1905 AGAATATGTGGCTGGGATCTTTGTCTTACATGATCCATCCGCTCTTGGGACATCTGTT 1964
DB 2063 AGAATATGTGGCTGGGATCTTTGTCTTACATGATCCATCCGCTCTTGGGACATCTGTT 2122
QY 1965 TTGAATTTGAAAAATTTGCGGTTTATCATGTCTGTGAAAGAAACTATGCGGGGTTTC 2024
DB 2123 TTGAATTTGAAAAATTTGCGGTTTATCATGTCTGTGAAAGAAACTATGCGGGGTTTC 2182
QY 2025 CTTACCAACATGGAAGCATGACGATGAGCACTGAGATGATGATGATCTTCAAA 2084
DB 2183 CTTACCAACATGGAAGCATGACGATGAGCACTGAGATGATGATGATGATCTTCAAA 2242
QY 2085 ACAACATGAGCTCTTTCACAGACCTCGAGCGCAAAAGCTGTGTAATGGCGGTGCGC 2144
DB 2243 ACAACATGAGCTCTTTCACAGACCTGAGCGCAAAAGCTGTGTAATGGCGGTGCGC 2302
QY 2145 ATGACCTGGAACACAGGGGCTTTCAGTAAACAGCTACTGAGAAAGTTGCAACACCCCTGG 2204
DB 2303 ATGACCTGGAACACAGGGGCTTTCAGTAAACAGCTACTGAGAAAGTTGCAACACCCCTGG 2362
QY 2205 CGGCGCTGTACTTCCACTTCCATGAGCAACCACTTCTCCAGACGGTGTTCATCC 2264
DB 2363 CTGCGTTGTACTTCCACTTCCATGAGCAACCACTTCTCCAGACGGTGTTCATCC 2422

Oy		2265	TTCAAGCTGGAAGGGCACAATATCTTCTTCACACTTGAGCTCCAGCGAGTAAGAAGAGGTGC	2234
Dd		2423	TCCAGCTGGAGGGGACAAACATCTTCTTCCACCCTGAGCTCCAGCGAGTAAGAAGAGGTGC	2482
Oy		2325	TGGAGATCATCCGCAAAAGCCATCATCGCACCCGACTCGGCCCTAATTACTTTGGAAACAGSA	2384
Dd		2483	TGGAGATCATCCGCAAAAGCCATCATCGCACCTGCACTGCACTGTACTTTGGAAACAGSA	2542
Oy		2385	AGCAGTTGAGAGAGANTGTACCAGA CAGGGTGCCTGAACCTTCACAACGATGCCAATCGAG	2444
Dd		2543	AGCAGTTGAGAGAGANTGTACCAGA CAGGGTGCCTGAACCTTCACAACGATGCCAATCGAG	2602
Oy		2445	ACCCTGTTCATCGGCTTTGATGATGTACCTGCTCTGTATCTTTGCTCTGTACCAAATGATGGC	2504
Dd		2603	ACCCTGTTCATCGGCTTTGATGATGTACCTGCTCTGTATCTTTGCTCTGTACCAAATGATGGC	2662
Oy		2505	CAGTTACAAAATTTGACAGCGAATGATATATATGTAGCAATTCCTGGCTGAGGGGTGATGAGA	2564
Dd		2663	CAGTTACAAAATTTGACAGCGAATGATATATATGTAGCAATTCCTGGCTGAGGGGGATGAGA	2722
Oy		2565	TGAAGAACCTGGGCATACAGCCCCATTCCTATGATGTGACAGAGACAGCGAATGAATGCC	2622
Dd		2723	TGAAGAACCTGGGGATACAGCCCATCCCTATGATGTGACAGAGACAGCGAATGAATGCC	2782
Oy		2625	CTCAAGGGGACACTCGGATTTCTACATGTCTGTGGCCATTCCTGCTATPACACCTTGAGCGC	2684
Dd		2783	CTCAAGGACACTGTGATTTCTACAAATGTCTGTGGCCATTCCTGCTATPACACCTTGAGCGC	2844
Oy		2685	AGATCTCTCCACCCACAGAGCTCTGTCTGAAGGCTCTGACGGGATTAACCTCAATCAGTGGG	2744
Dd		2843	AGATCTCTCCACCCACAGAGCTCTGTCTGAAGGCTCTGACGGGATTAACCTCAATCAGTGGG	2902
Oy		2745	AGAAAGTAATTCGCGGGGAAGAAGACAGCAATGTGATTTCAAGGCCCAAGGCCGCGGCTCTA	2804
Dd		2903	AGAAAGTAATTCGAGGGGAAGAAGACAGCAATGTGATTTCAAGGCCCA-----GCAACTTA	2954
Oy		2805	GCAAGAGACACCTGAGAAAGCTGGAAGCTGGAAGGTGAAGACTGATCTGGAATGACGTCC	2864
Dd		2957	GCAAAAGCACATCTGAHAAGCCGACACAGAAAGGTGAGTGAATCTGAGS-----	3008
Oy		2865	TGATGTCTGCCCAAGCAACCGACTCAACCTGCTCTGTGTGAATTGCTTTGTTTTTCA	2923
Dd		3009	TGATGTCTGCCCAAGCACTGAATCAACTGCTTCTGTGAATTGCTTTGTTTTTCA	3067
RESULT 10				
ID	ADM34017	ADM34017 standard; cDNA; 4388 BP.		
XX	ADM34017;			
AC				
DT	03-JUN-2004	(first entry)		
XX				
DE	DNA encoding human phosphodiesterase 8A1 (PDE8A1) splice variant.			
XX	ss: EST; expressed sequence tag; gene; phosphodiesterase 8A; PDB8;			
KW	cyclic nucleotide pathway; human.			
XX				
OS	Homo sapiens.			
XX				
PH	Key	Location/Qualifiers		
FT	CDS	3..2414		
FT		/*tag= a		
FT	/product= "Splice variant phosphodiesterase 8A1 (PDE8A1)"			
FT	/partial			
XX		/note= "No start codon"		
PD	US2003215919-A1.			
XX				
XX	20-NOV-2003.			
Pf	19-MAY-2003; 2003US-00440998.			

	XX	PR	16-OCT-1997;	97US-00951648-
	XX	PR	16-OCT-1998;	98US-00174437-
	XX	PR	11-OCT-2000;	2000US-00686055.
	PA	(LOUG/) LOUGHNEY K.		
	XX	Loughney K;		
	XX	WPI; 2004-021844/02.		
	DR	P-PDB; ADM34018.		
	XX	New phosphodiesterase 8 (PDE8) polypeptide, useful in preparing a		
	PT	composition for treating conditions associated with aberrant cyclic		
	PT	nucleotide pathways.		
	PS	Claim 7, SEQ ID NO 3; 39pp; English.		
	XX	The invention relates to purified and isolated phosphodiesterase 8 (PDE8)		
	CC	polypeptides and polynucleotides. Also described is a method of		
	CC	identifying a specific binding partner compound of a PDE8 polypeptide or		
	CC	polynucleotide comprising: (i) contacting the polypeptide or		
	CC	polynucleotide with a compound; (ii) detecting binding of the compound to		
	CC	the polypeptide or polynucleotide; and (iii) identifying the compound as		
	CC	a specific binding partner. The specific binding partner enhances or		
	CC	inhibits expression of the PDE8 polypeptide or polynucleotide. The		
	CC	phosphodiesterase 8 (PDE8) polypeptide is useful in preparing a cyclic		
	CC	composition for treating conditions associated with aberrant cyclic		
	CC	nucleotide pathways. The present sequence represents the coding sequence		
	CC	of human PDE8A1, a splice variant of PDE8.		
	XX			
	SQ	Sequence 4388 BP; 1315 A; 922 C; 920 G; 1231 T; 0 U; 0 Other;		
	Query March	51.9%; Score 1871.8; DB 12; Length 4388;		
	Beech Local Similarity	86.5%; Pred. No. 0;		
	Matches 2065; Conservative	0; Mismatches 322; Indels 0; Gaps 0;		
Oy	415	CTTCCCGGTCACACCGTTTGCCGCTGCCCTTCGGCTCCGACATGGAAGTAGACCCTC	474	
Db	2	CTTGCGCCCTCGCCGCCCGCGCGCGCGGTCTTTCGGCTCCGACATGGAAGTAGACTTTC	61	
Oy	475	TAAACATGCGAGTTGCTTCCGAAAGCTGACCGAGTGTTCCTCAAGCCCCAGTTGACGGA	534	
Db	62	TAAATAATGCGAGCTGCCTCCGAAAGCTGACCGAGTGTTCCTCAAGCCCCAGTTGACGGA	121	
Oy	535	TGAAGAAGTGAAGGCGCATCTTTCTCTCCATCCCACGAGTATTAGTAATTTGTTCTGA	594	
Db	122	TGAANAATGGAAGGATATCTTTCTCTCACCCCCAGGATATTAGTAATTTGTTATCTGA	181	
Oy	595	AAGGTATGTCAGAGACTGTGGAANAATGAGCTGAGAGAAAACAACAAGCAAAGA	654	
Db	182	AAGGTATGTCAGAGACAGTATGGAANAATGAGCTGAGAGAAAACAACAATCAGAAGA	241	
Oy	655	TGAACATCTCCCAAGGAAGTACAGAGGTACAGAGTACGAATATGACAGGAGTGTGTGA	714	
Db	242	TGAATCGGCTCTTAAGGAAGTACAGAGGTACCAAAATACGAATATGACAGGAGTGTGTGA	301	
Oy	715	GAGGTGAACAGCTATATGAGACAGCGCTGGAACAGCGGCGGGAACAACACTGCTCT	774	
Db	302	TGAATTAACAGCTATATGAGAACAGGCTTGAACACAGAGGAGAACACAGCTACTCT	361	
Oy	775	CTATGAGCTCAGACATCATCAGATAGCCAACAAAGCCGACGGATTGCACTGTACTT	834	
Db	362	CTATGAGCTCAGACATCATTAATAATATGCCACAAAGCCGATGATTGCACTGTACTT	421	
Oy	835	CCTTGAAGTGCATTAATAGCTGTGTGTTCATACACCCGGGATGAAGAGGCCA	894	
Db	422	CCTTGAAGTGCATTAATAGCTGTGTGTTCATACCGCACTGAGATGAAGAGGAAAA	481	
Oy	895	ACCCGGGCTATCCCTGACGGGCCCATCAACCAAGGGTACACCATCTCTGACTGAGC	954	
Db	482	ACCCGGGCTATCCCTGCTGGGCCCATCACTCAAGGACACACCGTCTCTGCTTAATGTGC	541	

QY 955 CAAGCTAGAGAGACGTTGGTAGAGATATCCTTGGGAGTAGACGATTTCTCGAGG 1014
DB 542 CAAGCTCAGAGAAAACATCTAGTAGAGACATCTTGAGATGAAAGATTTTCCAAAGG 601
QY 1015 TACTGGCTGGAATCAGAAACCCGCAATCCAGTCTGTTCTTTGCTTGGCCATTTGCACTGC 1074
DB 602 TACTGAGACTGGAATCAGGGACTGTATCCAGTCTGTTCTTTGCTTAACTAATGTCACTGC 661
QY 1075 CATTGGAGACTTGATGGATCTTGAATGTATCAGGCACTGGGGCAAGAGAGCCCTTCG 1134
DB 662 AATTGGATCTTGATTTGATTTCTGAGCTGTATCCGCACTGGGGCAAGAGAGCCCTTCG 721
QY 1135 CCTCAGCCATCAGAGAGTTGCAACAGCCAAATCTTGCTGGGCTTCCGTAGCAATACCA 1194
DB 722 TCTTAGTACCAAGAGTTGCAACAGCAAAATCTTGCTGGGCTTCAGTAGCAATACATA 781
QY 1195 GGTGCAAGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGATTTCTTACTGACGT 1254
DB 782 GGTGCAAGTGTATCAGAGGCTTGCCAAACAGACAGAAATGAATGATTTCTTACTGACGT 841
QY 1255 ATCAAAAGACATCTTGTATTAACATAGTTGCCATAGCTCTTCACTTTGAACATCATGAT 1314
DB 842 ATCAAAACATATTTTGTATTAACATAGTTGCCAATAGATTTCTTCACTTTGAACATATATGAT 901
QY 1315 ATATGCAAAAATCTAGTGAAGCCGACCGCTGCGGCTCTTCCAGGTGACCAACAAGA 1374
DB 902 ATATGCAAAAACCTGGTGAATGCCGATGTTGTGCACTTTTCCAGGTGACCAATAGAA 961
QY 1375 CAAGAGCTGTACTCGGACCTGTTTGAATTTGGGAGAGAAAGAGGGAGACCCATCTT 1434
DB 962 CAAGAGTGTATATTCAGACCTTTTGAATTTGGAAGAGAAAGAAAGAAACCTGTCTT 1021
QY 1435 CAAGAAAGACCAAGAGATCAAGTTTTCCATTGAGAAAGGAGTTGCTGTGCAATGCGCAG 1494
DB 1022 CAAGAAAGACCAAGAGATTAAGATTTTCAATTAAGAAAGGAATTTGCTGCGCAAGTATGCAAG 1081
QY 1495 AACAGGCAAGCTTGAACATTTCCGATGCTACGCGGACCTCTGCTTTAAAGAGAGGT 1554
DB 1082 AACAGGCAAGCTTGAACATTTCCGATGCTACGCGGACCTCTGCTTTAAAGAGAGGT 1141
QY 1555 GGAAGCTGTACAGAGCTACACAGAGAAATTTCTGTATGCTCCATATGAGCCGAGG 1614
DB 1142 AGACTTTGTACAGAGCTACACAGCGGAAATCTCTGTCATGCCATGTCAGCCGAGG 1201
QY 1615 CAGCGTATTTGGCGTGTGTCAGATGTTGAACAAAGATCAGCGGTAGGCTTTTCCAAAGC 1674
DB 1202 CAGCGTATGAGTGTGTGTCAGATGTTGAACAAAGATCAGTGGCAGTCTTCTTAAAC 1261
QY 1675 AGACGAGAACAACTTCAAGATGTTTGTCTTCTTGTGCGCACTGGCTTGCATGTGCTAA 1734
DB 1262 AGATGAGAAACAACTTCAAAATGTTTGTGCGTCTTTTGTGCTTAAAGCTTAACTGATCA 1321
QY 1735 CATGTACCAACAGGATCCGCACTCAGAAATGATCTACAGGGTTTACATGAGAGGCTTTC 1794
DB 1322 TATGTATATATAGAAATTCGCACTCAGAGTGCATTTTACGGGTATACGATGAGAAAGCTGTC 1381
QY 1795 CTACCAACAGCATCTGCACTCCGAGAGTGGCAAGGCTTCAATGCGCTTCAACTACAGC 1854
DB 1382 CTACCATAGCATTTGTATCTTCAGAAAGTGGCAAGGTCTCAGCAATTCACCTTCCCGT 1441
QY 1855 ACGCATTCGCGGAGCATGAGCTATTCACCTTTGACATTTGGTCTTTGAGAACATGTC 1914
DB 1442 GGTCTCTGCAAAAGAAATTTGAATTTATTCACCTTTGACATTTGATGTTTGAAGATGTG 1501
QY 1915 GCTTGGGATCTTTGTCTACATGATCATCGATCTTGTGGGACATCTGTATTTGAACCTTGA 1974
DB 1502 GCTTGGGATTTTGTCTACATGATCATCGATCTTGTGGGACATCTGTATTTGAAGCTTGA 1561
QY 1975 AAAATTTGGCGTTTATATATGTCTGTGAAGAAAGATATGCGCGGCTTCTTACCAAA 2034
DB 1562 AAAAGTTGTGTCTTTATATATGTCTGTGAAGAAAGATATGCGCGGCTTCTTATACAAA 1621
QY 2035 CTGGAAGCATGACGCTGAGCACTGCAATGTATGCAATTAATCTTCAAAACAAACATAG 2094

DB 1622 CTGGAAGCATGCGGTCACTGTAGACACACTGATATGCCATTAATCTTACAAACAAATCACAC 1681
QY 2095 CCTCTTCAACAGACCTCGAGCCGCAAGAGCTGTATATTCGCTGTCTGTCCCATGACCTGGA 2154
DB 1682 GCTTTTCAACAGACCTTGTAGCCGAAAGACCTGTATTCGCTGTCTGTCTGTATGACCTGGA 1741
QY 2155 CCAACAGGGCTTCAAGTAAACAGTACCTTCAGAGAGTTCAGACCAACCCCTGTGGCGGCTGTGA 2214
DB 1742 CCAACAGGGCTTCAAGTAAACAGTACCTTCAGAGAGTTCAGACCAACCCCTGTGGCGGCTGTGA 1801
QY 2215 CTCACCTTCAACATGAGACCAACCACTTCTCCAGACGCTGTCACTTCACTGAGTGA 2274
DB 1802 CTCACCTTCAACATGAGACCAACCACTTCTCCAGACGCTGTCACTTCACTGAGTGA 1861
QY 2275 AGGGCAATATCTTCTTCAACCTTGAAGCTTCAAGAGATTAAGAGAGGCTGTGAGATCAT 2334
DB 1862 AGGGCAATATCTTCTTCAACCTTGAAGCTTCAAGAGATTAAGAGAGGCTGTGAGATCAT 1921
QY 2335 CCGCAAGCCCATCATTCGCAACGACCTGCGCTTATTAATTTGGGAAACAGAGAGTGTGA 2394
DB 1922 CCGCAAGCCCATCATTCGCAACGACCTTGTATTAATTTGGGAAACAGAGAGTGTGA 1981
QY 2395 GGAATGTACCAAGACAGGAGTGTGAACTTCCACCAACGATCCCATGAGACCGTGTAT 2454
DB 1982 AGAATGTACCAAGACAGGATCATTAACCTTAAATTAATCAATCACTAAGACCGTGTAT 2041
QY 2455 GCGCTTGAATGATGATGCTGCTGTGATCTTTGCTGTGTGACAAACATATGCGCATTAACAA 2514
DB 2042 TGTGTTGATGATGATGCTGCTGTGATCTTTGTTGTGTGACAAACATGTCGCGCTTAAACAA 2101
QY 2515 ATTGACAGCATGATATATATATGAGAAATTTCTGGCTGAGGGTGTATGATGAAGAGCT 2574
DB 2102 ATTGACAGCAATATATATATATGAGAAATTTCTGGCTGAGGGTGTATGAAATGAATAT 2161
QY 2575 GGGCATACAGCCCATCTTATATGATGAGACAGACAAAGGAGATGAAGTCTCTCAAGGCA 2634
DB 2162 GGGATTAACAGCTTATTTCTATATGATGAGACAGACAAAGAGATGAAGTCTCTCAAGGCA 2221
QY 2635 GCTCGAATTTCAATATGCTGTGGCCATTTCCCTGCTATACCACTTGAAGCAGATCTCTCC 2694
DB 2222 GCTTGGGTTTCAATATGCTGTGGCCATTTCCCTGCTATACCACTTGAAGCAGATCTCTCC 2281
QY 2695 ACCGACAGAGCCTTGTGAGAGCCTTGCAGAGGATTAACCTCATCATGAGGAGAGTAAAT 2754
DB 2282 TCCACAGAGCCTTCTTGAAGCATGAGGATTAATCTCAGTCAAGTGGAGAGTGAAT 2341
QY 2755 TCGCGGGAGAGACAGCAATGTGATTTCAAGCCCAAGGCCCGGCGC 2801
DB 2342 TCGAGGGAGAGAGACTGCACCTGGAATTTCAATCCCATCGGTGCTC 2388

RESULT 11
AAK36711
ID AAK36711 standard; DNA; 4389 BP.
XX
XX
XX AAK36711;
XX
XX
XX 14-JUL-1999 (first entry)
XX
XX
XX Human phosphodiesterase, PDE8, coding sequence.
DE
XX
XX
XX Phosphodiesterase 8; PDE8; human; cyclic nucleotide pathway; therapy;
KM intracellular cyclic nucleotide level modulation; cAMP; cGMP; ss.
OS Homo sapiens.
XX
XX
XX MO9919495-A1.
PN
XX
XX 22-APR-1999.
PD
XX
XX 16-OCT-1998; 98WO-US021956.
PF
XX

PR 16-OCT-1997; 97US-00951648.
XX (ICOS-) ICOS CORP.
XX
PI Loughney K;
XX WPI; 1999-277645/23.
XX P-PSDB; AAY13935.
XX
PT New isolated phosphodiesterase genes and polypeptides for identifying
specific binding partners.
PS Claim 7; Page 50-55; 80pp; English.
XX
XX
XX This sequence encodes the human phosphodiesterase 8 (PDE8) of the
XX invention. The phosphodiesterase genes and polypeptides are used to
XX develop products for treating conditions in which cyclic nucleotide
XX pathways are aberrant and for modulation of intracellular cyclic
XX nucleotide levels. The PDE8 polypeptides exhibit high affinity for
XX hydrolysis of both cAMP and cGMP but relatively low sensitivity to enzyme
XX inhibitors specific for other PDE families. The PDE8A polypeptides and
XX polynucleotides can be used for identifying their specific binding
XX partners. The products can provide approaches for treating conditions in
XX which cyclic nucleotide pathways are aberrant as well as conditions in
XX which modulation of intracellular cAMP and/or cGMP levels in certain cell
XX types is desirable

Sequence 4389 BP; 1315 A; 922 C; 920 G; 1232 T; 0 U; 0 Other;

Query Match 51.9%; Score 1871.8; DB 2; Length 4389;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

QY	415	CTTCCCTCCCTGCGACCGTTTGGCGGCTGCGCTCGGCTCGACATGGAAGATGACCTTC	474
DB	2	CTTGGCCCTCGCGCGCGCGCGCGCGCTGCTCTTGGCTCGACATGGAAGATGACCTTC	61
QY	475	TAAACAATGCGAGTGGCTTCGGAAGCTGACCGAGTGTTCCTCAGCCCACTTTGACGA	534
DB	62	TAAATAATGCGAGTGGCTTCGGAAGCTGACCGAGTGTTCCTCAGCCCACTTTGACGA	121
QY	535	TGAAAAGTGAAGGCTTATCTTCTCCATCCCGAGGTTTGAATTTGTTCTGA	594
DB	122	TGAAAAGTGAAGGCTTATCTTCTCCATCCCGAGGTTTGAATTTGTTCTGA	181
QY	595	AAGTGTTAATGTCAGACATCTGTGAAGAGGCTGAAGAGGAAAACAACAAGCAAAAG	654
DB	182	AAGTGTTAATGTCAGACATCTGTGAAGAGGCTGAAGAGGAAAACAACAAGCAAAAG	241
QY	655	TGAACCATCTCCCAAGGAAGTCAAGAGTACAGAGTATGCAAGGAGTCTGTGA	714
DB	242	TGAATGCGCTCTTAAGGAGTCAAGAGTACAGAGTATGCAAGGAGTCTGTGA	301
QY	715	CGAGTGAACAGCTATACATAGACAGCGCTGGAACAGCGGCGGGAACAACACTGCTCT	774
DB	302	TGAACCTAAACAGCTATATAGAACACAGGTTGGAACAAGAGAGAACACACAGTACTCT	361
QY	775	CTATGAGCTCAGACATCATCAGATAGCCACAAAAGCCGACGAGTTTGCATTTACTT	834
DB	362	CTATGAGCTCAGACATCATTTAAATAGCCACAAAAGCCGATGAGTTTGCATTTACTT	421
QY	835	CGTTGAGAGTGAATTAATAGCGTGTGTGTTTATATCAACCCGAGATGAAGAGGCA	894
DB	422	CGTTGAGAGTGAATTAATAGCGTGTGTGTTTATATCAACCCGAGATGAAGAGGAAA	481
QY	895	ACCCGCGCTATCTCTGACAGGCGCCATACCCAGGATACCAATCTCTGCTACGTTGC	954
DB	482	ACCCGCGCTATCTCTGACAGGCGCCATACCAAGGAGCAACCGCTCTCTGCTATGTTGC	541
QY	955	CAAGTCTAGAGAGAGCTTTGTTGTAAGAGATATCTTTGGGATGAAGGATTTCTCAGG	1014
DB	542	CAAGTCTAGAGAGAGCACTGCTAGTAAGACATCTTTGAGATGAAGATTTCCAAAGG	601

QY	1015	TACTGCGCTGGAATCAGGAACCCGCAATCCAGTCTGTTGCTTGGCTTGGCCATTTGCACTGC	1074
DB	602	TACTGAGCTGGAATCAGGAATCTGATCCAGTCTGTTGCTTGGCTTACCAATTTGTCAGTGC	661
QY	1075	CATTGAGACTTGAATTTGCAATCTTTGAACTGTACAGGCACTGGGGCAAAAGAGCTTTCTG	1134
DB	662	AATTGAGACTTGAATTTGATTTCTGAGCTGTATCGGCACTGGGGCAAAAGAGCTTTCTG	721
QY	1135	CCTCAGCAATCAGAGAGTTTGCAACAGCCAAATCTTGGCTTCCGATAGCAATACACA	1194
DB	722	TCTTAGTACCAAGAGGTTTGCAACAGCAAAATCTTGGCTTCCGATAGCAATACATCA	781
QY	1195	GGTGAGGTTGTAGAGTCTGCGCAACAGCCGAATGATGACTTCTTACTGACGT	1254
DB	782	GGTGAGGTTGTAGAGGCTTGGCCAAACAGCAAGATTTGATGACTTCTTACTGACGT	841
QY	1255	ATCAAGACATATCTTGTATTAATATAGTTGCCATAGACTCTCTTATGAAACATCATGAT	1314
DB	842	ATCAAAAATATTTTGTATTAATATAGTTGCCATAGACTCTCTTATGAAACATCATGAT	901
QY	1315	ATATGCAAAAATCTATGTAAGCCGACCGCTGCGCTCTTCCAGTGGACCAAGAA	1374
DB	902	ATATGCAAAAATCTATGTAAGCCGATCGTTGTGCACTTTTCCAGTGGACCAATGAA	961
QY	1375	CAAGAGCTGTACTGGAACCTGTTTGAATTTGGAGAGAGAGAGGAGCCCATCTT	1434
DB	962	CAAGAGTTATATTCAGACCTTTTGTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG	1021
QY	1435	CAAGAAAGCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTCAAGTGGCAAG	1494
DB	1022	CAGAAAGCAAGAGATTAAGTTTTCATTGAGAAAGGATTTGCTGTGCGCAAGTACAG	1081
QY	1495	AAACAGCGAAGTCTTGAACATTTCCGATGCTTACCGGACCTCTGCTTTTAAACAGGAGT	1554
DB	1082	AAACAGGGAAGTCTTGAACATTTCCAGATGCTTATGCAAGCCCACTTTTAAACAGAAAT	1141
QY	1555	GGAATCTGTACAGGTTTAAACCAAGAGAAATTCGTGTATGGCCATATGAGAGGAGG	1614
DB	1142	AGAATTTGTACAGGTTTAAACCAAGAGAAATTCGTGTATGGCCATATGAGAGGAGG	1201
QY	1615	CAGCGTATTTGGCGTGTGCAAGATGTTGAACAAGATCAAGCGTATGAGCTTCTCAAGAC	1674
DB	1202	CAGCGTATAGTGTGTGTGCAAGATGTTGAACAAGATCAAGCGTATGAGCTTCTCAAGAC	1261
QY	1675	AGAAGAAACAATTCAGATGTTTGTCTCTTCTGCGCATGAGCTTGTGCACTGTCTTA	1734
DB	1262	AGATGAAACAATTCAGATGTTTGTCTCTTCTGCGCATGAGCTTGTGCACTGTCTTA	1321
QY	1735	CATGTACCAAGATTCGCGCATCTCAAGATGCAATCAAGGTTTACATGAGAGAGCTTC	1794
DB	1322	TATGTATCAAGATTCGCGCATCTCAAGATGCAATCAAGGTTTACATGAGAGAGCTTC	1381
QY	1795	CTACCAACAGATTCGCAACCTCCAGAGTGGCAAGGCTCATGCGCTTCAACCTTACAG	1854
DB	1382	CTACCAACAGATTTTGTATCTTCAAGAGTGGCAAGGCTCATGCAATTACCTTCCCGT	1441
QY	1855	ACGCACTGCGCGGACATCAGAGTATTCATTGACATTTGCTTTGAGAAATGTG	1914
DB	1442	GCGTCTCTGCAAGAAATTAATTAATTCATTGACATTTGCTTTGAGAAATGTG	1501
QY	1915	GCGTGGATCTTTGCTTCAATGATCAATGCTTTGTGGGACATCTGTTTGAACCTTGA	1974
DB	1502	GCGTGGATTTTGTCTTCAATGATCAATGCTTTGTGGGACATCTGCTTTGAGCTTGA	1561
QY	1975	AAAATTTGCGCTTTTATATATGCTGTGAAGAACTATCGCGGATTCCTTACCAAA	2034
DB	1562	AAAGTTGTGCTTTTATATATGCTGTGAAGAACTATCGCGGATTCCTTATCAAA	1521
QY	2035	CTGGAAGCATGCACTGCGTGGCACTGTCATGTATGCCATATCTTCAAAACAACATGG	2094
DB	1622	CTGGAAGCATGCGGTCACTGTACACATGCAATGTATGCAATCTTCAAGAACATACAC	1681
QY	2095	CTCTTTCACAGACCTGAGCGCAAGGCTGTAAATTTGCGTGTCTGTGCAATGACCTGGA	2154


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Db      1682 GCTTTTCACAGACCTTGAGCGGAAAGACGTGCTGATGCTGTGTCATGACCTGGA 1741
Qy      2155 CCACAGGGGGCTTCAGTAACGCTACCTGACAGAAAGTTGACACACCCCTGGCGGCTGTA 2214
Db      1742 CCACAGGGGGCTTCAGTAACGCTACCTGACAGAAAGTTGACACACCCCTGGCGGCTGTA 1801
Qy      2215 CTCACCTCCACATGAGGACACACCTTCTCCAGACGGTGTCAATCCTCACTGGA 2274
Db      1802 CTCACCTCCACATGAGGACACACCTTCTCCAGACGTGTCTCATCTCCAGTTGGA 1861
Qy      2275 AGGGCACAATATCTTCTCCACCTGAGCTCCAGCAGATGACAGAGTGGTGGATCAT 2334
Db      1862 AGGGCACAATATCTTCTCCACCTGAGCTCCAGTGAATGAGCAGGTCTTGAATCAT 1921
Qy      2335 CCGCAAGCCATCATCGCCACCGACCTGCGCTTATATCTTTGGGAAACAGAGACAGTTGA 2394
Db      1922 CCGCAAGCCATCATTTGCCACAGACCTTGCTTATATCTTTGAAAACAGGAAACAGTTGGA 1981
Qy      2395 GGAATGTATCCAGACAGAGGTCCGTGAACCTCCAAACCAAGTCCCATCCAGACCCGTGCT 2454
Db      1982 AGAATGTATCCAGACCGGATCACTAAACCTTAAATATCATATCAATAGACCCGTGTAAT 2041
Qy      2455 CGGCTTGATGATGATGCTGCTGATCTTGTGCTGTGACCAAACTATGGCCAGTTACAA 2514
Db      2042 TGGTTTGAATGATGATGCTGCTGATCTTGTGCTGTGACCAAACTATGGCCAGTTACAA 2101
Qy      2515 ATTGAACAGGAATGATATATATGACAAATTTCTGGGCTGAGGGTGAATGAGTAAGAAGCT 2574
Db      2102 ATTGAACAGGAATGATATATATGACAAATTTCTGGGCTGAGGGTGAATGAGTAAGAAT 2161
Qy      2575 GGGCATACAGCCCATTTCTATATATGACAGAGACAGATGAAATGCCCTCAAGGGGA 2634
Db      2162 GGGAAATACAGCCTATATCTATATGACAGAGACAGAAAGATGAAGTCCCAAGGGCA 2221
Qy      2635 GCTCGATTCTACAAATGCTGTGGCCATTCCTGTCTATATACACCTTGAACGAGATCCTCCC 2694
Db      2222 GCTTGGGTTCTACAAATGCTGTGGCCATTCCTGTCTATATACACCTTGAACGAGATCCTCCC 2281
Qy      2695 ACCCAGAGGCTCTGTGTAAGGCTGTGACGAGGATTAACCTCAATCAGTGGAGAGAGTAA 2754
Db      2282 TCCCAACGAGGCTCTTCTGAAGGATGACGAGGATATCTCACTCAGTGGGAGAGAGTAA 2341
Qy      2755 TCGCGGGGAGAGACAGCAATGTGATTTCAAGGCCCAAGGCCCGGGGC 2801
Db      2342 TCGAGGGGAGAGACTGCAACCTGATTTCAATCCCATCCGTGGCTC 2388

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RESULT 12

AC63696
ID AAC63696 standard; cDNA; 4389 BP.

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XX AC AC AAC63696;
XX DT 13-FEB-2001 (first entry)
XX DE Human phosphodiesterase 8A1 PDE8A1 coding sequence.
XX KW Human; PDE8A1; phosphodiesterase 8A1; chromosome 6p26-27; ss.
XX OS Homo sapiens.
XX PN US6133007-A.
XX PD 17-OCT-2000.
XX PF 16-OCT-1998; 98US-00174437.
XX PR 16-OCT-1997; 97US-00951648.
XX PA (ICOS-) ICOS CORP.
XX PT Loughney K.

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XX DR MPI: 2001-006138/01.
XX DR P-PDB; AAB28257.
XX PT New phosphodiesterase 8A (PDE8A) polypeptides useful in the
XX PT systematic analysis of the structure and function of PDE8, and for
XX PT identifying molecules with which PDE8A will interact.
XX PS Example 3; Col 31-40; 37pp; English.
XX CC The present sequence is the coding sequence for human phosphodiesterase
XX CC 8A1 (PDE8A1). Phosphodiesterases hydrolyse 3', 5' cyclic nucleotides to
XX CC their respective nucleoside 5' monophosphates. The present sequence is a
XX CC splice variant of PDE8 (AAC63695). This sequence may be used in the
XX CC systematic analysis of the structure and function of PDE8, and for the
XX CC identification of molecules with which PDE8 will interact. The present
XX CC sequence may be used in hybridisation assays to detect the capacity of
XX CC cells to express PDE8, and as a basis for diagnostic methods useful for
XX CC identifying a genetic alteration in a PDE8 locus that underlies a disease
XX CC state or states. The human PDE8 gene has been localised to chromosome
XX CC 6p26-27.
XX SQ Sequence 4389 BP; 1315 A; 922 C; 920 G; 1232 T; 0 U; 0 Other;
XX
XX Query Match 51.9%; Score 1871.8; DB 4; Length 4389;
XX Best Local Similarity 86.5%; Pred. No. 0;
XX Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
Qy 415 CTTCCCTTCCACCGTTTGCGCGCTGCGCTTGGCTCCGACATGAAATGACCTC 474
Db 2 CTTGCCCTCCGCGCGCGCGCGCTGCTCTTGGCTCCGACATGAAATGACCTTC 61
Qy 415 TAACAATGCGAGTCTTCCGAAAGCTGACCGAGTGTTCCTCAGCCCCAGTTGACGGA 534
Db 62 TAAATATGCGAGCTGCTTCCAAAGCTGACCGAGTGTTCCTCAGCCCCAGTTGACGGA 121
Qy 535 TGAAGAGTGAAGGCTATCTTCTCTCATCCCAAGTATTAATGATGATTTGTTCTGA 594
Db 122 TGAATTAATGAAAGCATATCTTCTCTCACCCCAAGTATTAATGATGATTTGTTCTGA 181
Qy 595 AAGTTAGTCCAGAGCTGTGAAAGTGTGCTGAAAGGAAACCAACAAAGCAAAAGA 654
Db 182 AAGTTAGTCCAGAGCTGTGAAAGTGTGCTGAAAGGAAACCAACAAATCAGAAAGA 241
Qy 655 TGAACATCTCCCAAGAGATCAGAGTACCAAGATTCGAATATGCGAGAGTGTGTTA 714
Db 242 TGAATCGGCTCTTAAGAAATCAGAGGATACCAAGATTCGAATATGCGAGAGTGTGTTA 301
Qy 715 CGAGCTGAACAGCTACATAGAGCAGCGCTGAGACACGCGCGGGAACAACCTGCTCT 774
Db 302 TGAATTAACAGCTATATAGAACACAGGTTGACACAGAGAGAGAACACAGCTACTCT 361
Qy 775 CTATAGCTCAGCAGCATCATCAGGATAGCAACAAAGCCGACGAGATTGCACTGACTT 834
Db 362 CTATAGCTCAGCAGCATCATTAATAATAGCCAAACCCAGTGAATTTGCACTGATTT 421
Qy 835 CTTGGAAGTGCATATATAGCTGTGTGTGTTCAATACACCCGGGATGAAGAGAGGCCA 894
Db 422 CTTTGAAGTGCATATATATAGCTGTGTGTGTTCAATACACCCGGGATGAAGAGAGGAA 481
Qy 895 ACCCGGCTCATCCCTGACGGGGCCATCACCGAGGATACCAACATCTGTGCTACGTGGC 954
Db 482 ACCCGGCTCATCCCTGTGGGCCCATATCTCAGGGCACACCGCTGTGCTATATGTGGC 541
Qy 955 CAAGTCTAGAAAGCTTGTGTGTAAGAGATATCTTTGGGATGAAGCATTTCTCGAGG 1014
Db 542 CAAGTCTAGAAAGACATGCTAGTGAAGACATCTTGAAGTGAAGCATTTCCAAAGG 601
Qy 1015 TACTGAGCTGGAATCAGAAACCCGATCATCACTGTTCTTTGCTTGGCCATTTGTAATGC 1074
Db 602 TACTGAGCTGGAATCAGGAACCTGATCATCACTGTTCTTTGCTTGAACAAATTTGTAATGC 661
Qy 1075 CATTGGAACCTTGAATGAGCATCTTGAACCTGTAACGAGCATGAGGCAAGAGGCTTCTG 1134

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PA (ICOS-) ICOS CORP.
XX
PI Loughney K;
XX WPI; 2003-719642/68.
DR P-PEDB; AAE39535.
XX
XX Identifying a specific binding partner of phosphodiesterase 8 (PDE8)
PI useful for purifying PDE8 products in fluid samples comprises contacting
PI PDE8 with a compound and detecting binding.
XX
XX Example 3; Col 31-40; 37p; English.
XX
XX The invention relates to a method for identifying a specific binding
CC partner of phosphodiesterase 8 (PDE8). The method is useful for
CC identifying a specific binding partner of PDE8, which inhibits or
CC enhances activity of PDE8. The binding partners of PDE8 are useful for
CC purification, detection or quantification of PDE8 products in fluid and
CC tissue samples using immunological procedures. Modulators of PDE8
CC activity are useful in treating a wide range of diseases and
CC physiological conditions in which PDE8 activity is known to be involved.
CC The present sequence is human PDE8 A2 splice variant cDNA
XX
XX Sequence 4389 BP; 1315 A; 922 C; 920 G; 1232 T; 0 U; 0 Other;

Query Match 51.9%; Score 1871.8; DB 10; Length 4389;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
SQ
415 CTTCCCTCCGCGCCGCTTGGCCGCTCCGCTCCGATGAGATGACCTTC 474
2 CTTCCCTCCGCGCGCGCGCGCTCTTCCGCTCCGATGAGATGACCTTC 61
475 TAACAATGGAATGCTTCCGAAAGCTGACCGAGTGTTCCTCAAGCCCATTTGACGGA 534
62 TAAATATCGAGCTCTTCGAAAGCTGACCGAGTGTTCCTCAAGCCCATTTGACGGA 121
535 TGAAGAAGTGAAGGCTATCTTCTCCATGCCAGGATAGATGAATTTGTTCTGA 594
122 TGAAGAAGTGAAGGCTATCTTCTCCATGCCAGGATAGATGAATTTGTTCTGA 181
595 AAGTTAGTGAAGAGCTGTGGAAGAGTGTGTAAGAGAAACCAACAAAGCAAGA 654
182 AAGTTAGTGAAGAGCTGTGGAAGAGTGTGTAAGAGAAACCAACAAATCAGAAGA 241
655 TGAACCATCTCCCAAGAAAGTGAAGAGTGTGTAAGAGAAACCAACAAATCAGAAGA 714
242 TGAATCGCTCTTAAGAAAGTGAAGAGTGTGTAAGAGAAACCAACAAATCAGAAGA 301
715 CGAGCTGAAGAGCTATGATAGAGAGAGCTGGAACGCGCGGGGCAACCACTGCTCT 774
302 TGAATGAAGAGCTATGATAGAGAGAGCTGGAACGCGCGGGGCAACCACTGCTCT 361
775 CTATAGAGCTGAGAGCATCATCAGATAGAGCAACAAGCCGAGATTTGCACTGACTT 834
362 CTATAGAGCTGAGAGCATCATCAGATAGAGCAACAAGCCGAGATTTGCACTGACTT 421
835 CTTTGAAGAGTGAATTAATAGCTGTGTGTGTTCAATACCAACCGGAGTGAAGAGGCA 894
422 CTTTGAAGAGTGAATTAATAGCTGTGTGTGTTCAATACCAACCGGAGTGAAGAGGAA 481
895 ACCCGGCTCATCCCTGAGAGGCGCATCAACCGAGGATACCAACATCTGCTTAAGTGC 954
482 ACCCGGCTCATCCCTGAGAGGCGCATCAACCGAGGATACCAACATCTGCTTAAGTGC 541
955 CAAGCTGAGAGAGAGCTGT 1014
542 CAAGCTGAGAGAGAGAGCTGT 601
1015 TACTGAGCTGGAATCAGAAACCGCATTCAGTCTGTCTTTGCTTTGCTTTGCTTTGCTTTG 1074
602 TACTGAGCTGGAATCAGAAACCGCATTCAGTCTGTCTTTGCTTTGCTTTGCTTTGCTTTG 661

QY 1075 CATGAGAGCTGATTTGGCATCTTGAAGTGAACAGGACATGGGGCAAGAGCCCTTCG 1134
DB 662 AATTGTAATCTTGAATTTGATTTCTGAGCTGTATGTGGACATGGGGCAAGAGCCCTTCG 721
QY 1135 CTTGAGCATCAGAGAGTTGGCAACAGCAATCTTTGGGCTTCGTAGCAATACACCA 1194
DB 722 TCTTAGTACAGGAGGTTGGCAACAGCAATCTTTGGGCTTCGTAGCAATACATCA 781
QY 1195 GGTGAGAGTGTGTAAGGCTTCGCAACAGACCGAATGAAATGAACTTCTGATGAGAGT 1254
DB 782 GGTGAGAGTGTGTAAGGCTTCGCAACAGCAATGAAATGAACTTCTGATGAGAGT 841
QY 1255 ATCAAGAATATCTTGAATTAATAGTGGATGATCTCTCACTTGAACATCATGAT 1314
DB 842 ATCAAGAATATCTTGAATTAATAGTGGATGATCTCTCACTTGAACATCATGAT 901
QY 1315 ATATGCAAAAAATCTAGTGAACGCGGACCGCTTCGCTTCAGGTGACACCAAGAA 1374
DB 902 ATATGCAAAAAATCTAGTGAACGCGGATCGTTGTGCACTTTCCAGGTGACATAGAA 961
QY 1375 CAAGAGCTGTACTGCGACCTGTTGACATTTGGGAGGAGAAAGGAGGAGCCATCTT 1434
DB 962 CAAGAGCTGTACTGCGACCTTGTGATTTGAGAGAGAAAGAAAGAAAGAAAGCTGTCTT 1021
QY 1435 CAAGAAGACCAAGAGATCAGATTTTCCATTGAGAAAGGATGCTGTCAAGTGGCAAG 1494
DB 1022 CAAGAAGACCAAGAGATGATGATTTTCAATTGAGAAAGGATGCTGTGCAAGTGGCAAG 1081
QY 1495 AACAGCGAAGTCTTGAACATTTCCGATGCTTACGCGGACCTTCGCTTTAACAGGAGT 1554
DB 1082 AACAGCGAAGTCTTGAACATTTCCAGATGCTTATGACACCAAGCTTTAACAGGAGT 1141
QY 1555 GACCTGTACACAGGCTACACCAAGAGAAATCTGTGTATGCCCCAATGAGGCGGAG 1614
DB 1142 AGACTTGTACACAGGCTACACCAAGGAAACATCTGTGATGCCATGTCAGGCGGAG 1201
QY 1615 CAGCGTGAATGGCGGTGAGAGATGTAACAAGATCAGCGGTAGCGCTTCTCAAGAC 1674
DB 1202 CAGCGTGAATGGGT 1261
QY 1675 AGACGAGAACCACTTCAAGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1734
DB 1262 AGATGAGAACCACTTCAAGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1321
QY 1735 CATGTACCAAGATCCGCGCTCAGAAATGATCTACAGGCTTACAGGAGAAAGCTTTC 1794
DB 1322 TATGTATGATGAATTTGCACTCAGAGTGAATTTACGCGGTAAAGATGAGAAAGCTGTC 1381
QY 1795 CTACCAAGCATCTGCACTCCAGAGAGTGGCAAGGCTCAGTGCCTTCAACTACAGC 1854
DB 1382 CTACCAAGCATCTGCTTCAAGAGAGTGGCAAGGCTCAGTGCCTTCAACTACAGC 1441
QY 1855 ACGCATCTGCGGGACATGAGCTATTTCACTTTGACATTTGCTTTTGAAGACATGTG 1914
DB 1442 GCGTCTGCAAGAAATTTGAATTAATTCACCTTGAACATTTGCTTTTGAAGACATGTG 1501
QY 1915 GCGTGGAGTCTTTGTCTACATGATTCATCGGCTTTGAGGACATCTGTTTGAACCTTGA 1974
DB 1502 GCGTGGAGTCTTTGTCTACATGATTCATCGGCTTTGAGGACATCTGTTTGAACCTTGA 1561
QY 1975 AAAATGTGCGGTTTTATCATGTCTGTGAAGAAAGAACTATGCGGCGGTTCTTACCAAA 2034
DB 1562 AAAATGTGCGGTTTTATCATGTCTGTGAAGAAAGAACTATGCGGCGGTTCTTACCAAA 1621
QY 2035 CTGAAAGCATCAGTCAAGTGGGACACTGTGATGTATGCAATCTTCAAAACCAATGTG 2094
DB 1622 CTGAAAGCATCAGTCAAGTGGGACACTGTGATGTATGCAATCTTCAAAACCAATGTG 1681
QY 2095 CCTCTTCAACAACCTCGAGCGCAAGGCTGTCTAATGCGGTCTGTGTGCTTGTGACTGAG 2154
DB 1682 GCTTTTCAACAACCTTGTGCGCAAGGACTGTCTAATGCGGTCTGTGTGCTTGTGACTGAG 1741
QY 2155 CCAAGGGGCTTCAAGTAAACAGCTACCTGCAAGAGTTCACACCCCTGTGGGCGCTGTA 2214

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Db      1742  CCACAGGGGCTTCACTAACAGCTACCTGAGAGTTCACCACTCTGCGCCCTCTCTCTA 1801
QY      2215  CTCGACCTTCCACCATGAGACAACCACTTCTCCAGACGCTGTCATCTTCAAGCTGGA 2274
Db      1802  CTCGACCTTCCACCATGAGACAACCACTTCTCCAGACGCTGTCATCTTCAAGTGA 1861
QY      2275  AGGGGCAATATCTTCTCCACCTGAGCTCCAGCGATACGAGCAGCTGCTGAGATCAT 2334
Db      1862  AGGGGCAATATCTTCTCCACCTGAGCTCCAGCGATACGAGCAGCTGCTGAGATCAT 1921
QY      2335  CCGCAAGCATCATATGCGACCACTGCGCCCTATATCTTTGGAGACAGAGATGGA 2394
Db      1922  CCGCAAGCATCATATGCGACCACTGCGCCCTATATCTTTGGAGACAGAGATGGA 1981
QY      2395  GAGAGATGATACAGACAGGCTGCGTGAACCTCAACAACGATCCATCGAGCCGTCTAT 2454
Db      1982  AGAGATGATACAGACAGGCTGCGTGAACCTCAACAACGATCCATCGAGCCGTCTAT 2041
QY      2455  CGGCTTGATGATGATGCTGCTGATCTTGTGTGACCAACTATGSCCAAGTTACAA 2514
Db      2042  TGGTTTGATGATGATGCTGCTGATCTTGTGTGACCAACTATGSCCAAGTTACAA 2101
QY      2515  ATTGACAGCGAATGATATATATGCAAAATTTGGGCTGAGGGTGAAGATGAAGAAGT 2574
Db      2102  ATTGACAGCGAATGATATATATGCAAAATTTGGGCTGAGGGTGAAGATGAAGAAT 2161
QY      2575  GGGCATACAGCCCATCTTATGATGAGACAGACAGAGATGAAGTCCCTCAAGGCA 2634
Db      2162  GGGCATACAGCCCATCTTATGATGAGACAGACAGAGATGAAGTCCCTCAAGGCA 2221
QY      2635  GCTCGATTTCTACATGCTGTGCGCATTCCTGCTATACCACTTGACGAGATCTCTCC 2694
Db      2222  GCTGCGTTCTACATGCGGTGCGCATTCCTGCTATACCACTTGACGAGATCTCTCC 2281
QY      2695  ACCCAGACAGCTCTGCTGAGGCTGCGAGGATTAACCTCAATCATGAGGAGAAAGTAT 2754
Db      2282  TCCCAAGGAGCCCTCTTCTGAAACATGACAGGATTAATCTCAGTGGAGAAAGTAT 2341
QY      2755  TGGCGGGGAGAGACAGCAATGATTTGAGGCCAGGCCCGCGGC 2801
Db      2342  TCGAGGGAGAGACATGCACTGAGATTTCATCCATCCGTGGCTC 2388

RESULT 14
AAA09590 standard; cDNA to mRNA; 2406 BP.
AC      AAA09590;
AC      AAA09590;
DT      29-JAN-2001 (first entry)
XX      Human phosphodiesterase 10 (PDE10) nucleotide sequence SEQ ID 2.
XX      Phosphodiesterase 10; PDE10; human; ss.
XX      Homo sapiens.
XX      JF2000224992-A.
XX      15-AUG-2000.
XX      11-MAY-1999; 99JF-00129343.
XX      30-NOV-1998; 98JF-00338861.
XX      (TANA ) TANABE SEIYAKU CO.
XX      WPI; 2000-605129/58.
XX      P-PSDB; AAB26854.
XX      Novel phosphodiesterase and its gene for research on complex mechanism of
PT      intracellular information transfer.

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XX      Claim 2; Page 16-19; 29pp; Japanese.
PS      Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
XX      proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful
CC      for research on the complex mechanism of intracellular information
CC      transfer. The invention includes a recombinant vector containing a PDE10
CC      gene, and a cell transformed with the vector. Sequences AAA09593-A09606
CC      represent PCR primers used in the isolation of the PDE10 polynucleotide
XX      sequences of the invention.
SQ      Sequence 2406 BP; 692 A; 551 C; 562 G; 601 T; 0 U; 0 Other;
Query Match      51.7%; Score 1864.2; DB 3; Length 2406;
Best Local Similarity 86.9%; Pred. No. 0; Mismatches 308; Indels 0; Gaps 0;
Matches 2049; Conservative 0;
QY      445  CTTGCGCTCCGACATGAGAAATGACCTCTAACATGCGAGTTGCTTCCGAGGCTGAC 504
Db      2  CTTGCGCTCCGACATGAGAAATGAGACCTTCTAATATGAGCTGCTTCCGAGGCTGAC 61
QY      505  CGAGTGTTCCTCAGCCCCAGTTTGAACGATGAAAAGGTGAAGGCTATCTTCTCTCA 564
Db      62  CGAGTGTTCCTCAGCCCCAGTTTGAACGATGAAAAGGTGAAGGCTATCTTCTCTCA 121
QY      565  TCCCGAGTATTAATGATGATTTGTTCTGAAAGTGTATGTGACAGACTGTGAAAAGTG 624
Db      122  CCCCAGGTATTAATGATGATTTGTTCTGAAAGTGTATGTGACAGACTGTGAAAAGTG 181
QY      625  GCTGAAGAGAAACCAACAAAGAAAGATGAAACCATCTCCCAAGAAAGTCAAGGATGA 684
Db      182  GCTGAAGAGAAAGAAACCAACCAATCAGAAATGATATAGTCTTGAAGAAAGTCAAGGATGA 241
QY      685  CCAGATACGAATATGACAGAGAGTGTGTACAGCTGAACAGCTACATGAGCAGGCTT 744
Db      242  CCAAGTACGAATATGACAGAGAGTGTGTATGATTAACATTAACAGCTATATGAACAACGCTT 301
QY      745  GGAACAGGCGGGGAGACAAACCACTGCTCTCTATAGCTCAACAGCATCATAGATAGC 804
Db      302  GGAACAGGAGAGAGACAAACCACTGCTCTCTATGACATGAGAGCATATTAATTAATAGC 361
QY      805  CACAAAAGCGACGAGATTTGACATGATCTCTCTGAGAGTGCATATATAGCTGTGTGT 864
Db      362  CACAAAAGCGAGATGATTTGACATGATTTCTCTGAGAGTGCATATATATAGCTGTGTGT 421
QY      865  GTTCATACCAACCGGATGAGAAAGCCCAACCCGCGCTCATTCCTGCAAGGCCCATTCAC 924
Db      422  ATTCAAGCCACCTGGGATTAAGAGAAACCCGCGCTCATTCCTGCGGCGCCATTCAC 481
QY      925  CCAAGGTACCACTTCTGCTGCTGAGGCAAGTCTAGAGAAAGCTGTGTGTAGAGA 984
Db      482  TCAAGGCAACACCTGCTGCTGCTGAGGCAAGTCTAGAGAAAGCTGTGTGTAGAGA 541
QY      985  TATCTTGGGATGAGAGATTTCTCTGAGATCTGAGCTGGAATCAGAAACCGCATTCGA 1044
Db      542  CATCTTGGAGATGAGAGATTTCTCTGAGATCTGAGCTGGAATCAGAAACCGCATTCGA 601
QY      1045  GTCTGTTCTTTGCTTGGCCCATTTGTCACTGCCATTGGAGACTTGATTTGCAATCTTGAAC 1104
Db      602  GTCTGTTCTTTGCTTGGCCCATTTGTCACTGCCATTGGAGACTTGATTTGCAATCTTGAAC 661
QY      1105  GTAAGGCACTGGGGCAAAAGGCTTGTGCTTCAAGCCATCAGAGAGTTGCAACAGCCAA 1164
Db      662  GTAAGGCACTGGGGCAAAAGGCTTGTGCTTCAAGCCATCAGAGAGTTGCAACAGCCAA 721
QY      1165  TCTTGCTTGGGCTTCCGTAGCAATACCAAGGTCAGAGTGTGTAGAGTCTCGCAACA 1224
Db      722  TCTTGCTTGGGCTTCCGTAGCAATACCAAGGTCAGAGTGTGTAGAGTCTCGCAACA 781
QY      1225  GACGAACTGAATGACTTCTCTACAGCATATCAAGCAATCTTTGATTAATAGTTGC 1284
Db      782  GACGAACTGAATGACTTCTCTACAGCATATCAAGCAATATTTGATTAATAGTTGC 841

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PT modulate phosphodiesterase11 activity.

XX Claim 4; Fig 4A; 158bp; English.

XX The present sequence encodes a human phosphodiesterase enzyme, designated
 CC PDE11A1. A second isoform, PDE11A2, also exists, which is believed to be
 CC a splice variant of PDE11A1. PDE11 sequences from mouse and rat are also
 CC disclosed. PDE11 is found in the striatum and corpus cavernosum. PDE11 is
 CC believed to catalyze the conversion of cGMP to GMP. As cGMP is the
 CC messenger in the male erectile process, inhibiting the activity of PDE11
 CC is likely to increase the concentration of cGMP and so enhance the male
 CC erectile process. The PDE11 enzymes are used in assays for identifying
 CC agents which can affect PDE11 activity or expression. They are also used
 CC to screen for agents useful in the treatment of sexual dysfunction. The
 CC identified agent can be used in a pharmaceutical compositions to treat a
 CC disease or condition associated with PDE11. A PDE11 gene or expression
 CC product can be used to prepare a medicament for the treatment or
 CC modulation of disturbances associated with a PDE11 imbalance. The gene or
 CC expression product can also be used to screen for modulators of PDE11
 CC activity or expression

SO Sequence 2554 BP; 743 A; 582 C; 592 G; 637 T; 0 U; 0 Other;

Query Match 51.5%; Score 1858.4; DB 3; Length 2554;

Best Local Similarity 86.8%; Pred. No. 0;

Matches 2045; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

QY 446 TTCGGCTCGACATGGAAGTGAACCTCTAACATGCGAGTGTCTCCGAAGCTGACC 505

DB 1 TTCGGCTCGACATGGAAGTGAACCTCTTAATATGCGAGCTCTCCGAAGCTGACC 60

QY 506 GAGTGTCTCTCAAGCCAGTTTGAAGATGAAGGAGTGAAGGCTATCTTCTTCAT 565

DB 61 GAGTGTCTCTCAAGCCAGTTTGAAGATGAAGGAGTGAAGGCTATCTTCTTCAC 120

QY 566 CCCGAGTATTAGATGATTTGTTTCTGAAAGTTTATGTCAGAGACTGTGAAAGTGG 625

DB 121 CCCGAGTATTAGATGATTTGTTTCTGAAAGTTTATGTCAGAGACTGTGAAAGTGG 180

QY 626 CTGAAGAGGAAACCAAGCAAGCAAGATGAACATCTCCAGAGAGTCAAGAGTAC 685

DB 181 CTGAAGAGGAAACCAAGCAAGATGAACATCTCCAGAGAGTCAAGAGTAC 240

QY 686 CAGGATACGAATATGAGGAGTGTGTATGAGCTGAGAGCTATACATAGAGACGCTTG 745

DB 241 CAGGATACGAATATGAGGAGTGTGTATGAGCTGAGAGCTATACATAGAGACGCTTG 300

QY 746 GACACGGGCGGGGCAACCACTGCTCTCTATGAGCTCAGAGCATCATCAGATAGCC 805

DB 301 GACACGGGCGGGGCAACCACTGCTCTCTATGAGCTCAGAGCATCATTAATAATAGCC 360

QY 806 ACAAAGCCGAGATTTGACCTGTACTTCTTGAGAGTGAATTAATACCTGTGTGG 865

DB 361 ACAAAGCCGAGATTTGACCTGTACTTCTTGAGAGTGAATTAATACCTGTGTGG 420

QY 866 TTCAATACCAACCGGAGTGAAGAGCCCAACCCGCTCATCCCTGAGGAGCCCATACC 925

DB 421 TTCAATACCAACCGGAGTGAAGAGCCCAACCCGCTCATCCCTGAGGAGCCCATACC 480

QY 926 CAGGAGTACCAACATCTCTGCTTACGTGGCAAGTCTTAGAAGACGTTTGTGTAGAGAT 985

DB 481 CAGGAGTACCAACATCTCTGCTTACGTGGCAAGTCTTAGAAGACGTTTGTGTAGAGAT 540

QY 986 ATCTTGGAGATGAGCATTTCTCGAGGTATCGGCTGGAATCAGGACCCGATCAG 1045

DB 541 ATCTTGGAGATGAGCATTTCTCGAGGTATCGGCTGGAATCAGGACCCGATCAG 600

QY 1046 TCTGTTCTTTGCTTGCATTTGTCACTGCAATGGAAGCTTGAATGCACTCTTGAAC 1105

DB 601 TCTGTTCTTTGCTTGCATTTGTCACTGCAATGGAAGCTTGAATGCACTCTTGAAC 660

QY 1106 TACAGGACCTGGGCAAGAGGCTTGTGCTCAGCAATCAGAGGTTTGAACAGCAAT 1165

DB 661 TATCGGCACTGGGGCAAGAAAGCTTCTGTCTTAGTACACGAGAGTTGCAACAGCAAT 720

QY 1166 CTTCCTGGGCTTCCGTAGCAATATACAGAGTGCAGGTGTGTAGAGTCTGCCAAACAG 1225

DB 721 CTTCCTGGGCTTCCGTAGCAATATACAGAGTGCAGGTGTGTAGAGTCTGCCAAACAG 780

QY 1226 ACCGAACTGAATGACTTCTCTACTGACAGTATCAAGAATATCTTGTATTAATAGTGGC 1285

DB 781 ACCGAACTGAATGACTTCTCTACTGACAGTATCAAGAATATCTTGTATTAATAGTGGC 840

QY 1286 ATAGACTCTTACTTGAACATCATGATATATGCAAAAAATCTAGTGAACGCCGACGC 1345

DB 841 ATAGACTCTTACTTGAACATCATGATATATGCAAAAAATCTAGTGAACGCCGACGC 900

QY 1346 TCGCGCTCTTCAAGTGAACCAAGAAACAGAGGCTGTACTCGAGCTGTGTAACAT 1405

DB 901 TCGCGCTCTTCAAGTGAACCAAGAAACAGAGGCTGTACTCGAGCTGTGTAACAT 960

QY 1406 GGGGAGGAGGAGGAGGAGGAGCCATCTTCAAGAAAGCAAGAGATCAGATTTTCCAT 1465

DB 961 GGGGAGGAGGAGGAGGAGGAGCCATCTTCAAGAAAGCAAGAGATCAGATTTTCCAT 1020

QY 1466 GAGAAAGGATGCTGTGTCAGTGCAGAGCAAGGCAAGTCTTGAACATTCGAGTGC 1525

DB 1021 GAGAAAGGATGCTGTGTCAGTGCAGAGCAAGGCAAGTCTTGAACATTCGAGTGC 1080

QY 1526 TACGGGACCTCGCTTTTACAGGAGGTGACCTGTACACAGGCTACACCAAGAGAAC 1585

DB 1081 TACGGGACCTCGCTTTTACAGGAGGTGACCTGTACACAGGCTACACCAAGAGAAC 1140

QY 1586 ATTCTGTATATCCCATATGTGACCGAGGACGAGTGTGGGTGGTGCATATGAGTAA 1645

DB 1141 ATTCTGTATATCCCATATGTGACCGAGGACGAGTGTGGGTGGTGCATATGAGTAA 1200

QY 1646 AAGATCAGCGGTAGCGCTTCTCAAGACAGACGAGAACATTTGATGTTTGTCTGTC 1705

DB 1201 AAGATCAGCGGTAGCGCTTCTCAAGACAGACGAGAACATTTGATGTTTGTCTGTC 1260

QY 1706 TTTCTGCACTGGCTTGCATGTGTGTAATGTATACACAGATCCGCACTCAGATGTC 1765

DB 1261 TTTCTGCACTGGCTTGCATGTGTGTAATGTATACACAGATCCGCACTCAGATGTC 1320

QY 1766 ATCTACAGGTTTACATGAGAGAGCTTCTTACACAGATCTGCACTCCGAGAGTGG 1825

DB 1321 ATCTACAGGTTTACATGAGAGAGCTTCTTACACAGATCTGCACTCCGAGAGTGG 1380

QY 1826 CAGGCTCATGCGCTTCAACCTTACAGAGCAGCATCTGCCGAGACATCGAGCTATTCC 1885

DB 1381 CAGGCTCATGCGCTTCAACCTTACAGAGCAGCATCTGCCGAGACATCGAGCTATTCC 1440

QY 1886 TTTGACATTTGCTCTTTCAGAGACATGTGGCTGGAGCTTTGTCTTACATGATCCATCG 1945

DB 1441 TTTGACATTTGCTCTTTCAGAGACATGTGGCTGGAGCTTTGTCTTACATGATCCATCG 1500

QY 1946 TCTTGTGGGACATCTCTGTTTGAATTTGAAAATTTGTGCGCTTTTATCATATCTGTGAAG 2005

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    |||||
Db 2341 TCCCACTCCGTGGCTC 2356
    |||||
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Search completed: January 12, 2006, 03:53:23
Job time : 2039 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 02:12:24 ; Search time 13496 Seconds
(without alignments)
12501.054 Million cell updates/sec

Title: US-10-618-252-14
Perfect score: 3606
Sequence: 1 acgcgtccgcctccatctg.....aatttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
3: gb_est3:*
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6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3066	85.0	3611	4 AK039249	AK039249 Mus muscu
2	1703.2	47.2	2340	11 DQ048769	DQ048769 Homo sapi
3	1596.6	44.3	2237	11 DQ048770	DQ048770 Pan trogl
4	797.8	22.1	820	8 CX241410	CX241410 NMA04348
5	759.2	21.1	836	8 CX562742	CX562742 UI-M-IBO-
6	755.2	20.9	772	6 CD805436	CD805436 UI-M-GMO-
7	752	20.9	755	6 CB249359	CB249359 UI-M-PCO-
8	722	20.0	736	6 CB245079	CB245079 UI-M-PCO-
9	720.8	20.0	861	6 CX238886	CX238886 NMA06506
10	690.2	19.1	702	6 CF182788	CF182788 UI-M-EYO-
11	681.4	18.9	683	7 CP913876	CP913876 B0955F07-
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18	605.8	16.8	815	7 CK597964	CK597964 AGENCOURT
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23	553	15.3	553	2 BE861486	BE861486 UI-M-API-
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25	537	14.9	676	5 BY723598	BY723598 BY723598
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27	528.4	14.7	782	1 AU120086	AU120086 AU120086
28	525.4	14.6	527	7 CN679364	CN679364 B0147F11-
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30	516	14.3	516	6 CA888663	CA888663 B0147F11-
31	512	14.2	512	6 CA560184	CA560184 K0268H06-
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33	509.6	14.1	517	5 BK527582	BK527582 BK527582
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45	463.6	12.9	687	8 DR000181	DR000181 TC115943

ALIGNMENTS

RESULT 1
AK039249
LOCUS
DEFINITION
Mus musculus adult male spinal cord cDNA, RIKEN full-length
enriched library, clone:A33007F15 product:phosphodiesterase 10A,
full insert sequence.

ACCESSION
AK039249
VERSION
AK039249.1 GI:26333148
KEYWORDS
HTC, CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
10349636
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
11042159
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

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AUTHORS
TITLE
JOURNAL
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3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komno, H., Akiyama, J., Nishii, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Iehli, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsui, J.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

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PUBMED
5
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
The FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3611)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haseizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirokane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, S., Kagawa, I., Kanda, M.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koyama, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
COMMENT Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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FEATURES
source

CDS

ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 3072; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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Qy 3285 GGAACATGTAATGAAGTCAAGTCAAGTCAAGGTGACAGAAATCCAACTGTTGATTAC 3344
Db 3208 GGAACATGTAATGAAGTCAAGTCAAGTCAAGGTGACAGAAATCCAACTGTTGATTAC 3267
Qy 3345 AGGTGACATACAGATATGCTCTTTCAAGTCTATCTGGGGGCAATAGAGTGTGCTCCA 3404
Db 3268 AGGTGACATACAGATATGCTCTTTCAAGTCTATCTGGGGGCAATAGAGTGTGCTCCA 3327
Qy 3405 CTCAAGAAAGAAATGATCTCTGCTCATCAAGGGGCAAGGGTACATCCAGGGCATGG 3464
Db 3328 CTCAAGAAAGAAATGATCTCTGCTCATCAAGGGGCAAGGGTACATCCAGGGCATGG 3387
Qy 3465 GGGAACTGAAGCTCTGACTTCAAAACCATGTCAAAAGATTAAAAACCTTCCCTCCCTC 3524
Db 3388 GGGAACTGAAGCTCTGACTTCAAAACCATGTCAAAAGATTAAAAACCTTCCCTCCCTC 3447
Qy 3525 ACTGTAGCTTTGGGCAATCGCCCATTCCTTTATCAAAAGAAATTAAGTAAGGCAAT 3584
Db 3448 ACTGTAGCTTTGGGCAATCGCCCAATTCCTTTATCAAAAGAAATTAAGTAAGGCAAT 3507
Qy 3585 TAAATTTAAAAAATAAAAAA 3606
Db 3508 TAAATTTCTCCAGCAAGCAAA 3529

RESULT 2
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LOCUS DQ048769
DEFINITION Homo sapiens PDB10A gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ048769
VERSION DQ048769.1 GI:66901968
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

RESULT 3				
LOCUS	DQ048770			
DEFINITION	DQ048770	2237 bp	DNA	linear
	Pan troglodytes PDE10A gene, VIRTUAL TRANSCRIPT, partial sequence,			GSS 02-JUN-2005
	genomic survey sequence.			
ACCESSION	DQ048770			
VERSION	DQ048770.1	GI:665901969		
KEYWORDS	GSS.			
SOURCE	Pan troglodytes (chimpanzee)			
ORGANISM	Pan troglodytes			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Euarchonta; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Pan.			
REFERENCE	1 (bases 1 to 2237)			
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees (ex) Plos Biol. 3 (6), E170 (2005) 15869325			
JOURNAL	2 (bases 1 to 2237)			
PUBMED	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submissioin Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
REFERENCE				
AUTHORS				
TITLE				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of			

FEATURES	alignment.	Location/Qualifiers
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Best Local Similarity	79.6%; Pred. No. 0;	
Matches 1752;	Conservative 0; Mismatches 448; Indels 0; Gaps 0;	
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Qy	585 TTGTTCTGAAAGGTTAGTGCAGAGACTGTGAAAAAGTGGCTGAAGAGAAACAAACA	644
Db	98 TTGATCTGAAAGGTTAGTGCAGAGACAGTAGAGAAATGGCTGAAGAGAAACAAACA	157
Qy	645 AAGCAAAAGATGAACCATCTCCCAAGAGTCAAGAGTACAGAGATACGAATATGACAG	704
Db	158 AATGCAAG	217
Qy	705 GAGTCGTGACGAGCTGAACAGCTACATAGAGCAGCCCTGGAACAGGGGGGCAACC	764
Db	218 NNN	277
Qy	765 AACTGCTCTATAGAGCTCAGACGATCATCAGATATGCCAAGAGCCGACCGATTG	824
Db	278 NNN	337
Qy	825 CACTGTACTTCTCTGAGAGTGCATATATAGCTGTGTGTGTTCAATCAACCCGGAGTA	884
Db	338 CACTGTATTCTTCTGAGAGTGCATATATAGCTGTGTGATTAATCAACCTGGAGTAA	397
Qy	885 AAGAAAGCCAAACCCCGCTCATCCCTGCAAGGCCCATCAACCCAGGGTACCAATCTCG	944
Db	398 AAGAAAGCAAAACCCCGCTCATCCCTGTGGGCCCATCAACAGGGCAACACCGTCTTG	457
Qy	945 CCTAGTGGCCAAAGCTAGGAAGAGCTGTGTGTAGAGATATCTTGGGGATGAGCAT	1004
Db	458 CTTATGTGGCCAAAGCTAGGAAGAGCTGTGTGTAGAGATATCTTGGGGATGAGCAT	517
Qy	1005 TTCTCTGAGAGTACTGGCTGTGATCAGGAACCCGCATCAGTCTGTCTTGTCTTGCCA	1064
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Qy	1065 TTGTCACTGCCATTGGAGACTTGAATGGCAATCTTGAACCTGACAGGACTGGGGCAAG	1124
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Qy	1125 AAGCCTTCTGCTCAGCATCAGAGAGGTGGAACAGCAATCTTGGCTTGGCTTCCGAG	1184
Db	638 AAGCCTTCTGCTTATGATCAGAGAGGTGGAACAGCAATCTTGGCTTGGCTTCCGAG	697
Qy	1185 CAATACACCAAGGTGAGGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCC	1244
Db	698 CAATACATAGGTGAGGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCC	757
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Qy	1305 AACTATGATATATGCAAAATCTAGGAAGCCGACGCTGCGCTCTTCCAGGTGG	1364
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Db      878  ACCATAGAACAGAGATTATATGACCTTTTGTATTTGAGAGAGAAAAAGAGAA 937
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Db      998  AAGTAGCAAGAAACAGGGGAAGTCTGAACATTTCCAGATGCTTATGAGACCCACGCTTTA 1057
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Db      1058  ACAGNNNNNNNNCTTGTATACAGAGCTACACCAAGGGAACATCTGTGTGATGCCATACG 1117
Oy      1605  TGAGCCGAGAGCGCTGATTTGGCGTGTGTGATGAGTGAACAGATACAGCGGTAGCGCT 1664
Db      1118  TCAGCCGAGAGCGCTGATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1177
Oy      1665  TCTCCAGACAGACGAGAACTTCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1724
Db      1178  TCTTAAACAGATGAAAACTTCAAAATGTTTGCCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1237
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Db      1298  AAAAGCTGTCTTACCAATAGCATTTTGTACTTCCGAAAGATGGGAAAGGCTCATGCAATTC 1357
Oy      1845  ACCTACCAAGCAGCATCTGCGCGGACATGAGCTATTCACATTTTGAATTTGTCTTTTGG 1904
Db      1358  CCGTCCCGGTGGTCTGTGCAAAAGAAATGANNNTTCCACTTGAACATTTGTCTTTTGG 1417
Oy      1905  AGAATGTGTGCTGTGGATCTTTTGTCTATCATATCATGCGTCTTGTGGACATCTGTT 1964
Db      1418  AAAACATGTGTGCTGGAATTTTGTCTATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1477
Oy      1965  TTGAAGCTTGAAGAAATTTGTGCGTCTTATCATGTGTGAAGAAACATATGGCGGGTTC 2024
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Db      1538  CTTTATCAACATGGAAGATGAGTCAAGTGTGGCACTGTCATGTATGTCATCTTCAA 1597
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Db      1658  ATGAGCTTGAAGCAAGGGGCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1717
Oy      2205  CGGCGCTTACTCACTTCAACATGAGAGCAACCACTTCTCCAGAGCGGTGTCCATCC 2264
Db      1718  CGGCTCTTACTCACTTCAACATGAGAGCAACCACTTCTCCAGAGCGGTGTCCATCC 1777
Oy      2285  TTCAAGCTGGAAGGGCAATATCTTCTCAACCTTGAAGTCCAGCGAGTACAGAGCGTGC 2324
Db      1778  TCCAGTTGGAAGGGCAATATCTTCTTACTTGAAGTCCAGTGAATATGAGCGGTGC 1837
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Db      1838  TTGAGATATCCGCAAGCAATCATTTGCAACAGACTTGTCTTAACTTTGGGAACAGGA 1897
Oy      2385  AGCAGTTGGAAGAGATGTACAGAGAGGGTGTGTAACCTTCAACCAAGTCCCATCAG 2444
Db      1898  AGCAGTTGGAAGAGATGTACAGAGAGGGATCATTAACCTTAAATATCAATCACTAAG 1957
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Db      1958  ACCGTGTATGAGGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2017

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Oy      2505  CAGTTACAAATTGACAGCAATGATATATATGCAATTCGTGGCTGAGGGTATGAGA 2564
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Oy      2565  TGAAGAGCTGGGCAATACAGCCCATTTCTATATGAGACAGACAGCAAGCAATGAAATGCC 2624
Db      2078  TGAAGAAATTTGGAAATACAGCCTATTCTNNNNGAAGACAGANANNNGAAGATGAATGCC 2137
Oy      2625  CTCAGAGGCACTGGGATTTCTACAAATGCTGTGGCATTCCTGCTATACCACTTGAAGC 2684
Db      2138  CCCANNNNNNCTTGGGTTCTTACATATGCGTGGCATTTCTGTGCTATACCACTTACC 2197
Oy      2685  AGATCTCCCAACCAAGAGCCTGTGCTGAAGGCGCTGAG 2724
Db      2198  AGATCTCTCCCTCCACGAGGCTCTTCTGAAAGCATGAG 2237

RESULT 4
CX241410
LOCUS
DEFINITION
  Mus musculus Lateral Ventricle Wall C57BL/6 adult Mus
ACCESSION
  CX241410
VERSION
  CX241410.1 GI:56896702
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridae; Muridae; Mus.
REFERENCE
  1 (bases 1 to 820)
  Williams, C., Wita, W., Wikstrom, L., Lundberg, J. and Friisen, J.
  Expressed sequence tags of cDNA clones from Mus Musculus Lateral
  Ventricle Wall
  Unpublished (2005)
  Contact: Erlendsson, R.
  Target Identification
  NeuroNova AB
  Flskartorpsvagen 15A-D, S-11433 Stockholm, Sweden
  Tel: +46 8 786 0915
  Fax: +46 8 786 0911
  Email: rikard.erlndsson@neuronova.com
  Seq primer: M13FWD.

FEATURES
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                Site_2: EcoRV; An oligo(dT) primed library was constructed
                in pCMVSPORT6 from RNA isolated from lateral ventricle
                wall tissue of adult male and female mice."

ORIGIN
Query Match      22.1%; Score 797.8; DB 8; Length 820;
Best Local Similarity 99.0%; Pred. No. 2.1e-189;
Matches 813; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

Oy      2753  ATTGCGGGGGAAGAGACAGCATGTGATTTCAAGGCCAGGCGCGGCTTGAAGAGAGC 2812
Db      1      ATTGCGGGGGAAGAGACAGCATGTGATTTCAAGGCCAGGCGCGGCTTGAAGAGAGC 60
Oy      2813  ACACTTGAAGAGCTGAACGTGAAGATTGAAGACTGATCTGAAGTGAAGTCTGATGTCT 2872

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QY 1203 TGTGTAGAGTCTCGCCAAACAGACCGAATGATCTTCTACTCGACGTATCAAGA 1262
 Db 491 TGTGTAGAGTCTCGCCAAACAGACCGAATGATCTTCTACTCGACGTATCAAGA 550
 QY 1263 CATCTTGTGATTAACATGTTGCGATAGACTCTCTACTTGAACAATCATGATATATGCAA 1322
 Db 551 CATCTTGTGATTAACATGTTGCGATAGACTCTCTACTTGAACAATCATGATATATGCAA 610
 QY 1323 AAAATCTGTGTAACGCCGACCGCTGGGCTCTTCCAGGTGAGCCAAAGAACAGAGGAGC 1382
 Db 611 AAAATCTGTGTAACGCCGACCGCTGGGCTCTTCCAGGTGAGCCAAAGAACAGAGGAGC 670
 QY 1383 TGTACTCGGACCTGTTTGAATTTGGGAGAGAGAGAGGAGGAGG-AGGCCATCTTCAAGAG 1441
 Db 671 TGTACTCGGACCTGTTTGAATTTGGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 730
 QY 1442 ACCAAGAGATCAATTTTCCATTTGAGAAAGGAGATTCTGTCAAGTGCGAAGAACAGGC 1501
 Db 731 ACCAAGAGATCAATTTTCCATTTGAGAAAGGAGATTCTGTCAAGTGCGAAGAACAGGC 790
 QY 1502 GAAGCTTGAACATTCGCGATGCGGAGCGGACCCCTCGCTTTAAACA 1547
 Db 791 GAAGCTTGAACATTCGCGATGCGGAGCGGACCCCTCGCTTTAAACA 836

RESULT 6
 CD805436 772 bp mRNA linear EST 15-JUL-2003
 DEFINITION UT-M-GW0-cl-j-04-0-0-UT.r1 NIH_BMAP_GW0 Mus musculus cDNA clone

IMAGE:30541947 5', mRNA sequence.
 CD805436
 VERSION CD805436.1 GI:32464262
 KEYWORDS EST

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 JOURNAL Sciurionath; Muridae; Muridae; Murinae; Mus.
 COMMENT 1 (bases 1 to 772)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyx-5.
 Location/Qualifiers
 1. 772

FEATURES
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 /tissue_type="whole eye"
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 /note="Organ: Eye; Vector: pyx-Asc; Site: 1: EcoR I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pyx-Asc vector. The library tag

sequence located between the Not I site and the polyA tail
 is CTGCGTCTC. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 20.9%; Score 755.2; DB 6; Length 772;
 Best Local Similarity 99.0%; Pred. No. 1.2e-178;
 Matches 757; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 660 CATCTCCCAAGAGTCAAGAGTCAAGATACGAATATGCAAGAGTCTGTACAGC 719
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 Db 61 TGAACGCTACATAGAGCAGCGGCTTGACACGGGCGGGGACACCACTGCTCTATG 120
 QY 780 AGCTCAGAGATCATCAGATAGCCACAAAAGCCGAGATTGCACTGTACTCTTG 839
 Db 121 AGCTCAGAGATCATCAGATAGCCACAAAAGCCGAGATTGCACTGTACTCTTG 180
 QY 840 GAGAGTGCATATATAGCTGTGTGTTCATACCAACCCGGATGAGAGAGCCACCC 899
 Db 181 GAGAGTGCATATATAGCTGTGTGTTCATACCAACCCGGATGAGAGAGCCACCC 240
 QY 900 GGCTCATCTCTGCAAGGCGCCATCACCCAGGGTACACATCTTGCCTACGTGGCAAGT 959
 Db 241 GGCTCATCTCTGCAAGGCGCCATCACCCAGGGTACACATCTTGCCTACGTGGCAAGT 300
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 Db 301 CTAGGAAGACGTTGTGTAGAGATATCTTGGGATGAGAGATTTCTGAGGATCTG 360
 QY 1020 GCTTGGAATCAGAACCCGATCCAGTCTGTTCTTGTGCTTCCATTGTCACTGCGATTG 1079
 Db 361 GCTTGGAATCAGAACCCGATCCAGTCTGTTCTTGTGCTTCCATTGTCACTGCGATTG 420
 QY 1080 GAGACTTGATGGCATCTTGAACGTACAGGACACTGGGGCAAGAGGCTTTGCTTCA 1139
 Db 421 GAGACTTGATGGCATCTTGAACGTACAGGACACTGGGGCAAGAGGCTTTGCTTCA 480
 QY 1140 GCCATCAGAGGTTGCAACAGCAATCTTGTGGGCTTCGGTAGCAATACCAAGGTGC 1199
 Db 481 GCCATCAGAGGTTGCAACAGCAATCTTGTGGGCTTCGGTAGCAATACCAAGGTGC 540
 QY 1200 AGTGTGTAGAGTCTCGCCAAACAGACCGAATGATGATCTTCTACTCGACGTATCA 1259
 Db 541 AGTGTGTAGAGTCTCGCCAAACAGACCGAATGATGATCTTCTACTCGACGTATCA 600
 QY 1260 AGACATCTTGTGATTAACATGTTGCGCATAGACTCTTAAGTGAACATCATGATATG 1319
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 QY 1320 CAAAAAATCTAGTAACGCCGACCGCTGGGCTCTTCCAGGTGAGCCAAAGAACAGG 1379
 Db 661 CAAAAAATCTAGTAACGCCGACCGCTGGGCTCTTCCAGGTGAGCCAAAGAACAGG 720
 QY 1380 AGCTGTACTCGACCTGTTTGAATTTGGGAGAGAGAGAGAGGAGGAG 1424
 Db 721 AGCTGTACTCGACCTGTTTGAATTTGGGAGAGAGAGAGAGAGAGAGAG 765

RESULT 7
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 DEFINITION UT-M-FC0-byt-j-21-0-0-UT.r1 NIH_BMAP_FC0 Mus musculus cDNA clone
 IMAGE:5720180 5', mRNA sequence.
 ACCESSION CB249359
 VERSION CB249359.1 GI:28388695
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 755)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cga@b-remail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers
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 /note="Organ: brain; Vector: pyx-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pyx-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is TAGAGAGCC. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP). 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
 Query Match 20.9%; Score 752; DB 6; Length 755;
 Best Local Similarity 99.7%; Pred. No. 7.4e-178;
 Matches 752; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 2 GTTTGACGATGAAAGGTGAAGCCCTATCTTCTCCATCCCGAGTATTGATGAAT 61
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 Db 585 TTGTTCTGAAAGTGTAGTGAAGAGCTGTGAAAAGTGGCTGAAGAGAAAACACA 644
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 Db 645 AAGCAAAAGATGAACATCTCCCAAGAGAGTCAAGATACGATATATGACAG 704
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 122 AAGCAAAAGATGAACATCTCCCAAGAGAGTCAAGATACGATATATGACAG 181
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 Db 705 GAGTCGTGTAAGAGCTGAACAGTACATAGAGAGCCCTTGAGACACGGCGGGGACAAC 764
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 182 GAGTCGTGTAAGAGCTGAACAGTACATAGAGAGCCCTTGAGACACGGCGGGGACAAC 241
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 Db 765 ACCTGCTCCCTTATGAGCTCAGAGCATCATCGAGATAGCAAAAGCGAGGATTTG 824
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 242 ACCTGCTCCCTTATGAGCTCAGAGCATCATCGAGATAGCAAAAGCGAGGATTTG 301
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QY 825 CACTGTACTCTTCTGAGAGTGAATATATAGCTGTGTGTTCATATACACCCGGATGA 884
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 QY 1065 TTGTACTGCTCATTTGAGAGCTTGTATGAGCTTGTAACTGTACAGGACTGGGGCAAG 1124
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 Db 542 TTGTACTGCTCATTTGAGAGCTTGTATGAGCTTGTAACTGTACAGGACTGGGGCAAG 601
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 QY 1125 AGGCTTGTGCTTCCATCCCATCAAGAGCTTGTACAAAGCCCAATCTTCTGCTTCCCA 1184
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 Db 602 AGGCTTGTGCTTCCATCCCATCAAGAGCTTGTACAAAGCCCAATCTTCTGCTTCCCA 661
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 QY 1185 CAATACACAGGTGAGAGTGTAGAGGCTGCGCAACAGACCAACTGATGACTTCC 1244
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 Db 662 CAATACACAGGTGAGAGTGTAGAGGCTGCGCAACAGACCAACTGATGACTTCC 721
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 QY 1245 TACTGACGTATCAAGAATCTTGTATGATCAT 1278
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 Db 722 TACTGACGTATCAAGAATCTTGTATGATCAT 755
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RESULT 8
 CB245079 736 bp mRNA linear EST 09-JUL-2003
 LOCUS
 DEFINITION
 IMAGE:6833690 5', mRNA sequence.
 ACCESSION
 CB245079 GI:28366723
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 736)
 NIH-MGC http://mgc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT Robert Strausberg, Ph.D.
 Email: cga@b-remail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
 http://image.llnl.gov
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pyx-5.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6833690"
 /issue_type="whole brain"
 /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_1ib="NIH_BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I. The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chirn, Ph.D., Program coordinator."

20.0%; Score 722; DB 6; Length 736;

Best Local Similarity 99.6%; Pred. No. 2.7e-170;

Matches 722; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 2759 GGGGAGAGACAGCAATGTGATTTCAAGCCCGGCCCTTAGCAAGCACACT 2818
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Db 12 GGGGAGAGACAGCAATGTGATTTCAAGCCCGGCCCTTAGCAAGCACACT 71
    |||||
QY 2819 GAGAGCTGAACGTGAAGTTGAAGACTGATCTGAAGTGAAGTCTGATGTCGCCAG 2878
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Db 72 GAGAGCTGAACGTGAAGTTGAAGACTGATCTGAAGTGAAGTCTGATGTCGCCAG 131
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QY 2879 CAACCGACTCAACTGCTTGTGTGACTTGTCTTTTGTTCAGAGGGGTGAACCC 2938
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Db 132 CAACCGACTCAACTGCTTGTGTGACTTGTCTTTTGTTCAGAGGGGTGAACCC 191
    |||||
QY 2939 CTGTCAAGAGGTACCGTGTGATATTCATGTGAAGCAAGCACTCCCTGTCGCCACAC 2998
    |||||
Db 192 CTGTCAAGAGGTACCGTGTGATATTCATGTGAAGCAAGCACTCCCTGTCGCCACAC 251
    |||||
QY 2999 AACTCGGACAGTGAACAACCGGCTGCGGTTCAGAGTGGCTACTCCGTTGCGTC 3058
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Db 252 AACTCGGACAGTGAACAACCGGCTGCGGTTCAGAGTGGCTACTCCGTTGCGTC 311
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QY 3059 CACCTGACCTCCGATGCTATTTGCTCCAGGCGCAGCACTGCACTGTCTGAGGGGGCAG 3118
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Db 312 CACCTGACCTCCGATGCTATTTGCTCCAGGCGCAGCACTGCACTGTCTGAGGGGGCAG 371
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QY 3119 AGACCAAGAGAGGTTCTTGTGCTGATCTTCCATGAGGGTGTGCGCATTCCTGCTT 3178
    |||||
Db 372 AGACCAAGAGAGGTTCTTGTGCTGATCTTCCATGAGGGTGTGCGCATTCCTGCTT 431
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QY 3179 CTGTGCGCATGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3238
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Db 432 CTGTGCGCATGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 491
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QY 3239 AAGTTTACATGATGACCTTCTTATAGGTTAACTGAGTTTGTGCTTGGGACATGTAATG 3298
    |||||
Db 492 AAGTTTACATGATGACCTTCTTATAGGTTAACTGAGTTTGTGCTTGGGACATGTAATG 551
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QY 3299 AAGGTCAAGTCAAGGTGACAGAAATCCAACTGTTGTTATTCAGGTGCACTACAG 3358
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Db 552 AAGGTCAAGTCAAGGTGACAGAAATCCAACTGTTGTTATTCAGGTGCACTACAG 611
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QY 3359 TATGCTCTTTAGTATCTGAGGGGACATAGTGAAGTCTGCTCACTGAGAAAGAGA 3418
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Db 612 TATGCTCTTTAGTATCTGAGGGGACATAGTGAAGTCTGCTCACTGAGAAAGAGA 671
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QY 3419 TACCTCTGCTCATTCAGGGGACACAGGGTACATCCAGGATCGGGGAATGAAAGCTC 3478
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Db 672 TACCTCTGCTCATTCAGGGGACACAGGGTACATCCAGGATCGGGGAATGAAAGCTC 731
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QY 3479 TCACCT 3483
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Db 732 TCACCT 736
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RESULT 9
CX238886 861 bp mRNA linear EST 29-DEC-2004
LOCUS NM006506 Mus Musculus lateral Ventricle wall C57BL/6 adult Mus
DEFINITION Musculus CDNA 5', mRNA sequence.

ACCESSION
CX238886
KEYWORDS
CX238886.1 GI:56894178
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 Williams,C., Witra,W., Wikstrom,L., Lundberg,J. and Priesen,J.
Expressed sequence tags of cDNA clones from Mus Musculus lateral
ventricle wall

JOURNAL
Unpublished (2005)
CONTACT: Erlendsson, R.
COMMENT Target Identification

NeuroNova AB
Fiskarörvägen 15A-D, S-11433 Stockholm, Sweden
Tel: +46 8 786 0915
Fax: +46 8 786 0911
Email: rikard.erlandsson@neuronova.com
Seq primer: M13FWD.

FEATURES
source
location/Qualifiers

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/sex="Male and Female"
/tissue_type="lateral Ventricle Wall"
/cell_type="Not applicable"
/dev_stage="Adult"
/lab_host="NeuroNova AB"
/clone_lib="Mus Musculus lateral Ventricle Wall C57BL/6
adult"
/note="Organ: Brain; Vector: pCMVport6; Site 1: NotI;
Site 2: EcorV; An oligo(dT) primed library was constructed
in pCMVport6 from RNA isolated from lateral ventricle
wall tissue of adult male and female mice."

ORIGIN

Query Match 20.0%; Score 720.8; DB 8; Length 861;

Best Local Similarity 98.6%; Pred. No. 5.6e-170;

Matches 759; Conservative 0; Mismatches 7; Indels 4; Gaps 3;

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QY 585 TTGTTTCTGAAAGTTTATGTCAGAGACTGTGAAAAGTGTGAAAGAGAAAACCAACA 644
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Db 156 TTGTTTCTGAAAGTTTATGTCAGAGACTGTGAAAAGTGTGAAAGAGAAAACCAACA 215
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QY 645 AAGCAAAAGATGAACATCTCCCAAGAAAGTCAGAGTACCAAGATACGAATATGCAAG 704
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Db 216 AAGCAAAAGATGAACATCTCCCAAGAAAGTCAGAGTACCAAGATACGAATATGCAAG 275
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QY 705 GAGTCGTGTAGAGTGAACAGCTACATAGAGCAGCGCTGGACACGGGCGGAGCAACC 764
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Db 276 GAGTCGTGTAGAGTGAACAGCTACATAGAGCAGCGCTGGACACGGGCGGAGCAACC 335
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QY 765 AACTGCTCTCTATAGAGTCAAGCAGCATCATCAGGATAGCCACAAAGCCGACGATTTG 824
    |||||
Db 336 AACTGCTCTCTATAGAGTCAAGCAGCATCATCAGGATAGCCACAAAGCCGACGATTTG 395
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QY 825 CACTGTACTCTCTTGAAGTGAAGTCAATATAGCTGTGTGTTCTTATACACCCCGGAGTGA 884
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Db 396 CACTGTACTCTCTTGAAGTGAAGTCAATATAGCTGTGTGTTCTTATACACCCCGGAGTGA 455
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885 AGAAGGCCAACCCCGCTATCCTCGAGGAGGCCATCAACCGGATACCATCTCTG 944
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945 CCTAGTGGCCAAATTTAGAGAGCTTTGGTATAGATATCTTTGGGATAGACCAT 1004
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516 CCTAGTGGCCAAATTTAGAGAGCTTTGGTATAGATATCTTTGGGATAGACCAT 575
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1005 TTCCTGAGGTACTGGCTGGAATCAGAAACCCGATCCAGTCTTTCTTTGCCCA 1064
576 TTCCTGAGGTACTGGCTGGAATCAGAAACCCGATCCAGTCTTTCTTTGCCCA 635
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1065 TTGTCACTCCATTGAGATCTTATTTGCAATCTTGAAGTATCAGGACATGAGGCAAG 1124
|||||
636 TTGTCACTCCATTGAGATCTTATTTGCAATCTTGAAGTATCAGGACATGAGGCAAG 695
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1125 AGGCTTTGCTCTGAGCCATCAGAGAGTTTGCAACAGCAATCTTTGGGCTTCCGTAG 1184
696 AGGCTTTGCTCTGAGCCATCAGAGAGTTTGCAACAGCAATCTTTGGGCTTCCGTAG 753
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1185 CAATACACAGAGTGGAGTGTGTAGAGTCTGCGCAAAAGAGACCAATGATGATCTCC 1244
754 CAATACACAGAGTGGAGTGTGTAGAGTCTGCGCAAAAGAGACCAATGATGATCTCC 812
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1245 TACTGACGTATCAAGACATCTTGTATATACATAGTTGCCATAGACTCT 1294
813 TACTGACGTATCAAGACATCTTGTATATACATAGTTGCCATAGACTCT 861

RESULT 10 702 bp mRNA linear EST 29-JUL-2003
CF182788
LOCUS UI-M-Eyo-bw7-p-12-0-UT-r1 NIH_BMAP_Eyo Mus musculus cDNA clone
DEFINITION IMAGE: 5705339 5', mRNA sequence.
CF182788
CF182788.1 GI:33314670

EST.
Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Dr. James Iain, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP).
Seq primer: pyx-5.
location/Qualifiers
1. 702
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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/clone="IMAGE: 5705339"
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/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH_BMAP_Eyo"
/note="Organ: Brain; Vector: pyx-Aagc, Site 1: Ecor I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with Ecor I adaptor, digested with Not I, and then
cloned directionally into pyx-Aagc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGGCGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 19.1%; Score 690.2; DB 6; Length 702;
Best Local Similarity 99.4%; Pred. No. 2,8e-162;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1983 GCGGTTTATCATATGCTGTGAGAAAGAACTATCGGCGGCTTCTTACCAACTGGAAC 2042
1 GCCGTTTATCATATGCTGTGAGAAAGAACTATCGGCGGCTTCTTACCAACTGGAAC 60
2043 ATGCAATCAGGTGGGACATGATATGATGATGATGATGATGATGATGATGATGATGAT 2102
61 ATGCAATCAGGTGGGACATGATATGATGATGATGATGATGATGATGATGATGATGAT 120
2103 CAGACTGAGCGGCAAGAGGCTGCTATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2162
121 CAGACTGAGCGGCAAGAGGCTGCTATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 180
2163 GCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
181 GCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
2223 CCACATGAGGCAACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2282
241 CCACATGAGGCAACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
2283 ATATCTTCTCCACCTGAGCTCGAGGAGTACGAGAGGCTGAGATGATGATGATGATGAT 2342
301 ATATCTTCTCCACCTGAGCTCGAGGAGTACGAGAGGCTGAGATGATGATGATGATGAT 360
2343 CCATATCGGCAACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2402
361 CCATATCGGCAACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
2403 ACCAGACAGGAGTGGTGAACCTCCACCAACGATCCATGAGACCGTGTATGAGCTTGA 2462
421 ACCAGACAGGAGTGGTGAACCTCCACCAACGATCCATGAGACCGTGTATGAGCTTGA 480
2463 TGATGACTGCTGTGATCTTTGCTGTGTGACCAAACTATGAGGCAATTTGACAG 2522
481 TGATGACTGCTGTGATCTTTGCTGTGTGACCAAACTATGAGGCAATTTGACAG 540
2523 CGAATGATATATATGCAAAATTTCTGGCTGAGGCTGATGATGATGATGATGATGATGAT 2582
541 CGAATGATATATATGCAAAATTTCTGGCTGAGGCTGATGATGATGATGATGATGATGAT 600
2583 AGCCCATTCCTATGATGAGACAGAGCAAGGAGATGAAGCTCTCAAGGCGAGCTGGAT 2642
601 AGCCCATTCCTATGATGAGACAGAGCAAGGAGATGAAGCTCTCAAGGCGAGCTGGAT 660
2643 TCTACATGCTGTGGCATTCCCTGCTATACCACT 2678
661 TCTACATGCTGTGGCATTCCCTGCTATACACTT 696

RESULT 11 683 bp mRNA linear EST 05-NOV-2003
CF913876
LOCUS B0955F07-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
DEFINITION musculus cDNA clone NIA:B0955F07 IMAGE:30477570 5', mRNA sequence.
ACCESSION CF913876

VERSION CF913876.1 GI:38185078
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 683)
 AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 TITLE Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
 PUBMED 11544199
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: B0955 row: F column: 07
 Seq primer: M13 Reverse
 High quality sequence stop: 683
 POLYA=No.
 FEATURES
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 /strain="C57BL/6J"
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 /dev_stage="Unfertilized Eggs"
 /lab_host="DH10B"
 /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (long 1)"
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). (PMID: 11544191). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dt) primer (Invitrogen): 5'-pGACATGCTTCATGATCGAGCGGCCCTTTT-3', treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

ORIGIN
 Query Match 18.9%; Score 681.4; DB 7; Length 683;
 Best Local Similarity 99.9%; Pred. No. 4.5e-160;
 Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1 AAGAGACCAAGAGATGATTTTCATTGGAAGGAGATTGCTCAAGTGCAGGA 1495
 Oy 1436 AAGAGACCAAGAGATGATTTTCATTGGAAGGAGATTGCTCAAGTGCAGGA 1495
 Db 1 AAGAGACCAAGAGATGATTTTCATTGGAAGGAGATTGCTCAAGTGCAGGA 60
 Oy 1496 ACAGCGCAAGTTTAACTTCCCGATCGCTACCGGACCCCTGTTTAAAGGAGAG 1555
 Db 61 ACAGCGCAAGTTTAACTTCCCGATCGCTACCGGACCCCTGTTTAAAGGAGAG 120
 Oy 1556 GACCTGTACACAGGCTACACAGAGAACTTGTGTATGCCCATAGTAGCGAGGC 1615

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 DEFINITION B0993E08-5 NIA Mouse Unfertilized Egg cDNA Library (long 1) Mus
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 ACCESSION CF916322
 VERSION CF916322.1 GI:38187524
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 681)
 AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
 TITLE Construction of long-transcript enriched cDNA libraries from
 submicrogram amounts of total RNAs by a universal PCR amplification
 method
 JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
 PUBMED 11544199
 COMMENT Contact: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: B0993 row: F column: 08
 Seq primer: M13 Reverse
 High quality sequence stop: 681
 POLYA=No.

Db 121 GACCTGTACACAGGCTACACAGAGAACTTGTGTATGCCCATAGTAGCGAGGAC 180
 Oy 1616 AGCGATTTGGCGTGTGACAGATGGTGAACAAGATCAGCGTAGGCGCTTCCAAAGCA 1675
 Db 181 AGCGATTTGGCGTGTGACAGATGGTGAACAAGATCAGCGTAGGCGCTTCCAAAGCA 240
 Oy 1676 GACGGAACAACCTTCAAGATGTTTGTCTCTTCTGCGCACTGCGCTTGCACTGTGCTAAC 1735
 Db 241 GACGGAACAACCTTCAAGATGTTTGTCTCTTCTGCGCACTGCGCTTGCACTGTGCTAAC 300
 Oy 1736 ATGTACACAGGATCCGCACTCAGATGATCTTACAGGTTTACATGAGAGACTTTCC 1795
 Db 301 ATGTACACAGGATCCGCACTCAGATGATCTTACAGGTTTACATGAGAGACTTTCC 360
 Oy 1796 TACACAGCATCTGCACCTCCGAGAGTGGCAAGGCCCTCAGCGCTTCAACTACCTACAGA 1855
 Db 361 TACACAGCATCTGCACCTCCGAGAGTGGCAAGGCCCTCAGCGCTTCAACTACCTACAGA 420
 Oy 1856 GCGATCTGCCGGGACATCGACTATTCCACTTGTGACATTTGATGATGATGATG 1915
 Db 421 GCGATCTGCCGGGACATCGACTATTCCACTTGTGACATTTGATGATGATGATG 480
 Oy 1916 CCGGATCTTTGTCTTACATGATTCATCGTCTTGTGGACATCTGTTTGAACCTTGA 1975
 Db 481 CCGGATCTTTGTCTTACATGATTCATCGTCTTGTGGACATCTGTTTGAACCTTGA 540
 Oy 1976 AATATGCGCGTTTATCATGCTGTGAAGAAAGATTCGCGCGGCTCTTACACAGCAAC 2035
 Db 541 AATATGCGCGTTTATCATGCTGTGAAGAAAGATTCGCGCGGCTCTTACACAGCAAC 600
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 Db 601 TGAAGCATGACATCGATGCGACACTGATGTATGCCATTAATCAACAACATGAGC 660

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 /clone="NIA:B093E08 IMAGE:30481207"
 /dev_stage="unfertilized Egg"
 /lab_host="DH10B"
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 /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):
 5'-pGACTGATCTAGATCGAGCGCCCTTTT-3',
 treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."

ORIGIN

Query Match 18.8%; Score 677.8; DB 7; Length 681;
 Best Local Similarity 99.7%; Pred. No. 3.7e-159;
 Matches 679; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1436 AAGAGACCAAGAGATGATGATTTTCATTGAGAGAGGATGCTGTCAGATGGCAAG 1495
 1 AAGAGACCAAGAGATGATGATTTTCATTGAGAGAGGATGCTGTCAGATGGCAAG 60

1496 ACAGGCGAAGTCTTGAACATTTCCGATGCTTACCGGACCTTGTCTTAAACAGGAGG 1555
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1556 GACCTGTACACAGGCTTACACAGAGAGAAATCTGTATGCGCACTAGGAGCGAGG 1615
 121 GACCTGTACACAGGCTTACACAGAGAGAAATCTGTATGCGCACTAGGAGCGAGG 180

1616 AGCGTATGCGGTGGTGCAGATGTGTAACAAGATCAGCGGTAGCGGCTTCTCAAGACA 1675
 181 AGCGTATGCGGTGGTGCAGATGTGTAACAAGATCAGCGGTAGCGGCTTCTCAAGACA 240

1676 GACGAGAACAACTTCAAGATGTTGCTGTTCTGCGCACTGCGCTTCACTGTGTAAC 1735
 241 GACGAGAACAACTTCAAGATGTTGCTGTTCTGCGCACTGCGCTTCACTGTGTAAC 300

1736 ATGTACCAACAGATCCGCCACTCAGATGATCTTACAGGGTTACCATGAGAGCTTTC 1795
 301 ATGTACCAACAGATCCGCCACTCAGATGATCTTACAGGGTTACCATGAGAGCTTTC 360

1796 TACACAGCATCTGCACCTCCGAGAGTGGACAGGCTTCACTGCGCTTCACTTACAGCA 1855
 361 TACACAGCATCTGCACCTCCGAGAGTGGACAGGCTTCACTGCGCTTCACTTACAGCA 420

1856 CGCATTCGCCGAGCATCGAGCTATTCACCTTGAACATTTGCTTTCGAGAAATGTGG 1915
 421 CGCATTCGCCGAGCATCGAGCTATTCACCTTGAACATTTGCTTTCGAGAAATGTGG 480

1916 CTTGGGATCTTTTGTCTACATGATCATCGGCTTGTGGGACATCTCTTTTGAACCTTGA 1975
 481 CTTGGGATCTTTTGTCTACATGATCATCGGCTTGTGGGACATCTCTTTTGAACCTTGA 540

QY 1976 AATTTGTCCTTTTATCATGTCGTGTAAGAAACTATGCGCGGTTCTTACCACAC 2035
 DB 541 AATTTGTCCTTTTATCATGTCGTGTAAGAAACTATGCGCGGTTCTTACCACAC 600

QY 2036 TGGAGCATGACATGACCGGTGGACACATGTCATGTCATTAACCTTCAAAACAAATGGC 2095
 DB 601 TGGAGCATGACATGACCGGTGGACACATGTCATGTCATTAACCTTCAAAACAAATGGC 660

QY 2096 CTCTTACAGACCTTCGAGCGC 2116
 DB 661 CTCTTACAGACCTTCGAGCGC 681

RESULT 13
 LOCUS BM230520/c 671 bp mRNA linear EST 07-JUN-2003
 DEFINITION musculus cDNA clone NIA:K0296G04 IMAGE:30053931 3', mRNA sequence.

ACCESSION
 VERSION BM230520
 KEYWORDS
 SOURCE

ORGANISM
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 671)
 Piao, Y., Ko, N.-T., Lim, M. K. and Ko, M. S. H.
 TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)

PUBMED 11544199

COMMENT On Dec 14, 2001 this sequence version replaced gi:17793762.

CONTACT: Dawood B. Dudekula
 Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@igsun.grc.nia.nih.gov
 Plate: K0296 row: G column: 04
 Seq primer: -21M13 Forward
 High quality sequence stop: 671
 POLY-A=Yes.

FEATURES

source

1..671
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="NIA:K0296G04 IMAGE:30053931"
 /issue_type="Unfertilized Egg"
 /lab_host="DH10B"
 /clone_1lb="NIA Mouse unfertilized Egg cDNA library (long)"
 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs (dt) Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen):
 5'-pGACTGATCTAGATCGAGCGCCCTTTT-3',
 treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes

and cloned into Sali/NciI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.5 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Query Match 18.6%; Score 671; DB 3; Length 671;
Best Local Similarity 100.0%; Pred. No. 1.9e-157; Mismatches 0; Indels 0; Gaps 0;
Matches 671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2878 GCAACCGACTCAACCTGCTTCTGTGACTCTCTCTTTTGTGTTTGAAGGGGTGAAAACCC 2937
671 GCAACCGACTCAACCTGCTTCTGTGACTCTCTCTTTTGTGTTTGAAGGGGTGAAAACCC 612

2938 CCTGTCAAGAGTACCGTGCATATTCATGTGAAGACAGCACTCCCTGCTTGGCCGACA 2997
611 CCTGTCAAGAGTACCGTGCATATTCATGTGAAGACAGCACTCCCTGCTTGGCCGACA 552

2998 CACCTCGGACAGTGAAGCAACCAAGGCTGCGGTGTGAGAGTGGGCTACTCCGAGCT 3057
551 CACCTCGGACAGTGAAGCAACCAAGGCTGCGGTGTGAGAGTGGGCTACTCCGAGCT 492

3058 CCACCTGACCTCCGATGCTATTTGCTCCAGGCGACACTGCTGTGAGAGGGGCGCA 3117
491 CCACCTGACCTCCGATGCTATTTGCTCCAGGCGACACTGCTGTGAGAGGGGCGCA 432

3118 GAGACCAAGAGAGTCTTCCCTGCACTCTCCCATGAGGGTGGCCAGTTCCCTGCT 3177
431 GAGACCAAGAGAGTCTTCCCTGCACTCTCCCATGAGGGTGGCCAGTTCCCTGCT 372

3178 TCTGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3237
371 TCTGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312

3238 GAAAGTTACATGACCTTCTTATAGTTAACTGAGTTTGGCTGGGACACATGTAT 3297
311 GAAAGTTACATGACCTTCTTATAGTTAACTGAGTTTGGCTGGGACACATGTAT 252

3298 GAAAGTCAAGTCCACAGGTGAAGAAATCCAACTGTTGATTAAGGTGCACTACAG 3357
251 GAAAGTCAAGTCCACAGGTGAAGAAATCCAACTGTTGATTAAGGTGCACTACAG 192

3358 GTAATCTCTTTCAGTCTATCTGGGGGCACTAGTGAAGTCTGCTCCTCCTCCTGAGGAAAGC 3417
191 GTAATCTCTTTCAGTCTATCTGGGGGCACTAGTGAAGTCTGCTCCTCCTCCTGAGGAAAGC 132

3418 ATACCTCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 3477
131 ATACCTCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 72

3478 CTGACTTCAAAACATGTCAAAAGATTAAACACCTCCCTCCTCCTCCTCCTGAGCCTTGC 3537
71 CTGACTTCAAAACATGTCAAAAGATTAAACACCTCCCTCCTCCTCCTCCTGAGCCTTGC 12

3538 GCAACTGGGCC 3548
11 GCAACTGGGCC 1

RESULT 14
CF725825 680 bp mRNA linear EST 09-OCT-2003
LOCUS CF725825 UI-M-G20-cjn-b-10-0-UI.r1 NIH_BMAP_G20 Mus musculus cDNA clone
DEFINITION IMAGE:30604737 5', mRNA sequence.
ACCESSION CF725825
VERSION CF725825.1 GI:37599993
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 680)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.

FEATURES

source

Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30604737"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_G20"
/note="Organ: Eye; Vector: PYX-Aac; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NciI and then cloned
directionally into PYX-Aac vector. The library tag
sequence located between the Not I site and the polyA tail
is TTAATGAAGT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 18.6%; Score 670.2; DB 6; Length 680;
Best Local Similarity 98.8%; Pred. No. 3e-157; Mismatches 8; Indels 0; Gaps 0;
Matches 672; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

677 AGCAGTACCAAGATACGAATATGCAAGGAGTCTGTGACAGCTGACACTTAAGAG 736
1 AGCAGTACCAAGATACGAATATGCAAGGAGTCTGTGACAGCTGACACTTAAGAG 60

737 CAGCGCTTGACACGGGCGGGGACCAACCACTGCTCTCTATAGCTACAGCAGCATATC 796
61 CAGCGCTTGACACGGGCGGGGACCAACCACTGCTCTCTATAGCTACAGCAGCATATC 120

797 AGGATGACCAAAAAGCCGAGGATTTGACATGTAATCTCTTGGAGAGTGCAATAATAGC 856
121 AGGATGACCAAAAAGCCGAGGATTTGACATGTAATCTCTTGGAGAGTGCAATAATAGC 180

857 CTGTGTGTTCATACCAACCGGAGTGAAGAGCCAAACCCGGCTCATCTCTGACGGG 916
181 CTGTGTGTTCATACCAACCGGAGTGAAGAGCCAAACCCGGCTCATCTCTGACGGG 240

917 CCCATCACCAAGGTTACCAACATCTCTGCTTACGTGGCAAGTCTAGAGAAGACCTTTGG 976
241 CCCATCACCAAGGTTACCAACATCTCTGCTTACGTGGCAAGTCTAGAGAAGACCTTTGG 300

977 GTAAGATATCTTGGGAGTGAAGGATTTCTCTGAGGATACAGGCTGGAATCAGAAAC 1036
301 GTAAGATATCTTGGGAGTGAAGGATTTCTCTGAGGATACAGGCTGGAATCAGAAAC 360

1037 CGCATTCAGTCTGTCTTGTGCTTGGCCCATGTGCACTGCGCATTTGAGACTTGAATTC 1096

Db 361 GCATCCAGTCTGTTCTTTCCTTCCCAATGTCACTGCCATTGGAGACTTGATTGGCATC 420
 Oy 1097 CTTGAACTGTACAGGCACTGGGGCAAGAAGGCTTCTGCTTCAGCCATCAGAGGTTTCA 1156
 Db 421 CTTGAACGTACAGGCACTGGGGCAAGAAGGCTTCTGCTTCAGCCATCAGAGGTTTCA 480
 Oy 1157 ACAGCCAATCTTGTGGGCTTCCTGAGCATACACAGGTGCAAGTGTATGAGGTCTC 1216
 Db 481 ACAGCAATCTTGTGGGCTTCCTGAGCATACACAGGTGCAAGTGTATGAGGTCTC 540
 Oy 1217 GCCAAGCAGACCGAAGTGAATCTTCTACTCGAGCATCAAGACATCTTGTATAC 1276
 Db 541 GCCAAGCAGACCGAAGTGAATCTTCTACTCGAGCATCAAGACATCTTGTATAC 600
 Oy 1277 ATAGTTGCATAGACTCTCTACTTGAACACATCATGATATATGCAAAAATCTAGTGAAC 1336
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 Oy 1337 GCCGACCGCTGCGGCTCTT 1356
 Db 661 GCCGACCGCTGCGGCTCTT 680

RESULT 15
 LOCUS CX241102 662 bp mRNA linear EST 29-DEC-2004
 DEFINITION NM003974 Mus Musculus lateral Ventricle Wall C57BL/6 adult Mus
 musculus cDNA 5', mRNA sequence.
 ACCESSION CX241102
 VERSION CX241102.1 GI:56896394
 KEYWORDS EST.
 SOURCE Mus musculus
 ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 662)
 Williams, C., Wirtz, W., Wikstrom, L., Lundberg, J. and Friese, J.
 Expressed sequence tags of cDNA clones from Mus Musculus lateral
 Ventricle Wall
 Unpublished (2005)
 JOURNAL CONTACT: Erlendsson, R.
 COMMENT Target Identification
 NeuroNova AB
 Piskarcorpavagen 15A-D, S-11433 Stockholm, Sweden
 Tel: +46 8 786 0915
 Fax: +46 8 786 0911
 Email: rikard.erlandsson@neuronova.com
 Seq primer: M13PMD.

FEATURES
 source
 1..662
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /sex="Male and Female"
 /tissue_type="Lateral Ventricle Wall"
 /cell_type="Not applicable"
 /dev_stage="Adult"
 /lab_host="Neuronova AB"
 /clone_lib="Mus Musculus lateral Ventricle Wall C57BL/6
 adult"
 /note="Organ: Brain; Vector: pCMVSPORT6; Site 1: NotI;
 Site 2: EcoRV; An oligo(dT) primed library was constructed
 in pCMVSPORT6 from RNA isolated from lateral ventricle
 wall tissue of adult male and female mice."

ORIGIN

Query Match 17.9%; Score 646.4; DB 8; Length 662;
 Best Local Similarity 99.7%; Pred. No. 3e-151; 1; Indels 1; Gaps 1;
 Matches 658; Conservative 0; Mismatches 1; Gaps 1;
 Oy 886 GGAAAGCCAAACCCGGCTATCCCTGCAAGGCCCATCACCAGGATACCAACATCTCTGC 945

Db 1 GGAAAGCCAAACCCGGCTATCCCTGCAAGGCCCATCACCAGGATACCAACATCTCTGC 60
 Oy 946 CTACGTGGCCAAAGTCTTAGAAGAAGTGTGTGTAGAGATATCTTGGGATAGACGATT 1005
 Db 61 CTACGTGGCCAAAGTCTTAGAAGAAGTGTGTGTAGAGATATCTTGGGATAGACGATT 120
 Oy 1006 TCTTCAGAGTACTGGCTCGAATCAGGAACCCGCAATCAGTCTGTCTTGGTGGCCAT 1065
 Db 121 TCTTCAGAGTACTGGCTCGAATCAGGAACCCGCAATCAGTCTGTCTTGGTGGCCAT 180
 Oy 1066 TGTCACTGCCAATGGAGACTTGAATGGCATCTTGAACCTGTACAGGCACTGGGGCAAGA 1125
 Db 181 TGTCACTGCCAATGGAGACTTGAATGGCATCTTGAACCTGTACAGGCACTGGGGCAAGA 240
 Oy 1126 GGCCTTCTGCTCAGCCATCAGAGGTTGCAACGCCAATCTTGGTGGCTTCCGTAGC 1185
 Db 241 GGCCTTCTGCTCAGCCATCAGAGGTTGCAACGCCAATCTTGGTGGCTTCCGTAGC 300
 Oy 1186 AATACACAGGTGCAAGGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCT 1245
 Db 301 AATACACAGGTGCAAGGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCT 360
 Oy 1246 ACTGACGATCAAGACATCTTGAATACATAGTTCATAGACTCTCTACTTGAACA 1305
 Db 361 ACTGACGATCAAGACATCTTGAATACATAGTTCATAGACTCTCTACTTGAACA 420
 Oy 1306 CATCATGATATATGCAAAAATCTAGTGAACGCCAGCGCTGCGCTTCTCAAGTGA 1365
 Db 421 CATCATGATATATGCAAAAATCTAGTGAACGCCAGCGCTGCGCTTCTCAAGTGA 480
 Oy 1366 CCACAAAGACAAAGAGCTGTACTCGAAGCTGTTTGAATTTGGGAGAGAAAGAGGGGA 1425
 Db 481 CCACAAAGACAAAGAGCTGTACTCGAAGCTGTTTGAATTTGGGAGAGAAAGAGGGGA 540
 Oy 1426 GCCCATCTTCAAGAAAGACCAAGAGATGATTTCCATTGAGAAAGGATGTGTCTCA 1485
 Db 541 GCCCATCTTCAAGAAAGACCAAGAGATGATTTCCATTGAGAAAGGATGTGTCTCA 600
 Oy 1486 AGTGGCAAGACA-GCCGAAGTCTTGAACATTCGCGATGCTTACCGGACCTCGCTTAA 1544
 Db 601 AGTGGCAAGACAAGGGCGGAAGTCTTGAACATTCGCGATGCTTACCGGACCTCGCTTAA 660

Search completed: January 12, 2006, 12:35:36
 Job time : 13505 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2006, 03:08:59 ; Search time 607 Seconds
(without alignments)
10559.946 Million cell updates/sec

Title: US-10-618-252-14

Perfect score: 3606
Sequence: 1 acgcgcgcgcctccatctg.....aatttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	1871.8	51.9	4389	2 US-08-951-648-3	Sequence 3, App1
2	1871.8	51.9	4389	3 US-09-174-437-3	Sequence 3, App1
3	1871.8	51.9	4389	3 US-09-686-055A-3	Sequence 3, App1
4	1787.4	49.6	3195	2 US-08-951-648-5	Sequence 5, App1
5	1787.4	49.6	3195	3 US-09-174-437-5	Sequence 5, App1
6	1787.4	49.6	3195	3 US-09-686-055A-5	Sequence 5, App1
7	1787.4	49.6	4381	3 US-09-420-190-2	Sequence 2, App1
8	1785	49.5	2298	2 US-08-951-648-1	Sequence 1, App1
9	1785	49.5	2298	3 US-09-174-437-1	Sequence 1, App1
10	1785	49.5	2298	3 US-09-686-055A-1	Sequence 3, App1
11	469.2	13.0	477	2 US-08-951-648-38	Sequence 38, App1
12	469.2	13.0	477	3 US-09-174-437-38	Sequence 38, App1
13	469.2	13.0	477	3 US-09-686-055A-38	Sequence 38, App1
14	333.8	9.3	404	2 US-08-951-648-33	Sequence 33, App1
15	333.8	9.3	404	3 US-09-174-437-33	Sequence 33, App1
16	333.8	9.3	404	3 US-09-686-055A-33	Sequence 33, App1
17	272.6	7.6	458	2 US-08-951-648-7	Sequence 7, App1
18	272.6	7.6	458	3 US-09-174-437-7	Sequence 7, App1
19	209.6	5.8	3044	2 US-07-872-644-7	Sequence 44, App1
20	209.6	5.8	3044	2 US-07-872-644-44	Sequence 44, App1
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27	209.6	5.8	3044	3 US-09-883-825-44	Sequence 44, App1
28	209.6	5.8	3044	6 PCT-US92-03222-44	Sequence 44, App1
29	209.6	5.8	4171	3 US-09-754-250-1	Sequence 1, App1
30	209.6	5.8	4171	3 US-10-094-989-1	Sequence 1, App1
31	209.6	5.8	4240	3 US-09-708-392-6	Sequence 373, App1
32	209.6	5.8	4240	3 US-09-949-016-373	Sequence 373, App1
33	201.6	5.6	1784	3 US-09-226-741-2	Sequence 2, App1
34	201.6	5.6	1784	3 US-09-595-514-2	Sequence 2, App1
35	192.8	5.3	3789	2 US-07-872-644-42	Sequence 42, App1
36	192.8	5.3	3789	2 US-08-297-494-42	Sequence 42, App1
37	192.8	5.3	3789	2 US-08-297-510-42	Sequence 42, App1
38	192.8	5.3	3789	2 US-08-479-532-42	Sequence 42, App1
39	192.8	5.3	3789	2 US-08-455-526-42	Sequence 42, App1
40	192.8	5.3	3789	2 US-08-455-525-42	Sequence 42, App1
41	192.8	5.3	3789	3 US-09-139-491-42	Sequence 42, App1
42	192.8	5.3	3789	3 US-09-883-825-42	Sequence 42, App1
43	192.8	5.3	3789	6 PCT-US92-03222-42	Sequence 42, App1
44	192.8	5.3	4131	2 US-07-872-644-38	Sequence 38, App1
45	192.8	5.3	4131	2 US-08-297-494-38	Sequence 38, App1

ALIGNMENTS

RESULT 1
US-08-951-648-3
Sequence 3, Application US/08951648

Patent No. 5932465

GENERAL INFORMATION:

APPLICANT: Loughney, Kate

TITLE OF INVENTION: Phosphodiesterase 8

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker, Sears Tower Suite 6300

CITY: Chicago

STATE: Illinois

COUNTRY: US

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/951,648

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/34038

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

SEQUENCE CHARACTERISTICS:

LENGTH: 4389 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 3..2411

US-08-951-648-3

Query Match 51.9%; Score 1871.8; DB 2; Length 4389;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0;

415 CTTCCCTGCGACCGTTTGCGCTTCCGATCGAATGAGATGACCCCTC 474
Db 2 CTTCCCTGCGCGCGCGCGCGCTGCTTTCCGCTCCGACATGGAAGATGACCTTC 61
475 TAACAATCGAAGTCTTCCGAAAGCTGACCGAGTGTCTTCCAGCCCCAGTTTGA 534
Db 62 TAAATATCGAGCTCTTCCGAAAGCTGACCGAGTGTCTTCCAGCCCCAGTTTGA 121
555 TGAAGAGTGAAGGCTATCTTCTCTCCATCCGAGATTAAGATGATTTGTTTCA 594
Db 122 TGAAGAGTGAAGGCTATCTTCTCTCCATCCGAGATTAAGATGATTTGTTTCA 181
595 AAGTTAGTGAAGAGCTGTGAAAAAGTGTGAAGAGAAAAACAACAAAGCAAGA 654
Db 182 AAGTTAGTGAAGAGAGAGTGAAGAAAAAGCTGAAGAGAAAGAAACAATAATCA 241
655 TGAACCATCTCCCAAGAAAGTGAAGAGTACCAAGATACGAATATGACAGAGT 714
Db 242 TGAATCGGCTCTTAAGAAAGTGAAGAGTACCAAGATACGAATATGACAGAG 301
715 CGAGCTGAACAGCTATATGAGACAGCGCTGGAACGCGCGGGGCAACCACTG 774
Db 302 TGAACCTAAACAGCTATATGAAACAAGTGAACAAGAGAGAAACAACAGCTA 361
775 CTATGAGCTCAGCAGCATCATCAGATAGAGTACCAAAAGCCGACGATTTGCA 834
Db 362 CTATGAGCTCAGCAGCATCATCAGATAGAGTACCAAAAGCCGATTTGCACT 421
835 CTTTGAAGTGAATATATAGCTGTGTGTGTATACCAACCCGAGATGAAGAG 894
Db 422 CTTTGAAGTGAATATATAGCTGTGTGTGTATACCAACCCGAGATGAAGAG 481
895 ACCCGGCTCATCCGTCAGAGGCGCATCACCGAGGTACCACTCTGCTTGA 954
Db 482 ACCCGGCTCATCCGTCAGAGGCGCATCACCGAGGTACCACTCTGCTTGA 541
955 CAAGCTCAGAAAGAGCTGTGTGTGTGTGTATCTTGGGAGTGAAGCATTTCT 1014
Db 542 CAAGCTCAGAAAGAGCTGTGTGTGTGTGTATCTTGGGAGTGAAGCATTTCT 601
1015 TACTGGCTGGAATCAGAAACCGCATTCAGTCTGTTCTTTGCTTGGCCATTT 1074
Db 602 TACTGGCTGGAATCAGAGGACTGTATCAGCTGTGTTCTTTGCTTGAACAT 661
1075 CATTGGAGACTTTGATTTGGATCTCTGAACTGTACAGGCACTGGGCAAGAG 1134
Db 662 AATTGGTACTTGAATTTGTATCTCGAGCTGTATCGGCACTGGGCAAGAG 721
1135 CCTCAGCATCAGAGAGTTGCAACAGCCAACTTGTCTTGGGCTTCCGTAGCA 1194
Db 722 TCTTAGTCAACAGAGAGTTGCAACAGCAAACTTGTCTTGGGCTTCCGTAG 781
1195 GGTGAGGTGTGTAGAGTCTGCGCAACAGACCGAATGAATGACTTCTTCA 1254
Db 782 GGTGAGGTGTGTAGAGAGCTTGGCAACAGACCAAAATGAATGACTTCTTCA 841
1255 ATCAAAGCATCTTGAATTAATAGTTGGCTAGACTCTCTCACTTGAACATGAT 1314
Db 842 ATCAAAGCATCTTGAATTAATAGTTGGCTAGACTCTCTCACTTGAACATGAT 901
1315 ATATCAAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTCAAGTGAACAA 1374
Db 902 ATATCAAAAAATCTAGTGAATGCCGATGTGTGTGCACTTTCCAGGTGAACA 961
1375 CAAGAGCTGTACTGCGACCTGTGTTGACATTTGGGAGAGAAAGAGGAGCC 1434
Db 962 CAAGAGCTGTACTGCGACCTTTTGATATGTGAGAGGAAAGGAAAGGAAAC 1021
1435 CAAGAGAGCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTGCA 1494
Db 1022 CAAGAGAGCAAGAGATTAAGATTTTCAATTTGAGAAAGGATTTGCTGTG 1081
1495 AACAGGCAAGCTTGAAACATTCGCCGATGCTACGCGGACCTCGCTTTAA 1554

1082 AACAGGCAAGCTTGAAACATTCGAGATGCTTATGACAGACCAAGCTTTAA 1141
Db 1555 GAGCTGTACACAGGCTACACCAAGAGAAATTTGTGTATATGCCAATGAGAG 1614
Db 1142 AGACTTTGACAGGCTACACCAAGGAAATCTTGTGATGCTTACGTCAGCG 1201
1615 CAGGCTGATTTGCGGTGTGAGATGATGTAACAAGATCAGCGGTAGCGCTTCCA 1674
Db 1202 CAGGCTGATTTGCGGTGTGAGATGATGTAACAAGATGATGCTTCTCAAA 1261
1675 AGACGAGAAACAATTTCAAGATGTTGTCTGTCTGCGCACTGCGCTTGA 1734
Db 1262 AGATGAAAAACAATTTCAAAATGTTTCCGCTTTTGTGCTTATGCTTAC 1321
1735 CATGTACACAGATCCGCCCTCAGAAATGATCTACAGGTTTACATGAGAA 1794
Db 1322 TATGTATCATGAAATTCGCCACTCAGAGTGAATTTACCGGTTACGATGA 1381
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Db 1682 GCTTTTCAACAATCTTGAAGGCCAAAGGCTCTTAAATTTGGTCTGTGCA 1741
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Db 2282 TCCCAACGAGGCTCTGTCTGAGAGGCTTCGACGGATTAACCTCAATCACTGGGAGAGATAT 2341
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RESULT 2
US-09-174-437-3
/ Sequence 3, Application US/09174437A
/ Patent No. 6133007
/ GENERAL INFORMATION:
/ APPLICANT: Loughney, Kate
/ TITLE OF INVENTION: Phosphodiesterase 8A
/ FILE REFERENCE: 27866/35047
/ CURRENT APPLICATION NUMBER: US/09/174,437A
/ EARLIER FILING DATE: 1998-10-16
/ EARLIER APPLICATION NUMBER: 08/951,648
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 4389
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3)..(2411)
US-09-174-437-3

Query Match 51.9%; Score 1871.8; DB 3; Length 4389;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;

QY 415 CTTCCCTCTTGCCACGCTTTGCGCTGCTCCCTTCCGCTCCGACATGGAAGATGACCTTC 474
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QY 475 TAAACATGCGAGTGTCTTCCGAAGGCTGACCGAGTGTTCCTGACGCCCACTTGAACGA 534
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Db 122 TGAAGAGTGAAGGCTATCTTCTCCATCCCGAGATTAAGATGATTTGTTCTGA 181
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Db 242 TGAATGGCTCCCTGAAGAGTCAAGAGTACCAAGATATGCAAGGAGTCCGTGA 301
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QY 775 CTATGAGCTCAGCAGCATCATCAGAGATGCCAAGAGCCGACGAGATTTGCACTGTATCTT 834
Db 362 CTATGAGCTCAGCAGCATCATTAATAATAGCCACAAAGCCGATGAGATTTGCACTGTATCTT 421
QY 835 CTTTGAAGATGCAATTAATAGCTGTGTGTTCATACACCCGGGATGAAGAGGCCA 894
Db 422 CTTTGAAGATGCAATTAATAGCTGTGTGTTCATACACCCGGGATGAAGAGGCCA 481

QY 895 ACCCGGCTCATCCCTGAGAGGCCCCCATGCCAGGGTACACACATCTGCTACAGTGGC 954
Db 482 ACCCGGCTCATCCCTGAGAGGCCCCCATGCCAGGGTACACACATCTGCTACAGTGGC 541
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QY 1015 TACTGGCTGGAATCAGAAACCCGATCCAGTCTGTCTTGTCTTGGCCCATTTGTCACTGC 1074
Db 602 TACTGGAAGTGAATCAGGAGCTCGATCCAGTCTGTCTTGTCTTGAACCAATTTGTCACTGC 661
QY 1075 CATTTGAGACTGATTTGGATCTCTTGAACCTGATCAGGACCTGGGGCAAGAGGCTTCTCG 1134
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QY 1135 CCTCAGCCATCAGAGAGTTGCAACAGCCAAATCTTGGGCTTCCGTGACAAATACCA 1194
Db 722 TCTTATGTCACAGAGAGTTGCAACAGCAAAATCTTGGGCTTCCGTGACAAATACCA 781
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QY 1615 CAGCGTATTTGCGGTGTCAGATGTTGAAACAAATCAAGTGCAGAGCTTCTTAAAC 1674
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QY 1675 AAGACGAAACACTTCAAGATTTTGTCTGTGCGGACTGGCTTGCATGTGCTAA 1734
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QY 1855 ACGCATCTGCGGAGATGAGCTATTTCACTTTGACATTTGCTTTGAGAAACATGTG 1914
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QY 1915 GCGTGGATCTTTGTATCATGATCCAGTCTTGTGGAACATCTCTGTTTGAACCTTGA 1974
Db 1502 GCGTGAATTTTGTCTATAGTTCATGAGTCTGTGGAACATCTCTGCTTGAAGCTTGA 1561

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QY 1975 AAAATTGCGGTTTATCATGCTGTGAGAGAACTATGCGGCGGTTCTTACACAA 2034
DB 1562 AAAATTGCTGTTTATATATGCTGTGAGAGAACTATGCGGCGGTTCTTACACAA 1621
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DB 1622 CTGGAAGCATGCGATCAGCGTGGCACTGTGATGTGCTATCTTCAAAACAATG 1681
QY 2095 CCTCTTCAAGACCTTCAGCGGCAAGGCGCTGTAATGGGTCTGTGCGCATGACTGGA 2154
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QY 2155 CCACAGGGGCTTCAGTAACAGTACCTGAGAAAGTTGACACACCCCGTGGCGGCTGTA 2214
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QY 2215 CTCCACTTCACATGAGAGCAACCACTTCTCCAGACGAGTGCATCTCTTCACTGGA 2274
DB 1802 CTCCACTTCACATGAGAGCAACCACTTCTCCAGACGAGTGCATCTCTTCACTGGA 1861
QY 2275 AGGGCAATATCTTCTCCACCTTGAAGTCCAGCGATACGACGAGTGTGGAATCAT 2334
DB 1862 AGGGCAATATCTTCTCCACCTTGAAGTCCAGCGATACGACGAGTGTGGAATCAT 1921
QY 2335 CCGCAAGCATCATGCGACCGACCTGCGCTTATCTTGGGAAACAGGAACAGTTGA 2394
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QY 2395 GAGAGTGAACAGAGAGGTCGCTGACCTCCACAAACGAGTCCATCGAGACGCTCAT 2454
DB 1982 AGAGATGAACAGAGAGGTCGCTGACCTCCACAAACGAGTCCATCGAGACGCTCAT 2041
QY 2455 CGGCTTGAATGATGATGCTGCTGATCTTGTGCTGTGACCAAACTATGGCCGTTACAA 2514
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RESULT 3

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US-09-686-055A-3
; Sequence 3, Application US/09686055A
; Patent No. 6566087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4389

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)..(2411)
US-09-686-055A-3
Query Match 51.9%; Score 1871.8; DB 3; Length 4389;
Beet Local Similarity 86.5%; Pred. No. 0;
Matches 2065; Conservative 0; Mismatches 322; Indels 0; Gaps 0;
QY 415 CTTCCCTTCGCAACCGTTTGGCGCTGACCTTGGCTCCGACATGGAATGACCTTC 474
DB 2 CTTGGCCTGCGCGCGCGCGCGCTGCTCTTGGGCTCCGACATGGAATGACCTTC 61
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Db 902 ATATGCAAAAACTGGTGAATGCCGATCGTGTGCACTTTTCAGGTGACCATTAAGAA 961
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Qy 2275 AGGAGCAAAATATCTTCTCAACCTGAGCTCAGAGAGTAAGAGAGGTGCTGAGATCAT 2334
Db 1862 AGGAGCAAAATATCTTCTCAACCTGAGCTCAGAGAGTAAGAGAGGTGCTGAGATCAT 1921
Qy 2335 CCGCAAAAGCCATCATGCGCAACCGACCTGCGCTTATCTTTGGAGAAAGAGAGCTTGA 2394
Db 1922 CCGCAAAAGCCATCATGCGCAACCGACCTTGTGCTTATATCTTTGAGAAAGAGAGCTTGA 1981
Qy 2395 GAGATGTATACAGAGAGGTGCTGAACTTCCACACACATGCTCATGAGAGCTGTGAT 2454
Db 1982 AGAGATGTATACAGAGCGGATCATTAACCTTAAATTAATCAATGAGAGCGGTGTAAT 2041

Qy 2455 CGGCTTGAATGATGATCTGCGCTGTGATCTTTGCTCTGTGACCAAACTATGGCCAGTTACAA 2514
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Db 2102 ATTTGACGGAATGATATATATATGAGAAATTTCTGGCTGAGGGTGTATGAAATGAAGAAAT 2161
Qy 2575 GGGCATACAGCCCATCTTATGATGAGACAGACAGAGATGAAGTCCCTCAAGGGCA 2634
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Db 2342 TCGAGGGAGAGAGACTGCAACTGGATTTCACTCCCATCCGTGGCTC 2388

RESULT 4
US-08-951-648-5
Sequence 5, Application us/08951648
Patent No. 5932465
GENERAL INFORMATION:
APPLICANT: Loughney, Kate
TITLE OF INVENTION: Phosphodiesterase 8
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker, Sears Tower Suite 6300
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/34038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..2403
US-08-951-648-5
Query Match 49.6%; Score 1787.4; DB 2; Length 3195;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

525 GTTGAAGGATGAAAAGGTGAAGGACCTATCTTCTCCATCCCGAGTATTAGTAAT 584
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705 GAGTGTGACAGAGTGAACAGCTACATAGACAGGCGCTGGAACGCGGCGGACCAAC 764
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344 AGCTACTCTCTATGAATGAGCAGCATCATTAATAAGCAAAAGCCGATGATTTG 403
825 CACTGTACTTCTTGAAGAGTGAATTAAGCTGTGTGTGTTCAATCAACCCCGGATGA 884
404 CACTGTATTTCTTGAAGAGTGAATTAAGCTGTGTATTAATCAAGCACTGGGATTA 463
885 AAGAAAGCCAAACCCGCGCTCATCCCTGACAGGCGCATCACCGAGGATCAACATCT 944
464 AAGAAAGAAACCCCGCGCTCATCCCTGCGGCGCATCATCAAGGACCAACGCTCT 523
945 CCTAGCGGCCAAGTCTAGAGAGAGCGTTGTGTGAAGATATCTTGGGGATGAGCAT 1004
524 CTATAGTGGCCAAAGTCCAGGAAAACTGTGTAGAGAACATCTTGGAGATGAGCAT 583
1005 TTCCCTGAGGTACTGGCCCTGGAATCAGGAACCGGATCCAGTCTGTCTTGGCCCA 1064
584 TTCCAAAGAGTACTGAGCTGGAATCAGGAGCTGTATCCAGTCTGTCTTCTTAACA 643
1065 TTGTCACTGCCATTGGAAGACTTGTGATCTTGAACCTGTATGTAAGGCACTGGG 1124
644 TTGTCACTGCCATTGGAATGATTTGTGATTTCTGAGTGTATGCGGCACTGGGCA 703
1125 AAGCCTTCTGCTCAGCCATCAGAGGTTGCAACAGCCAACTTGTGGGCTTCCGAT 1184
704 AAGCCTTCTGCTTGTGTCACAGAGGTTGCAACAGCCAACTTGTGGGCTTCAATG 763
1185 CAATCACAAGGTGAGGTGTAGAGTCTGGCCAAACAGACCAATGATGATCTCC 1244
764 CAATCACAAGGTGAGGTGTAGAGGCTTGGCCAAACAGACCAATGATGATCTCC 823
1245 TACTGACGATCAAGAATATCTTGTATATCATAGTTGCCATAGCTCTTACTTGAAC 1304
824 TACTGACGATCAAAAACATATTTTGTATATCATAGTTGCCATATGATTTCTTACT 883
1305 ACATCATGATATATGCAAAAACTGTGTATGCGATGCTGTGCACTTTTCAAGTGG 1364
884 ACATCATGATATATGCAAAAACTGTGTATGCGATGCTGTGCACTTTTCAAGTGG 943
1365 ACCAAGAAAGAGAGCTGTACTGGAACCTGTGTGAACATTTGGGAGAGAGAGGGA 1424
944 ACCAAGAAAGAGAGTATATGACCTTTTGTATTTGAGAGAAAAAGAGAGAA 1003
1425 AGCCCATCTTCAAGAGAACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGTG 1484
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1485 AAGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCGATGCTTACGCGGACCTTTA 1544
1064 AAGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCAGATGCTTATGACGACCTTTA 1123
1545 ACAGGAGAGTGAACCTGTATCAGAGCTACACAGAGAGAACTGTGTATGAGCCAT 1604
1124 ACAGGAGAGTGAACCTGTATCAGAGCTACACAGGCGAAGCTGTGTATGAGCCAT 1183
1605 TGAGCCGAGGAGCGTGAATTTGGCTGTGTGCAAGTGTGAACAAGATCAGCGGTAG 1664

1184 TCAGCCGAGGAGCGGTGATAGGTGTGTGAGATGTCAACAAATCAGTGGCAGTGCCT 1243
1665 TTCTCAACACAGAGAGAACCACTTCAAGATGTTGTGTCTTCTGCGGACCTGGCTTGC 1724
1244 TCTCTAAAAAGATGAAAAACCTTCAAAATGTTGGCTTTTGTGTCTTTAGCTTAC 1303
1725 ACTGTGTATCATGTATACCAAGATCCGCACTCGAATGATCTACAGGGTTACATG 1784
1304 ACTGTGTATATGTATATATATGATTTGGCCACTCAGATGTCAATTAACGGGATAC 1363
1785 AGAAGCTTCTTACCAACAGATCTGCACTCCGAGAGTGGCAAGGCTCATGCGCTTCA 1844
1364 AAAAGCTGTCTTACCAATGATTTGTATCTTCAAGAGATGGCAAGGTCTCATGCAAT 1423
1845 ACTTACCAACAGATCTGCGGAGATGAGCTATTTCACTTTGACATTTGTCTTTG 1904
1424 CCTTCCCGTGTGTCTTGAAGAAATTTGAATTAATTCACCTTGAACATTTGTCTTT 1483
1905 AGAATATGAGCGTGGATCTTTGTCTATGATCATCGGTCTTGTGGGACATCTGTT 1964
1484 AAAATATGAGCGTGGATTTTGTCTATGATTTATGATCTGTGTGAAGAACTATCG 1543
1965 TTGAACCTTGAAGAAATTTGTCCGTTTATCATGTCTGTGAAGAACTATCGCGGTT 2024
1544 TTGAGCTTGAAGAAATTTGTGTGTATTTATTTATGTCTGTGAAGAACTATCG 1603
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1604 CTTACCAACATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
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1664 ACAATATGAGCGCTTCTTCAACATCTTGAAGCGCAAGGCTGTGTGTGTGTGT 1723
2145 ATGACCTTGAACCAAGGCGCTTCAAGTACAGCTACCTGCAAGTGTGACCAACCC 2204
1724 ATGACCTTGAACCAAGGCGCTTCAAGTACAGCTACCTGCAAGTGTGACCAACCC 1783
2205 CCGGCTGTATCTTCAACCTTCAACATGAGGAAACCACTTCTCCAGAGCGGTTCAT 2264
1784 CCGGCTGTATCTTCAACCTTCAACATGAGGAAACCACTTCTCCAGAGCGGTTCAT 1843
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1904 TGAAGATATCTCGAAGACCATATCTTGCACAGACCTTGTATCTTTGAAACAG 1963
2385 AGCAGTTGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2444
1964 AGCAGTTGGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2023
2445 ACCGTGTATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2504
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2084 CCGTTACAAAATTTGACAGCGAATGATATATATGAGAAATTTGAGGCTGAGGTGAT 2143
2565 TGAAGAGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2624
2144 TGAAGAGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2203
2625 CTAAGGAGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2684
2204 CTAAGGAGTGTGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2263
2685 AGATCTTCCACCAAGAGCTTGTGAAAGGCTGAGGAGATTAACCTCAATCAGTGG 2744

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Db      2264 AGATCTCCCTCCACGAGCCTCTTCTGAAGCATGCAGGATATCTCACTCACTGGG 2323
QY      2745 AGAAGTATTCGCGGGGAGAGACAGCAATGTGATTTTCAGGCCCGCGGC 2801
      2324 AGAAGTATTCGAGGGGAGAGACTGCAACCTGATTTTCATCCCATCGTGGCTC 2380

RESULT 5
US-09-174-437-5
; Sequence 5, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(2403)
US-09-174-437-5

Query Match      49.6%; Score 1787.4; DB 3; Length 3195;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

QY      525 GTTTGACGATGAAGCTGAAGCCCTATCTCTCCATCCCGAGTATTGATGAAT 584
      104 GTTTGACAGATGAAGAAAGTGAAGCAATCTTCTCTTCACCCCAGTATTGATGAAT 163
QY      585 TTGTTCTGAAGTGTAGTGCAGAGACTGTGAAAAAGTGGCTGAAGAGAAAAACCA 644
      164 TTGTATCTGAAGTGTAGTGCAGAGACTGTGAAAAAGTGGCTGAAGAGAAAAACCA 223
QY      645 AAGCAAAAGATGAACCATCTCCAGAGAGTCAAGAGTACCAAGATACGAATATGCA 704
      224 AATCAGAAAGATGAATGAGCTCTTAAGAGAGTCAAGAGTACCAAGATATGCAAG 283
QY      705 GAGTCTGTACGAGCTGAACAGCTACATAGAGAGCGCTGGAACAGGGGGGGGCAAC 764
      284 GAGTGTATATGAAGCTAAGAGCTATATAGAACAGCGTTGACACAGAGAGAGAAC 343
QY      765 ACCTGCTCCTCTAGAGCTCAGAGCATCATCAGATAGCCAAAGCCGAGATTTG 824
      344 AGCTATCTCTCTATGAAGTGAAGCATCATTAATAATGCAAAAGCCGATGATTTG 403
QY      825 CACTGTATCTCTTGAAGAGTGAATATAGCCTGTGTGTTCATATCAACCCGGAGTGA 884
      404 CACTGTATCTCTTGAAGAGTGAATATAGCCTGTGTATTTCAACCCGATGATTTG 463
QY      885 AGAAGGCCAACCCCGGCTCATCTCTGAGGGCCCATCAACCGAGGTACCAACATCTCTG 944
      464 AGAAGGAAAAACCCCGCTCATCTCTGAGGGCCCATCAACCGAGGTACCAACATCTCTG 523
QY      945 CCTACGAGGCAAGTCTAGAGAGAGCTTTGTGTGAGAGATATCTCTTGGGAGAGCGAT 1004
      524 CTTATGTGGCAAGTCTAGAGAGAGAGCTGTATGAGAGAGATCTCTTGGAGATGAAGAT 583
QY      1005 TTCTCTGAGGTACTGAGCTGTGAATCAGGAAACCGCATCTCACTCTTCTTCTGCTCA 1064
      584 TTCTCAAGAGGTACTGAGCTGTGAATCAGGAAACCGCATCTCACTCTTCTTCTGCTCA 643
QY      1065 TTGTCACTGCAATGTGAGACTGTGATTTGCAATCTCTTGAACGTATACAGGCACTGGGGCAAG 1124
      644 TTGTCACTGCAATGTGAGACTGTGATTTGCAATCTCTTGAACGTATACAGGCACTGGGGCAAG 703
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QY      1125 AGCTCTTCTGCTCTCCGATCAGAGAGTGTGAACAGCCAACTTCTTGGGCTTCCGTAG 1184
      704 AAGCTCTTCTGCTTATGTACACAGAGAGTGTGAACAGCAAACTTCTTGGGCTTCAAGTAG 763
QY      1185 CAATACACAGAGTGCAGGTGTGTAGAGGTCTGCCAAAAGACCCAGACTGAATGACTTCC 1244
      764 CAATACATCAGGTGCAGGTATGCAAGGCTTGCAAAAGACAGATTTGAATGACTTCC 823
QY      1245 TACTGACGTATCAAAAGACATATCTTTGATATACATATGTTGCCATATACATCTCTTGAAC 1304
      824 TACTGACGTATCAAAACATATTTGATATACATATGTTGCCATATATCTCTTGAAC 883
QY      1305 ACATATATATATATCAAAAAATCTAGTGAAGCCGACCGCGCGGCTCTTCAAGTGG 1364
      884 ACATATATATATATCAAAAACTGTGTAATGCGATGTTGTGCACTTTTCCAGTGG 943
QY      1365 ACCACAAGAACAGAGAGCTGTACTGGAACCTGTTGACATTTGGGAGAGAGAGGGGA 1424
      944 ACCATAGAGAACAGAGATATATTTGAGACTTTTGAATTTGAGAGAGAGAGAGAA 1003
QY      1425 AGCCATCTTCAAGAGAACCAAGAGATCATTTTCCATTGAGAAAGGATTTGCTGTTC 1484
      1004 AACTGTCTTCAAGAGAACCAAGAGATGATTTTCAATTTAGAGAAAGGATTTGCTGTTC 1063
QY      1485 AAGTGCAGAGAACAGGCGGAAGCTTGAACATTCGCCGATGCTTACGCGGCTTTA 1544
      1064 AAGTGCAGAGAACAGGCGGAAGCTTGAACATTCGCCGATGCTTACGCGGCTTTA 1123
QY      1545 ACAGGAGGTGAGACCTGTACACAGGCTACACAGAGAGAACATTTGTGTATGCCATAG 1604
      1124 ACAGAGAGTGAATCTTTGATACAGGCTACACAGGAGAACATTCGTGATGATGCCATAG 1183
QY      1605 TGAGCGGAGGACCGGTGATTTGCGTGTGCAATGTGTGAACAAAGATCAAGGTCGCT 1664
      1184 TGAGCGGAGGACCGGTGATTTGCGTGTGCAATGTGTGAACAAAGATCAAGGTCGCT 1243
QY      1665 TCTCCAGACACAGAGAACCACTTCAAGATGTTTGTCTCTTCTGCGGACTGCGCTTGC 1724
      1244 TCTCTAAACAGATGAAGAACCTTCAAGATGTTTGTCTCTTCTGCGGACTGCGCTTGC 1303
QY      1725 ACTGTCTAACTGTACACAGAGATCCGCACTCAGATATGCAATCTACAGGGTTAACATAG 1784
      1304 ACTGTCTAACTGTATATATATATATATATATATATATATATATATATATATATATAT 1363
QY      1785 AGAAGCTTCTTACCAACAGCATCTGCACTCCGAGAGTGGCAAGGCTCATAGCGCTTCA 1844
      1364 AAAAGCTTCTTACCAACAGCATCTTGTATGCAAGAGTGGCAAGGCTCATATGCAATTTCA 1423
QY      1845 ACCTTACAGACAGCATCTGCGGAGACATGAGCTATTTCACTTTGACATTTGCTCTTTCG 1904
      1424 CCCTTCCGTCGCTCTCTCAAGAAATTTGAATTTTCACTTTGACATTTGCTCTTTCG 1483
QY      1905 AGAAGATGTGGCTGTGGATCTTTGTCTACATGATCCATGAGTCTTGTGGGACATCTCTGT 1964
      1484 AAAAGATGTGGCTGTGAATTTTGTCTACATGATCCATGAGTCTTGTGGGACATCTCTGT 1543
QY      1965 TTGAATTTGAATAATTTGTGCGGTTTATCATATCTGTGTGAAGAACTATCGCGGTTTC 2024
      1544 TTGAATTTGAATAATTTGTGCGGTTTATCATATCTGTGTGAAGAACTATCGCGGTTTC 1603
QY      2025 CTTTACCAACATGGAAGCATGATGCAAGTGTGCAACATGATATGCAATCTTCAAA 2084
      1604 CTTTATCAACATGGAAGCATGCGGTACATGATGCAACATGATATGCAATCTTCAAA 1663
QY      2085 ACAACATGAGCTCTTCAACAGACTGTGAGGCAAGGCTGTATATTTGAGTGTCTGTGCC 2144
      2145 ATGACCTGAGCAACAGGGGCTTCAATACATGATGCTTCAAGAGATTTGACATCCCTGTG 2204
      1664 ACATATCAACAGCTTTTCAACAGACTTGAAGGCAAGAGATGCTGTATGCTGTGTCTGTG 1723
QY      2145 ATGACCTGAGCAACAGGGGCTTCAATACATGATGCTTCAAGAGATTTGACATCCCTGTG 2204
      1724 ATGACCTGAGCAACAGGGGCTTCAATACATGATGCTTCAAGAGATTTGACATCCCTGTG 1783
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Qy	2205	CGGCGCTGATCTCCACCTTCCACCATGAGACACACCACTTCTCCAGACGGTGTCCATCC	2265
Db	1784	CGGCTCTCTACATCCACTTCCACCATGAGACACACCACTTCTCCAGACTGTGTCCATCC	1843
Qy	2265	TTCACTGGAAAGGACCAATATCTTCTCCACCTGAGCTCCAGCAGATACGACAGGTGC	2322
Db	1844	TCCAGTTGGAAAGGACCAATATCTTCTCCACTTGAAGCTCCAGTGAATATGACAGGTGC	1903
Qy	2335	TGAGATCATCCGCCAAAGCCATCATCGCCACCGACCTGCGCCCTATATCTTTGGAAACAGA	2384
Db	1904	TTGAGATCATCCGCAAGCCATCATTTGCCACAGACTTGTCTTATATCTTTGGAAACAGA	1963
Qy	2385	AGCAATTTGGAAGAGATGATACCAAGACAGAGGTGCGTGAACCTCCACAACAGTCCCATCGAG	2444
Db	1964	AGCAATTTGGAAGAGATGATACCAAGACCGGATCACTTAACTTATATATCAATCACTTAAG	2023
Qy	2445	ACCGTGTCAATCGGCTTGAATGATGATGCTGCTGATGACTTGTGCTGTGTGAACAACTATGCG	2504
Db	2024	ACCGTGTATTTGGTTTGAATGATGATGCTGCTGATGACTTGTGTGTGAACAAACTGTGCG	2083
Qy	2505	CAGTTACAAATTTGACAGCGAATGATATATATGCAAAATTCGTGGCTGAGGGTGAATGAGA	2564
Db	2084	CGGTTACAAATTTGACCGGAATGATATATATGAGAAATTCGTGGCTGAGGGTGAATGAAA	2143
Qy	2565	TGAAGAAGCTGGGCAATACAGCCCATTTCTATGATGACAGAGACAGAGCATGAAATGCC	2624
Db	2144	TGAAGAAATTTGGGAATACAGCCTTATCTATGATGACAGAGACAGAGCATGAAATGCC	2203
Qy	2625	CTCAAGGGAGAGTGGGATTTCTACATATGCTGATGCGATTCCTCGCTATACACTTGAATCG	2684
Db	2204	CCCAAGGCCAGTTTGGGATTTCTACATATGCGATGCGATTCCTCGCTATACAACTTGAATCC	2263
Qy	2685	AGATCTCTCCACCCACAGAGCCTCTGCTGAAGGCTGACGGGATTAAGCTCATAGTGGG	2744
Db	2264	AGATCTCTCTCTCCACCGAGAGCCTCTTGAAGAGATGACGGGATTAATCTCATAGTGGG	2323
Qy	2745	AGAGGTAATTCGCGGGGAGAGACAGACATGTGATTTCAAGGCCACGACCCCGGCGCG	2801
Db	2324	AGAGGTAATTCGAGGGGAGAGAGATGTAAGCTGATTTCAATCCCATCCGTGGCTC	2380
RESULT 6			
US-09-686-055A-5			
Sequence 5, Application US/09686055A			
Patent No. 6566087			
GENERAL INFORMATION:			
APPLICANT: Loughney, Kate			
TITLE OF INVENTION: Phosphodiesterase 8A			
FILE REFERENCE: 27866/35047			
CURRENT APPLICATION NUMBER: US/09/686, 055A			
CURRENT FILING DATE: 2000-10-11			
PRIOR APPLICATION NUMBER: 08/951, 648			
NUMBER OF SEQ ID NOS: 48			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 5			
LENGTH: 3195			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (67)..(2403)			
US-09-686-055A-5			
Query Match			
Best Local Similarity 49.6%; Score 1787.4; DB 3; Length 3195;			
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;			
Qy	525	GTTTGACGATGAAAAGGTGAAGGCTATCTTTCTCTCATCCCGAGGTATTAGATGAT	584
Db	104	GTTTGACGATGAAAAGGTGAAGGATATCTTCTCTTCAACCCCGATATTAGATGAT	163
Qy	585	TTGTTTCTGAAGTGTATTGTGACAGACTGTGAAAAGTGGCTGAGAGAGAAACACAA	644

Db	164	TTGTAATCGAAAGGTGTAAGTGACAGACAGTAGAGAAATGGCTGAAGAGAAACACACA	223
QY	645	AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAGCAGGTACCAGATACGAATATGCAAG	704
Db	224	AATCAGAAAGATGAANTCGGCTCCTTAAGAAAGTCAGCAGGTACCAAGATACGAATATGCAAG	283
QY	705	GAGTCGTGTACGAGCTGAACAGCTACATAGAGCAGCGCTTGACACCGGCGGGGACACAC	764
Db	284	GAGTGTGTATGAACATAACAGCTATATAGAACCAACGGTTGGACACAGAGAGAACCAAC	343
QY	765	AACGTCCTCTGATAGCTCAGCAGCATCATCAGGATAGGCCAAGAACCGCAGATTGG	824
Db	344	AGCTACTCTCTATGAACCTGAGCAGCATCATTAATAATGCCACAAAGCCGATGGAATTTG	403
QY	825	CAGTGTACTTCTCTTGAGAGATGACATAATATAGCTGTGTGTGTTCTATACACCCGGGATGA	884
Db	404	CAGTGTATTTCTTGAGAGATGACATAATATAGCTGTGTATATTCACGCGCATCTGGGATATA	463
QY	885	AGAAAGGCCAACCCCGGCTCATCTCCGCAAGGCCCCATACCCAGGGTACCAACATCTCTG	944
Db	464	AGAAAGGAAACCCCGCTCATCTCCGCGGCCCATCATCTCAGGGCACACCCGTCTCTG	523
QY	945	CCTAACGTGGCCAAAGCTTAGAGAAAGCTGTGTGTATAGAGATATCCTTGGGGATGAGCAT	1004
Db	524	CTTATGTGGCCAAAGCTCAGGAAACACGTCTATAGAAAGACATCTTGGAGATGAACAT	583
QY	1005	TTCTCGAGTACTGGCCTGGAAATCAGGAACCCGCATCAGTCTGTCTTTGCTTGCCCA	1064
Db	584	TTCCAAAGAGTACTGGAATGGAATCAGGGAATCGATACAGTCTGTCTTTGCTTACCA	643
QY	1065	TTGTCACTGCCATTGGAGACTTGATTTGGCATCTTGAACCTGTACAGGCACTGGGGCAAG	1124
Db	644	TTGTCACTGCAATTGGTGTAGCTTGATTTGGTATTTCTCGACCTGTATGGGCACTGGGGCAAG	703
QY	1125	AGGCTTCTGCTCTCAGGCATCAGAGAGGTTGCAACAGCCAACTTGTCTTGGGCTTCCGTA	1184
Db	704	AAGCTTCTGTCTTAGTCAACAGAGAGGTTGCAACAGCAAACTTGGCTCGGGGCTTAGTAG	763
QY	1185	CAATACACAGAGTGAGGTGTGTAGAGGCTCGCCAAACAGACCGMACTGAATGACTTCC	1244
Db	764	CAATACATCAGGTGAGGTATGCAAGGCTCTGGCCAAACAGACAGMAATTGAATGACTTCC	823
QY	1245	TACTCGAGTATCAAAAGCATACTTTGTATTAATAGTTCAGATAGACTCTCTACTTGAAC	1304
Db	824	TACTCGAGTATCAAAACATATTTTGTATTAATAGTTCAGATAGATTCTCTACTTGAAC	883
QY	1305	ACATCATGATATATGCAAAAATCTTAGTGAACGCCGACCGCTGCGGCTCTTCCAGGTGG	1364
Db	884	ACATATGATATATGCAAAAACCTGTGMAATGCCGATCGTTTGGCATTTTCCAGGTGG	943
QY	1365	ACCAACAAGAACAGAGAGCTGTACTCGGACCTGTTGACATTTGGGGAGAGAAAGAGGGA	1424
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QY	1425	AGCCCATCTTCAAGAAAGACCAAGAGATCAGATTTTCAATTGAGAAAGGAATGCTGTGTC	1484
Db	1004	AACCTGTCTTCAAGAAAGACCAAGAGATTAAGATTTTCAATTGAGAAAGGAATTTGCTGCC	1064
QY	1485	AAATGGCAAGACAGGCGAAGTCTTGAACATTTCCGATGCTTAGCGGACCTCGCTTTA	1544
Db	1064	AAATGAGCAAGAACAGGGGAGTCTCGAACATTTCCAGATGCTTAGCAGACCCACGCTTTA	1124
QY	1545	ACAGAGAGGTGGAACCTGTACACAGGCTACACAGAGGAACATTCGTGTATGCGCATAG	1604
Db	1124	ACAGAGAGGTGGAACCTGTACACAGGCTACACAGCGGAACATCTGTGACATGCCCATAG	1184
QY	1605	TGAGCCAGAGCAGCGTATTTGGCTGTGTCAGATGTGGAACAAATCAGCGGTAGCGCT	1664
Db	1184	TGAGCCAGAGCAGCGTATAGTGTGTGTGTGTCAGATGTGTCAAAATCAGTGGCAGTGGCT	1244
QY	1665	TCTTCAAGACAGACGAGAACCACTTCAAGATGTTTGTCTGTCTTGTGCGCATGGCTTGGC	1724

Db 1244 TCTTAAACAGATGAAAACAAATTCAAAATGTTGCCGTCTTTGTGCTTAACCTTAC 1303
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Db 1304 ACTGAGTAACTGATACCAAGAGATCCGCCACTCAGATATGCACTCAAGGTTTACCATGG 1363
Qy 1785 AGAAGCTTCTTACCAAGAGATCTGCACTCCGAGAGTGGCAAGGCTTCATGCGCTTCA 1844
Db 1364 AAAAGCTGCTTACCAAGAGATCTTGTGATCTTCAAGAGAGTGGCAAGGCTTCATGCAATTTCA 1423
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Db 1424 CCGTTCCTGCGGTCTGCAAGAAATTAATTTTCACTTTGACATTTGGCTTTGG 1483
Qy 1905 AGAAGAGTGGCTGGAGTCTTTGTCTACATGATCCATGCGTCTTTGGGACATCTCTTT 1964
Db 1484 AAAACATGAGGCTGGAAATTTTGTCTACATGATCCATGCGTCTTTGGGACATCTCTGT 1543
Qy 1965 TTGAACCTGAAAAATTTGCGGCTTTTATCATGTCTGTGAAGAAATCTATCGCGGCTTC 2024
Db 1544 TTGAGCTTAAAAAGTTGTGCGTTTATTTATGTCTGTGAAGAAATCTATCGCGGCTTC 1603
Qy 2025 CTTTACCAAACTGGAAGCATGCACTGCGTGGCACTGTCATGTAATGCTTCAAA 2084
Db 1604 CTTATCAAACTGGAAGCATGCGTCACTGTACACATGTCATGTAATGCTTCAAA 1663
Qy 2085 ACAAACAATGGCCCTTCAAGACCTGAGGCGAAAGGCGCTTAATTCGCTGTGCTG 2144
Db 1664 ACAATCAACGCTTTTCAAGACCTTGAAGGCAAGGAGCTGCTGATTTGCGTGTGCTG 1723
Qy 2145 ATGACCTGGAACAAGGCGCTTCAATACCTGCAAGATTCAGAACCTTCCCTG 2204
Db 1724 ATGACCTGGAACAAGGCGCTTCAATACCTGCAAGATTCAGAACCTTCCCTG 1783
Qy 2205 CCGCGCTGATCTCACTCTCACTCACTGAGGAACAACCTTCTCCAGACGCTTCCATCC 2264
Db 1784 CCGCTCTACTCTCACTCTCACTGAGGAGCAACCTTCTCCAGACGCTTCCATCC 1843
Qy 2265 TTCAGCTGGAAGGCAATATCTTCCACCTGAGCTCCAGAGTACGAGGCTG 2324
Db 1844 TCCAGTGGGAAGGCAATATCTTCTCCACCTGAGCTCCAGAGTACGAGGCTG 1903
Qy 2325 TGGAGATCAATCCGCAAGGCTCATGCGCAACGCTTCCGCTTATATCTTTGGGAACGA 2384
Db 1904 TTGAGATCAATCCGCAAGGCTCATGCGCAACGCTTCCGCTTATATCTTTGGGAACGA 1963
Qy 2385 AGCAGTTGGAAGATGATCAAGACAGGCTGCTGAACCTTCCACACCATGCTCATGAG 2444
Db 1964 AGCAGTTGGAAGATGATCAAGACAGGCTGCTGAACCTTCCACACCATGCTCATGAG 2023
Qy 2445 ACCGTGCTACCGGCTTGATGATGATGCTGCGTGTGATCTTTGCTGTGACCAAACTATG 2504
Db 2024 ACCGTGTAATTTGTTGATATGATGCTGCTGTGACCTTTGTTCTGTGACCAAACTATG 2083
Qy 2505 CAGTTACAAAATTTGACAGCAATGATATATATGAGCAATTTCTGGGCTGAGGGTATGAGA 2564
Db 2084 CCGTTACAAAATTTGACAGCAATGATATATATGAGCAATTTCTGGGCTGAGGGTATGAGA 2143
Qy 2565 TGAAGAACTGGGCAATCAAGCCATTTCTTATGATGACAGAGACAAAGGAGATGAATCC 2624
Db 2144 TGAAGAAATTTGGGAATCAAGCTTATCTTATGATGACAGAGACAAAGGAGATGAATCC 2203
Qy 2625 CTGAAGGAGCTGCGATTTCAAAATGCTGTGCGCATTTCCCTGTATACCACTTTGACGC 2684
Db 2204 CCAAGGCGAGCTTGGGTTCTACAAATGCGTGGCATTTCCCTGTATACCACTTTGACCC 2263
Qy 2685 AGATCTCTCCCAACCAAGAGCTTGTCTGAAGGCTTGAAGGATTAACCTCAATGAGGG 2744
Db 2264 AGATCTCTCTCCCAACCAAGAGCTTGTCTGAAGGATTAACCTCAATGAGGG 2323
Qy 2745 AGAAGGTATTTGCGGGGAGAGACAGCAATGTTGATTTCAAGGCCCAAGGCCCGCGC 2801
Db 2324 AGAAGGTATTTGCGGGGAGAGACAGCAATGTTGATTTCAATCCCAATCCCTGTGCTC 2380

RESULT 7
US-09-420-190-2
; Sequence 2, Application US/09420190
; Patent No. 6673564
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 4381
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67) ... (2403)
US-09-420-190-2
Query Match 49.6%; Score 1787.4; DB 3; Length 4381;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;
Qy 525 GTTTCAGATGAAAAGGAGGCGCTATCTTCTCCATCCCGAGTATTGATGAAT 584
Db 104 GTTTCAGATGAAAAGGAGGCGCTATCTTCTTCCATCCCGAGTATTGATGAAT 163
Qy 585 TTGTTCTGAAAGTGTAGTGCAGAGCTGTGAAAAAGTGTGTAAGAGAAAAACA 644
Db 164 TTGTTCTGAAAGTGTAGTGCAGAGCTGTGAAAAAGTGTGTAAGAGAAAAACA 223
Qy 645 AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAAGGTAACAGATTAAGATTTG 704
Db 224 AATCAAAAGATGAATGCGCTCTTAAGAAAGTCAAGGTAACAGATTAAGATTTG 283
Qy 705 GAGTGTGTAAGAGCTGAACAGTATGAGAGGCGCTGACAGAGGAGGGAAC 764
Db 284 GAGTGTGTAAGAGCTGAACAGTATGAGAGGCGCTGACAGAGGAGGGAAC 343
Qy 765 ACCTGCTCTCTATGAGCTCAGAGCATCATAGATAGCCAAAGCCGAGATTGG 824
Db 344 AGCTTACTCTCTATGAGCTGAGAGCATCTTAAATAGCCAAAGCCGAGATTGG 403
Qy 825 CACTGTACTCTCTTGAAGAGTGAATATAGCTGTGTGTCTATACACCCGGGATGA 884
Db 404 CACTGTATTTCTTGAAGAGTGAATATAGCTGTGTGTCTATACACCCGGGATGA 463
Qy 885 AGAAGGCAACCCCGGCTATCCCTGCGAGGCGCATCACCGAGGTAACACCATCTG 944
Db 464 AGAAGGCAACCCCGGCTATCCCTGCGAGGCGCATCACCGAGGTAACACCATCTG 523
Qy 945 CTAAGTGGCAAGTCTAGGAAGCTTGTGTGTAAGATATCTTTGGGATGAGGAT 1004
Db 524 CTTATGTGGCAAGTCTAGGAAGCTTGTGTGTAAGATATCTTTGGGATGAGGAT 583
Qy 1005 TTCTGAGGTAAGTGGCTGGAATCAGAAACCGCATCCAGTCTGTTCTTGTGCCA 1064
Db 584 TTCAGAGGTAAGTGGCTGGAATCAGAAACCGCATCCAGTCTGTTCTTGTGCCA 643
Qy 1065 TTGTCACTGCAATTTGAGAGCTTGTATGAGCATCTTTGAACGTAAGGCACTGGGGCAAG 1124
Db 644 TTGTCACTGCAATTTGAGAGCTTGTATGAGATTTCTGAGCTGTATGCACTGGGGCAAG 703
Qy 1125 AGGCTTCTGCTCAGGCACTAGAGGTTGCAACAGCAATCTTGTGGCTTCCGTAG 1184
Db 704 AAGCTTCTGCTTATGACACAGAGGTTGCAACAGCAATCTTGTGGCTTCACTAG 763

TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2298
OTHER INFORMATION:
OTHER INFORMATION: /note="The amino acid encoded by nucleotides 868-870 is
OTHER INFORMATION: either Pro or Lys."
US-08-951-648-1

Query Match 49.5%; Score 1785; DB 2; Length 2298;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 1968; Conservative 1; Mismatches 306; Indels 0; Gaps 0;

527 TTGACGATGAAAAAGGTGAAGGCTTCTTCTCTCCATCCCGAGTATTAGTGAATTT 586
1 TTGACGATGAAAAAGGTGAAGGCTTCTTCTCTCCATCCCGAGTATTAGTGAATTT 60
587 GTTCTGAAAAGTGTAGTGAGAGACTGTGAAAAAGTGTGAAGAGAAAAACAACAA 646
61 GATATCGAAAAGTGTAGTGAGAGACAGTAGAAGAAATGCTGAAGAGAGAAACAACA 120
647 GCAAAAGATGAACCATCTCCCAAGAAAGTCAAGAGGTAACCAAGATACGAATATGACAGGA 706
121 TCAGAAAGATGAATCGGCTCTTAAGAAAGTCAAGAGGTAACCAAGATACGAATATGACAGGA 180
707 GTCGTGACGAGCTGAACAGCTACATAGAGCAGCGCTGGAACAGGGCGGGACAACAC 766
181 GTTGTATATGAACTTAACAGCTATATGAACAAACGGTGGACACAGAGAGAACAAACAG 240
767 CTGCTCTCTATAGAGCTCAGACAGCATCATCAGATAGCAAAAGCCGAGATTTGCA 826
241 CTACTCTCTATGAACTGAGCAGCATCATTAATAATAGCCACAAAAGCCGATGATTTGCA 300
827 CTGTACTCTCTGAGAGAGTCAATATAGCTGTGTGTCTTACCAACCCCGAGTGAAG 886
301 CTGTATTTCTTGAAGAGTCAATATAGCTGTGTATATTCACGCCACTGAGATTAAG 360
887 GAAGGCAACCCCGGCTCATCCCTGCAAGGCCCATCAACCGAGGTACCAACATCTGACC 946
361 GAAGGAAACCCCGCTCATCCCTGCGGCGCATCATCAGAGGACCAACCGTCTGCT 420
947 TACGTGGCCAAAGCTTGAAGAGACGTTGTTGTAAGAGATATCTTGGGAGTGAACGATTT 1006
421 TAGTGGCCAAAGCTTGAAGAGACGTTGTTGTAAGAGACATCTTGGAGTGAACGATTT 480
1007 CCTGAGAGTATCGGCTGTGAATCAGAAACCCGATCCAGTCTGTTCTTCTGCCCCAT 1066
481 CCAAGAGTATCGGATCGGAATCAGGAGCTGTATCAGAGCTGTTCTTTCCTTAACCAATT 540
1067 GTCACTGCGCAATGGAGACTTGAATTGGCATCTTGAACCTGTACAGGCACTGAGGCAAGAG 1126
541 GTCACTGCGCAATGGAGACTTGAATTGGATTTCTGAGCTGTATCGGCACTGAGGCAAGAG 600
1127 GCCCTTCTGCTCAGCCATCAGAGGTTGCAACAGCCATCTTGTGAGGCTTCGTAAGCA 1186
601 GCCCTTCTGCTTATGTAACAGAGGTTGCAACAGCAAAATCTTGGCTGAGCTTCAATGTA 660
1187 ATACACCAAGGTGACGTTGTGTAGAGGTTGCGCCAAACAGACCGAACTGAATGACTTCTTA 1246
661 ATACATCAGGTTGACGTTGTGTAGAGGTTGCGCCAAACAGACAGAAATGAATGACTTCTTA 720
1247 CTGAGAGTATCAAGACATCTTGAATACATAGTTGCCATAGACTCTCTACTTGAACAC 1306
721 CTGAGAGTATCAAGACATCTTGAATACATAGTTGCCATAGACTCTCTACTTGAACAC 780
1307 ATCATGATATATGCAAAAAATCTAGTGAACGCGACCGCTGCGGCTCTTCCAGAGTGAAC 1366
781 ATATATGATATATGCAAAAAATCTGTTGAATGCGATGTTGTGCACTTTTCCAGAGTGAAC 840
1367 CACAAAGACAAAGAGCTGTACTCGGACTGTGTTTGAACATTTGGGAGAGAAAGAGGGAGAG 1426
841 CATTAAGAACAAAGAGTATATTCAGACCTTTTGTGATTTGAGAGAGAAAGAGAGAGAA 900

1427 CCCATCTTCAAGAGAACCAAGAGATCAGATTTTCCATTGAGAAAGGATTTGCTGTCAA 1486
901 CCTGTCTTCAAGAGAACCAAGAGATTAAGATTTTCAATTGAGAAAGAAATCTGAGCCAA 960
1487 GTGGCAAGAACAGGGAAGTCTTGAACATTTCCGATGCTTACGCGGACCTTGCTTTTAA 1546
961 GTAGCAAGAACAGGGAAGTCTTGAACATTTCCAGATGCTTATGCAAGCCCAAGCTTTTAA 1606
1547 AGGAGAGTGAACCTGTACACAGGCTTACACCAAGAGAACATTTCTGTATATGCCATAGTG 1606
1021 AAGAGAGTGAACCTGTACACAGGCTTACACCAAGAGAACATCTGTGATATGCCATAGTG 1080
1607 AGCCGAGGAGGCTGTATTTGCGTGTGTCAGATGTGTGAACAAATACGCGGTAGCCGCTTC 1666
1081 AGCCGAGGAGGCTGTATTTGCGTGTGTCAGATGTGTGAACAAATACGCGGTAGCCGCTTC 1140
1667 TCAGAGACAGAGAGAACATTTCAAGATGTTGCTGTCTTGTGCGCACTGAGCTTTCAC 1726
1141 TCTAAACAGATGAAGAACATTTCAAGATGTTGCTGTCTTGTGCGCACTGAGCTTTCAC 1200
1727 TGTGCTAACATGTACCAAGAGATCCGCACTCAGAAATGATCTTACAGGTTTACATGAG 1786
1201 TGTGCTAACATGTATGATATGAAATTTGCGCACTCAGAGTGCATTTTACCGGTTAAGATGAA 1260
1787 AAGCTTCTTACCAAGAGATCTGACCTTCAGAGAGTGGCAAGGCTTCAATGCGCTTCAAC 1846
1261 AAGCTTCTTACCAAGAGATCTGACCTTCAGAGAGTGGCAAGGCTTCAATGCAATTCACC 1320
1847 CTACAGACAGGATCTGCGGGGATCGAGGCTATTCCATCTTGAACATTTGATCTTTCAG 1906
1321 CTTCCTGCTGCTCTGCAAGAAATTTGATTTTCACTTTGACATTTGATCTTTCAG 1380
1907 AACATGTGCTGAGATCTTGTGTATCATGATTCATCGGCTTGTGAGACATCTGTTT 1966
1381 AACATGTGCTGAGATTTTGTGTATCATGATTCATCGGCTTGTGAGACATCTGTTT 1440
1967 GAACTTGAAGAAATTTGCGGTTTATCATGTCTGTGAAGAAACATATGCGGAGTTCCT 2026
1441 GAGCTTGAAGAAATTTGCGGTTTATCATGTCTGTGAAGAAACATATGCGGAGTTCCT 1500
2027 TACCAACATGGAAGATCAGTCAAGTGGGCACTGCAATGTATGCAATCTTCAAAAC 2086
1501 TATCAACATGGAAGATGAGTCAAGTGGGCACTGCAATGTATGCAATCTTCAAAAC 1560
2087 AACATGTGCTTCTTCAAGACCTCGAGCGCAAGGCTGTATGCTGTGCTGAT 2146
1561 AACATGTGCTTCTTCAAGACCTCGAGCGCAAGGCTGTATGCTGTGCTGAT 1620
2147 GACCTGAGACCAAGGGGCTTCAAGTACAGTACCTGCAAGTGTGCAACCCCTGAGG 2206
1621 GACCTGAGACCAAGGGGCTTCAAGTACAGTACCTGCAAGTGTGCAACCCCTGAGG 1680
2207 GCGCTGTATCTCCACTTCCACATGAGGCAACACATCTTCCGACGAGTGCATCTT 2266
1681 GCTCTGTATCTCCACTTCCACATGAGGCAACACATCTTCCGACGAGTGCATCTT 1740
2267 CAGCTGAAAGGACAAATATCTTCCACCTGAGTCCAGAGTGAAGAGAGTGTCTG 2326
1741 CAGTTGAAAGGACAAATATCTTCCACCTGAGTCCAGAGTGAAGAGAGTGTCTG 1800
2327 GAGATCATCCGCAAGGACATATCTTCCACCTGAGTCCAGAGTGAAGAGAGTGTCTG 2386
1801 GAGATCATCCGCAAGGACATATCTTCCACCTGAGTCCAGAGTGAAGAGAGTGTCTG 1860
2387 CAGTTGAAAGGATGTACAGAGAGGTCGCTGAACCTTCCAGAGTGAAGAGAGTGTCTG 2446
1861 CAGTTGAAAGGATGTACAGAGAGGTCGCTGAACCTTCCAGAGTGAAGAGAGTGTCTG 1920
2447 CAGTTGAAAGGATGTACAGAGAGGTCGCTGAACCTTCCAGAGTGAAGAGAGTGTCTG 2506
1921 CAGTTGAAAGGATGTACAGAGAGGTCGCTGAACCTTCCAGAGTGAAGAGAGTGTCTG 1980

Qy	2507	GTTCAAAATGACAGCGAATGATATATATATACAAATCTGGGCTGAGGGGATGAGATG	2566
Dp	1981	GTTCAAAATGACGCGCAATGATATATATACAAATCTGGGCTGAGGGGATGAAATG	2040
Qy	2567	AAGAAGCTGGGCATACAGCCCATTCCTATGATGACAGAGACAAGCGAGATGAAGTCCT	2626
Dp	2041	AAGAATATGGGAATACAGCCTATTCCTATGATGACAGAGACAAGAAAGATGAAGTCCG	2100
Qy	2627	CAAGGGCAGCTCGAATCTTACTACATGCTGTGGCCATTCCTCTATACACCTTACACCGAG	2686
Dp	2101	CAGGGCAGCTTGGATTCTACATGCTGTGGCCATTCCTCTATACACCTTACACCGAG	2160
Qy	2687	ATCTCTCCACCACAGAGCCTCTGTGTAGGCTCTGACGGATTAACCTCAATCAGTGGGAG	2746
Dp	2161	ATCTCTCCCTCCACAGAGCCTCTGTGAAACATGACGAGATTAATTCAGTCAATGAGGAG	2220
Qy	2747	AAGGTAATTCGGGGGAAGAGACAGCAATGTGATTTCAAGCCCAAGGCGCGGCGC	2801
Dp	2221	AAGGTGATTCAGGGGAGAGACATGCAACTGTGAATTCATATCCCATCGTGGCTC	2275

RESULT 9 :
US-09-174-437-1
; Sequence 1, Application US/09174437A

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1  APPLICANT: Loughney, Kate
2  TITLE OF INVENTION: Phosphodiesterase 8A
3  FILE REFERENCE: 27866/35047
4  CURRENT APPLICATION NUMBER: US/09/174,437A
5  CURRENT FILING DATE: 1998-10-16
6  EARLIER APPLICATION NUMBER: 08/951,648
7  EARLIER FILING DATE: 1997-10-16
8  NUMBER OF SEQ ID NOS: 48
9  SOFTWARE: PatentIn Ver. 2.0
10 SEQ ID NO 1
11 LENGTH: 2298
12 TYPE: DNA
13 ORGANISM: Homo sapiens
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (1)..(2298)
17 FEATURE:
18 NAME/KEY: misc feature
19 LOCATION: (866)..(870)
20 OTHER INFORMATION: The amino acid encoded by nucleotides 866-870 is
21 OTHER INFORMATION: either Pro or Leu
22 IS-09-174-437-1

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Query Match	49.5%	Score 1785	DB 3	Length 2298
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Matches 1968; Conservative 1; Mismatches 306; Indels 0; Gaps 0;

[illegible]

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QY	887	GAAAGGCCAACCCCGGCTCATCCCTGACAGGGGCCCATCAACCAGGGATCCACCATCTGCC	946
Db	361	GAAAGGAAACC CGGCTCATCCCTGTGGGGCCATCACTCAAGGGGACCAACGCTCTCTCT	420
QY	947	TACGTGGCCAAAGTTAGGAGAAGTTGGTATAGAGATATCTTTGGGGATGAGCGATTT	1006
Db	421	TATGTGGCCAAAGTCCAGGAAAAACCTGTACTAGAAAGCATCTTGGAGATGAACGATTT	480
QY	1007	CCCTGAGGGTATGTGGCTGGGAATCCAGSAAACCGGATCCAGCTGTGTTCTTTGGTGGCCATT	1066
Db	481	CCAAAGGATCTGAGCTGGAATCAAGGAGCTGTATCCAGTCTGTTCCTTTGCTTACAAATT	540
QY	1067	GTCACTGCCATTGGAGACTTGATTTGGCATCTCTTAACGTATACAGGCACTGGGGCCAAAG	1122
Db	541	GTCACTGCCAATTGGTGAATTGATTTGGTATTTCTGAGCTGTATTCGGCACTGGGGGAAAGAA	600
QY	1127	GCCTTCTGCTCAGCCATCAGAGGTTTGCAACAGCCAACTTTCCTTGGGGCTTCCGTAGCA	1186
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QY	1187	ATAACACAGGTGCGAGTGTGTAGAGGTCTGGCCAAACAGACCGGAACGAAATGACTTCTTA	1246
Db	661	ATATCATCAGGTGCGAGTGTGTAGAGGCTTGGCCAAACAGAAATGAAATGACTTCTCTTA	720
QY	1247	CTGACGCTATCAAGAACAATCTTGTATGATACATAGTCCATAGACTCTCTACTTGAACAC	1306
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QY	1307	ATCATGATATATGCAAAAAATCTTAGTGAACGCCGACCGCTGCGCTTTCAGGTTGAC	1366
Db	781	ATATGATATATGCAAAAAACCTGTGAATGCCATGTTGTGTGCACTTTTCAAGTGGAC	840
QY	1367	CACAAAGAACAGAGGCTGTACTCGGACCTGTGTTGACATTTGGGGAGAGAAAGAGGGAGAG	1422
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QY	1427	CCCATCTTCAAGAAAGCAAGAGAGATCAGATTTTCCATTGGAAGAGGATTTGCTGTCA	1486
Db	901	CTGTCTTTCAGAAAGACCAAGAGATAGATTTTCAATTGGAAGAAATTTGCTGGCCA	960
QY	1487	GTGGCAAGAACAGGCGAAGTCTTGAACAATTCGCCATGCTACGGCGAACCTTCGCTTTAAC	1546
Db	961	GTACCAAGAACAGGGGAAGTCTGAACAATTCAGATGCTATGCAAGACCCACGCTTTAAC	1020
QY	1547	AGGAGGTGGAACCTGTATACAGGCTTACACCAACGAGGAACAATTCGTGTATATGCCATAGTG	1606
Db	1021	AGAAAGGTAGACTTGTATACAGGCTTACACCAACGGGAACAATTCGTGTATATGCCATAGTG	1080
QY	1607	AGCGAGGACGCGGATTTGGCGTGTGTGAGATGAGTGAACAAGATCAGCGGTAGCGCTTTC	1666
Db	1081	AGCGAGGACGCGTGTATGTTGTGTGATGTGTCAACAAATCAAGTGGCAATGTGCTTTC	1140
QY	1667	TCCAAAGACAGCGAACAATTCMAAGATGTTTCTGTCTTCCGCACTGGCCTTGCAC	1726
Db	1141	TCTAAACAGATGAAACAATTCMAAATGTTTTCGCTTTTGTGTATAGCTTACAC	1200
QY	1727	TGTGTCAATGTATCCACAGGATTCGCGCACTCAGAAATGCAATCTACAGGGTTACATGAG	1786
Db	1201	TGTGTCAATGTATGTATCAGAAATTCGCGCACTCAGAGTGCATTTCGCGGTAAACATGAGA	1260
QY	1787	AAGTTTTCCTAACACAGATCTGCACTTCGAGGAGTGGCAAGGCTCATATGCGTTCAC	1846
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QY	1847	CTACACACAGCATCTGCGGGGACATGAGGCTATTTCACTTTGACATTTGTCCTTTGAG	1906
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1441 GAGCTTGAATGTTGTGTCTTTTATATGTCTGTGAAGAAATATCGGGGTTCT 1500
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1501 TATCAACAATGGAAGATGCACTGATGAGCACTGTGATGTATGCCATCTTCAAAAC 1560
2087 AACATGCGCTTTTCAACAATCTTCAAGGCGCAAGGCTCTTATTTGCGGTCTGAGCAT 2146
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2207 GCGCTGATCTCCACCTTCAACAATGAGCAACAACCTTCTCCAGACGAGTGTCTCATCTT 2266
1681 GCTCTCTACTCCACTTCCACATGAGAGCAACACTTCTCCAGACGAGTGTCTCATCTT 1740
2267 CAGCTGGAAGGCAATATCTTCTCCACCTGAGCTTCCAGAGATGACAGAGGCTG 2326
1741 CAGTTGGAAGGCAATATCTTCTCCACTGAGCTTCCAGAGATGAGCAAGGCTG 1800
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1801 GAGATCATCCGCAAAAGCATATCCGCAACGAGCTGCGCTTATCTTGGGAAACAGAAAG 1860
2387 CAGTTGGAAGGATGATACAGAGAGGCTGAGCACTTCCAGCAACAGTGTCTCATCTGAGAC 2446
1861 CAGTTGGAAGGATGATACAGAGAGGCTGAGCACTTCCAGCAACAGTGTCTCATCTGAGAC 1920
2447 CGTGTATCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2506
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2507 GTTACAAATTTGACAGGATGATATATATGAGAAATTTGAGGCTGAGGATGATGATGATG 2566
1981 GTTACAAATTTGACAGGATGATATATATGAGAAATTTGAGGCTGAGGATGATGATGATG 2040
2567 AAGAACTGGGCAATACAGCCATTTCTATGATGAGCAAGAGCAAGAGATGAGTCCCT 2626
2041 AAGAAATTTGGGATACAGCTTATTTCTATGATGAGCAAGAGCAAGAGATGAGTCCCT 2100
2627 CAAAGGCAAGCTGAGATTTTCAATGATGAGGCAATTTCTGCTATATACACTTGAAGCAG 2686
2101 CAAAGGCAAGCTGAGATTTTCTCAATGATGAGGCAATTTCTGCTATATACAACTTGAAGCAG 2160
2687 ATCTCTCCACCCACAGAGCTTCTGCTGAAAGGCTGAGGAGATTAACCTCATCATGAGGAG 2746
2161 ATCTCTCTCCACCCAGAGCTTCTGCTGAAAGGCAATGAGGAGATTAACCTCATCATGAGGAG 2220
2747 AAGGTAATTTGCGGAGGAG 2801
2221 AAGGTAATTTGAGGAGGAG 2275

RESULT 10
US-09-686-055A-1
Sequence 1. Application US/09686055A
Patent No. 6566087
GENERAL INFORMATION:
APPLICANT: Loughney, Kate
TITLE OF INVENTION: Phosphodiesterase 8A
FILE REFERENCE: 2786/35047
CURRENT APPLICATION NUMBER: US/09/686, 055A
CURRENT FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 08/951,648
PRIOR FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 48

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(2298)
NAME/KEY: misc_feature
LOCATION: (868)..(870)
OTHER INFORMATION: The amino acid encoded by nucleotides 868-870 is
US-09-686-055A-1
Query Match 49.5%; Score 1785; DB 3; Length 2298;
Best Local Similarity 86.5%; Pred. No. 0;
Matches 1968; Conservative 1; Mismatches 306; Indels 0; Gaps 0;
527 TTGAGGAGTGAAGAGTGAAGGCTATCTTCTTCCATCCCAAGATATTAGTGAATTT 586
1 TTGAGGAGTGAAGAGTGAAGGCTATCTTCTTCCATCCCAAGATATTAGTGAATTT 60
587 GTTCTGAAGTGTATGTCAGAGACTGTGAAAAGTGTGAAGAGAAAACAA 646
61 GTATCTGAAGGTTATGTCAGAGACTGTGAAAAGTGTGAAGAGAAAACAA 120
647 GCAAAAGATGAACATCTTCCAGAGAGTCAAGAGTACAGAGATACGAATATGACAGGA 706
121 TCAGAAAGATGATCGCTCTCTTAAGAGAGTCAAGAGTACGAATATGACAGGA 180
707 GTCTGTACAGAGTGAACAGCTATACATGAGAGAGGCTGGAACAGGCGGAGCAACAC 766
181 GTTGTATATGAATTAACAGCTATATATGAACAGGTTGACAGAGAGAGACACAG 240
767 CTGCTCTCTATAGCTCAGAGCATCATCAGATATAGCAAAAGCCGATTTGCA 826
241 CTATCTCTTATGAAGTGAAGCATCATTAATATGCAAAAGCCGATTTGCA 300
827 CTGTACTTCTTGAAGAGTGAATATATGCTGTGTGTGTCTATACACCCGGAGGAAG 886
301 CTGTATTTCTTGAAGAGTGAATATATGCTGTGTGTGTCTATACACCCGGAGGAAG 360
887 GAAAGGCAACCCCGGCTCATCCCTGAGGAGCCCATCAACGAGGTATCAACATCTGTGC 946
361 GAAAGGCAACCCCGGCTCATCCCTGAGGAGCCCATCAACGAGGTATCAACATCTGTGC 420
947 TACGTGGCAAGTCTAGAGAGAGTGTGTGTATGAGAGATATCTTGGGATGAGCATTT 1006
421 TATGTGGCAAGTCTAGAGAGAGTGTGTGTATGAGAGATATCTTGGGATGAGCATTT 480
1007 CTTGAGGTATCTGAGCTTGAATCAGGAACCCGATCAAGTCTGTCTTGTCTTGCCATT 1066
481 CCAAGAGTATCTGAGCTTGAATCAGGAACCCGATCAAGTCTGTCTTGTCTTGCCATT 540
1067 GTTACCTGCAATTTGGAATTTGATTTGCAATCTTGAATCTGAGGCAAGGCAAGAG 1126
541 GTTACCTGCAATTTGGAATTTGATTTGCAATCTTGAATCTGAGGCAAGGCAAGAG 600
1127 GCTTCTGCTCAGCATCAGAGGATTTGCAACAGCAATCTTGTGGCTTCCGATGCA 1186
601 GCTTCTGCTTATGTCACAGAGAGTGTGCAAGCAAAATCTTGTGGCTTCAATGCA 660
1187 ATACACCAAGTGAAGTGTGTAGAGTCTGCGCAACAGACGAACTGAATGATCTTCTTA 1246
661 ATACATCAAGTGAAGTGTGTAGAGTCTTGTCCAAACAGACAAATTTGAATGATCTTCTTA 720
1247 CTGAGATATCAAAAGCATCTTGAATATATGATGATGATGATGATGATGATGATGATGATG 1306
721 CTGAGATATCAAAAGCATCTTGAATATATGATGATGATGATGATGATGATGATGATGATG 780
1307 ATCATGATATATCAAAAGCATCTTGAATATATGATGATGATGATGATGATGATGATGATG 1366
781 ATATATGATATATCAAAAGCATCTTGAATATATGATGATGATGATGATGATGATGATGATG 840

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 DB CATTAGAAACAAGAGATTATATTCAGACCTTTTGATTTGAGAGAGAGAGAGAGAGAGAG 900
 QY 1427 CCCATCTTCAAGAAAGACCAAGAGATCAGATTTTCCATTGAGAAAGAGATGGTGTCA 1486
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 QY 1487 GTGGCAAGAAACGAGGAGTCTTTGAACATTTCCGATGCTTAGCGGAGACCTTGCTTAA 1546
 DB GTAGCAAGAAACGAGGAGTCTTGAACATTTCCAGATGCTTAGCAACCAAGCTTTTAA 1020
 QY 1547 AGGAGGTGAGCTGTGACAGGCTTACACAGAGAGAACTTGTGTATGCGCAATAGAG 1606
 DB AAGAAAGTAGATTTGACAGGCTTACACAGGCTTACACAGGAGAACTTGTGTATGCGCAATAGAG 1080
 QY 1607 AGCCGAGGAGGAGTGTGATGGCTGTGAGATGTGTAAGTAAGTACAGCGGTAGCGCTTC 1666
 DB AGCCGAGGAGGAGTGTGATGGCTGTGAGATGTGTAAGTAAGTACAGCGGTAGCGCTTC 1140
 QY 1667 TCBAAGACAGACGAGAAACAATTCAAGATGTTTCTGCTTCTGCGACATGCGCTTGCAC 1726
 DB TCTAAACAGATGAGAAACAATTCAAAATGTTTGCCTTTTGTGCTTTAGCCTTACAC 1200
 QY 1727 TGTGCTAATGATACACAGAGATCGGCACTGAGAAATGATCTACAGGAGTTACATGAGAG 1786
 DB TGTGCTAATGATGATGATGAAATTTGCTGACATGAGTGAATTTACCGGAGTAACGATGAGAA 1260
 QY 1787 AAGCTTTCTTACACAGACATCTGACCTTCGAGAGTGGCAAGGCTTACATGCGCTTCAAC 1846
 DB AAGCTGCTTACATGACATTTGTAATTGTAAGTAAGTGGCAAGGCTTACATGCAATTCAC 1320
 QY 1847 CTACACAGACGATCTGCGGAGACATCGAGCTATTCATTTGACATTTGCTCTTTCAG 1906
 DB CTTCCTGCTGCTCTGCAAAAGAAATTAATTCATTTGACATTTGCTCTTTCAG 1380
 QY 1907 AACATGTGGCTGGAGTCTTTGCTACATGATCCATCGGCTTGTGGGACATCGCTTTT 1966
 DB AACATGTGGCTGGAGTCTTTGCTACATGATCCATCGGCTTGTGGGACATCGCTTTT 1440
 QY 1967 GAATCTGAAAAATGTCGCTTTTATCATGTCTGTGAAAGAAACTATCGGCGGTTCT 2026
 DB GAGCTTGAATAATTTGTGTGTTTATATGTCTGTGAAAGAAACTATCGGCGGTTCT 1500
 QY 2027 TACCAAACTGGAAGCATGACGTACGCTGAGCACTGATGTATGCCATTTCAAAAC 2086
 DB TATCAAACTGGAAGCATGCGGTCACTGTAGCACTGATGTATGCCATTTCAAGAAC 1560
 QY 2087 AACATGTGCTCTTCAAGACCTTCAGAGGCAAAAGCGCTGTATGCGGTCTGTGGCAT 2146
 DB AATCAAGCTTTTCAAGACCTTCAGAGGCAAAAGCGCTGTATGCGGTCTGTGGCAT 1620
 QY 2147 GACCTGAGCAACAGAGGGCTTCACTAAGCTACTGCAAGATTTGACCAACCCCTGGG 2206
 DB GACCTGAGCAACAGAGGGCTTCACTAAGCTACTGCAAGATTTGACCAACCCCTGGG 1680
 QY 2207 GCGCTGTACTCCACTTCACATGAGCAACAATTCTCCAGACGCTGTCAATCTT 2266
 DB GCTCTACTCTCACTTCACATGAGCAACAATTCTCCAGACGCTGTCAATCTT 1740
 QY 2267 CAGCTGGAAGGAGCAATATCTTTCCACCTGAGACTCCAGAGATGACAGAGAGTGTG 2326
 DB CAGTTGGAAGGAGCAATATCTTTCCACTGTGAGCTTCAGAGATGAGAGAGAGTGTGCT 1800
 QY 2327 GAGATCATCCGAAAGCATCATCCGACCTGCGCCTTACTTTGGGAAACGAGAG 2386
 DB GAGATCATCCGAAAGCATCATTTGCAAGACCTTGTCTTATCTTTGAAACGAGAG 1860
 QY 2387 CAGTTGAGAGATGTACCAACAGAGGCTGTGAACCTTCACAAACAGTCCCATGAGAC 2446
 DB CAGTTGAGAGATGTACCAACAGAGGCTGTGAACCTTCAAACCTTAATATCAATCAATAGAGAC 1920

QY 2447 CGTGTATCGGCTTGATGATGATCTGCTGTGATCTTTGCTCTGTGACCAAACTATGSCCA 2506
 DB CGTGTATTTGTTGATGATGATGATCTGCTGTGATCTTTGTTCTGTGACAAACTGTGGCC 1980
 QY 2507 GTTACAAATTTGACACGGAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATG 2566
 DB GTTACAAATTTGACCGGCAATGATATATATGAGAAATTTGAGGCTGAGGCTGATGATG 2040
 QY 2567 AAGAGCTGGGATTCACCCCATTTCTATGATGACAGAGCAACGAGATGAATGCCCT 2626
 DB AAGAAATTTGGAAATACGCTTATTTCTATGATGACAGAGCAACGAGATGAATGCCCT 2100
 QY 2627 CAAGGCACTCGAATTTTCAATGCTGTGCAATTCCTGCTATACCACTTACGCAAG 2686
 DB CAAGGCACTGTGATTTTCAATGCTGTGCAATTCCTGCTATACCACTTACGCAAG 2160
 QY 2687 ATCTCCCAACCAAGACCTTGTGTAAGGCTTGCAGAGATTAACCTTAATGATGGAG 2746
 DB ATCTCCCTCCCAAGAGCTTCTTGAAGCATGCAAGGATTAATCTCAGTCAATGAGAG 2220
 QY 2747 AAGTAAATTTCCGGGAGAGAGACAGCAATGTGATTTCAAGCCCAAGCCCGGCGC 2801
 DB AAGGATTTCAAGGAGAGAGACAGCAATGTGATTTCAATCCCATCCGTGCTC 2275

RESULT 11

US-08-951-648-38
 ; Sequence 38, Application US/08951648
 ; Patent No. 5932465
 ; GENERAL INFORMATION:
 ; APPLICANT: Loughney, Kate
 ; TITLE OF INVENTION: Phosphodiesterase 8
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker, Sears Tower Suite 6300
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: US
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/951,648
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Williams Jr., Joseph A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/34038
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; INFORMATION FOR SEQ ID NO: 38:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 477 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; US-08-951-648-38

Query Match 13.0%; Score 469.2; DB 2; Length 477;

Best Local Similarity 99.4%; Pred. No. 5e-99;
 Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAGCCGACGAGATTGCACTGTACTTCTTGGAGAGTGCAATATATACCTGTGTGT 864
 DB 4 CCAAAAGCCGACGAGATTGCACTGTACTTCTTGGAGAGTGCAATATATACCTGTGTGT 63

QY 865 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAG 924
DB 64 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAG 123
QY 925 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 984
DB 124 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 183
QY 985 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 1044
DB 184 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 243
QY 1045 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 1104
DB 244 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 303
QY 1105 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 1164
DB 304 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 363
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 1224
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 423
QY 1225 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 1278
DB 424 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 477

RESULT 12
US-09-174-437-38
; Sequence 38, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-174-437-38

Query Match 13.0%; Score 469.2; DB 3; Length 477;
Best Local Similarity 99.4%; Pred. No. 5e-99;
Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAAGCCGAGCGATTTGCACTGTAATCTTCTTGAAGAGTGCAATATAGCTGTGTGT 864
DB 4 CCAAAAAGCCGAGCGATTTGCACTGTAATCTTCTTGAAGAGTGCAATATAGCTGTGTGT 63
QY 865 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAC 924
DB 64 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAC 123
QY 925 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 984
DB 124 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 183
QY 985 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 1044
DB 184 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 243
QY 1045 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 1104
DB 244 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 303

QY 1105 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 1164
DB 304 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 363
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 1224
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 423
QY 1225 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 1278
DB 424 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 477

RESULT 13
US-09-686-055A-38
; Sequence 38, Application US/09686055A
; Patent No. 6566087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; EARLIER FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-686-055A-38

Query Match 13.0%; Score 469.2; DB 3; Length 477;
Best Local Similarity 99.4%; Pred. No. 5e-99;
Matches 471; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 805 CACAAAAGCCGAGCGATTTGCACTGTAATCTTCTTGAAGAGTGCAATATAGCTGTGTGT 864
DB 4 CCAAAAAGCCGAGCGATTTGCACTGTAATCTTCTTGAAGAGTGCAATATAGCTGTGTGT 63
QY 865 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAC 924
DB 64 GTTCATACCAACCCGGAGTAAAGAGAGCCAAACCCGGCTCATCTTCGAGGGCCCATCAC 123
QY 925 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 984
DB 124 CCAAGGATACCAACCATCTTCGCTTACGTCGCAAGCTTAGAGAGACGTTGTTGGTAGAGGA 183
QY 985 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 1044
DB 184 TATCTTGGGGATGAGCGATTTCTCGAGGTACTGCGCTGGAATCAGAAACCCGCATCCA 243
QY 1045 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 1104
DB 244 GTCTGTCTTCTTCTGCTCCCATTTGTCACTGCGCATTTGAGACTTGATGCACTCTTGAAC 303
QY 1105 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 1164
DB 304 GTTACAGCACTGGGGGAAAGAGCCCTTTCGCTCAGCGCATCAGAGAGTTGCAACAGCCAA 363
QY 1165 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 1224
DB 364 TCTTGTGGGCTTCCGTAGCAATACACAGGTGAGGTGTAGAGGTCTCGCAAAACA 423
QY 1225 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 1278
DB 424 GACCGAAGTGAATGACTTCTTCTGCTGAGCGTATCAAGACATCTTGTGATTAACAT 477

RESULT 14
US-08-951-648-33
; Sequence 33, Application US/08951648


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; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker, Sears Tower Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-951-648-33

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Query Match          9.3%; Score 333.8; DB 2; Length 404;
Best Local Similarity 92.6%; Pred. No. 1.2e-67;
Matches 373; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 1298 CTTGAACATCATATATATGCAAAAAATCTAGTGAACGCCGCGCTGCGCTCTTC 1357
DB 1 CTTGAACATCATATATATGCAAAAAATCTAGTGAACGCCGCGCTGCGCTCTTC 60

QY 1358 CAGGTGACCAACAAGAGAGCTGTACTCGACCTGTTGACATTGGGAGAGAAAG 1417
DB 61 CAGGTGACCAACAAGAGAGCTGTACTCGACCTGTTGACATTGGGAGAGAAAG 120

QY 1418 GAGGGGAAGCCCATCTTCAAGAAAGCAAGAGATCAGATTTTCAATTGAGAAAGGATT 1477
DB 121 GAGGGGAAGCCCGTTTCAAGAAAGCAAGAGATCAGATTTTCAATTGAGAAAGGATT 180

QY 1478 GCTGCTCAAGTGGCAAGAACAGGCGAGTCTTGAACATTCGCCATGCTTACCGGACCT 1537
DB 181 GCTGCTCAAGTGGCAAGAACAGGCGAGTCTTGAACATTCGCCATGCTTACCGGACCT 240

QY 1538 CGCTTTAACAAGAGAGTGAACCTGTACACAGGCTACCAAGAGAACTTCTGTATG 1597
DB 241 CGCTTTAACAAGAGAGTGAACCTGTACACAGGCTACCAAGAGAACTTCTGTATG 300

QY 1598 CCCATAGTAGGCGGAGGCGAGCGTGAATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 1656
DB 301 CCCATAGTAGGCGGAGGCGAGCGTGAATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 360

QY 1657 TAGCCCTTCTCCAAGACAGACGAGAACTTCAAGATGTTT 1699
DB 361 CA--GGCCTTCCAAGACGAGATGAGAACACTTCAAGATGTTT 401

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RESULT 15
US-09-174-437-33
; Sequence 33, Application US/09174437A

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; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-174-437-33

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Query Match          9.3%; Score 333.8; DB 3; Length 404;
Best Local Similarity 92.6%; Pred. No. 1.2e-67;
Matches 373; Conservative 0; Mismatches 27; Indels 3; Gaps 2;

QY 1298 CTTGAACATCATATATATGCAAAAAATCTAGTGAACGCCGCGCTGCGCTCTTC 1357
DB 1 CTTGAACATCATATATATGCAAAAAATCTAGTGAACGCCGCGCTGCGCTCTTC 60

QY 1358 CAGGTGACCAACAAGAGAGCTGTACTCGACCTGTTGACATTGGGAGAGAAAG 1417
DB 61 CAGGTGACCAACAAGAGAGCTGTACTCGACCTGTTGACATTGGGAGAGAAAG 120

QY 1418 GAGGGGAAGCCCATCTTCAAGAAAGCAAGAGATCAGATTTTCAATTGAGAAAGGATT 1477
DB 121 GAGGGGAAGCCCGTTTCAAGAAAGCAAGAGATCAGATTTTCAATTGAGAAAGGATT 180

QY 1478 GCTGCTCAAGTGGCAAGAACAGGCGAGTCTTGAACATTCGCCATGCTTACCGGACCT 1537
DB 181 GCTGCTCAAGTGGCAAGAACAGGCGAGTCTTGAACATTCGCCATGCTTACCGGACCT 240

QY 1538 CGCTTTAACAAGAGAGTGAACCTGTACACAGGCTACCAAGAGAACTTCTGTATG 1597
DB 241 CGCTTTAACAAGAGAGTGAACCTGTACACAGGCTACCAAGAGAACTTCTGTATG 300

QY 1598 CCCATAGTAGGCGGAGGCGAGCGTGAATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 1656
DB 301 CCCATAGTAGGCGGAGGCGAGCGTGAATTGGCGTGTGACAGATGG-TGAACAAGATCAGCGG 360

QY 1657 TAGCCCTTCTCCAAGACAGACGAGAACTTCAAGATGTTT 1699
DB 361 CA--GGCCTTCCAAGACGAGATGAGAACACTTCAAGATGTTT 401

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Search completed: January 12, 2006, 12:45:48
J00 Time : 614 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OW nucleic - nucleic search, using SW model

Run on: January 12, 2006, 08:50:54 ; Search time 2719 Seconds
(without alignments)
10967.038 Million cell updates/sec

Title: US-10-618-252-14

Perfect score: 3606

Sequence: 1 acgcgtccgcctccatctg.....atttaaaaaaaaaaaaaa 3606

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_Main:*

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3606	100.0	3606	3	US-09-321-801-14
2	3606	100.0	3606	7	US-10-618-252-14
3	3064	85.0	7618	7	US-10-659-770-12
4	3050.4	84.6	7581	7	US-10-659-770-11
5	2610.6	72.4	3219	5	US-10-202-107-11
6	2610.6	72.4	3219	8	US-10-887-276-1
7	1871.8	51.9	4389	6	US-10-440-998-3
8	1858.4	51.5	2554	3	US-09-321-801-1
9	1858.4	51.5	2554	7	US-10-618-252-1
10	1790.2	49.6	2798	3	US-09-321-801-3
11	1790.2	49.6	2798	7	US-10-618-252-3
12	1787.4	49.6	3195	6	US-10-440-998-5
13	1787.4	49.6	4381	3	US-09-420-190-2
14	1787.4	49.6	4381	6	US-10-458-839-2
15	1785	49.5	2298	6	US-10-440-998-1
16	900.2	25.0	1068	7	US-09-321-801-12
17	900.2	25.0	1068	7	US-10-618-252-12
18	485.2	13.5	539	3	US-09-321-801-18
19	485.2	13.5	539	7	US-10-618-252-18
20	484.2	13.4	4446	9	US-10-450-763-23296
21	469.2	13.0	477	6	US-10-440-998-38
22	441.4	12.2	487	3	US-09-321-801-16
23	441.4	12.2	487	7	US-10-618-252-16

24	333.8	9.3	404	6	US-10-440-998-33	Sequence 33, Appl
25	272.6	7.6	458	6	US-10-440-998-7	Sequence 7, Appl
26	216.6	6.0	3489	6	US-10-168-402-5	Sequence 5, Appl
27	216.6	6.0	4167	6	US-10-168-402-38	Sequence 38, Appl
28	215.4	6.0	3855	10	US-11-097-143-42398	Sequence 42398, A
29	209.6	5.8	3044	3	US-09-883-825-44	Sequence 44, Appl
30	209.6	5.8	3044	7	US-10-697-894-44	Sequence 44, Appl
31	209.6	5.8	4145	7	US-10-236-417-77	Sequence 77, Appl
32	209.6	5.8	4171	5	US-10-094-989-1	Sequence 1, Appl
33	209.6	5.8	4171	10	US-11-044-015-1	Sequence 971, App
34	209.6	5.8	4240	3	US-09-954-531-971	Sequence 6, Appl
35	209.6	5.8	4240	8	US-10-686-390-6	Sequence 6, Appl
36	209.6	5.8	4240	9	US-10-686-282-6	Sequence 2038, Ap
37	209.6	5.8	4240	9	US-10-843-641A-2038	Sequence 6, Appl
38	209.6	5.8	4240	9	US-10-686-349-6	Sequence 1917, Ap
39	209.6	5.8	4240	9	US-10-756-149-1917	Sequence 485, App
40	207	5.7	3244	6	US-10-108-260A-485	Sequence 2, Appl
41	201.6	5.6	1784	5	US-10-094-168B-2	Sequence 6, Appl
42	201.6	5.6	1784	7	US-10-746-197-6	Sequence 2, Appl
43	201.6	5.6	2078	7	US-10-746-197-2	Sequence 8, Appl
44	201.6	5.6	2502	3	US-09-891-216-8	Sequence 9, Appl
45	201.6	5.6	2889	3	US-09-891-216-9	

ALIGNMENTS

RESULT 1									
US-09-321-801-14									
Sequence 14, Application US/09321801									
Patent No. US20020115176A1									
GENERAL INFORMATION:									
APPLICANT: Lanfear, Jeremy									
APPLICANT: Robas, Nicola M.									
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES									
FILE REFERENCE: PC9477A									
CURRENT APPLICATION NUMBER: US/09/321, 801									
CURRENT FILING DATE: 1999-05-27									
EARLIER APPLICATION NUMBER: 9826777.6									
EARLIER FILING DATE: 1998-12-04									
EARLIER APPLICATION NUMBER: 9823882.7									
EARLIER FILING DATE: 1998-10-30									
EARLIER APPLICATION NUMBER: 9811500.9									
EARLIER FILING DATE: 1998-05-28									
EARLIER APPLICATION NUMBER: 9908247.1									
EARLIER FILING DATE: 1998-04-09									
EARLIER APPLICATION NUMBER: 9910801.1									
EARLIER FILING DATE: 1999-05-10									
NUMBER OF SEQ ID NOS: 19									
SOFTWARE: PatentIn Ver. 2.1									
SEQ ID NO 14									
LENGTH: 3606									
TYPE: DNA									
ORGANISM: Mouse									
US-09-321-801-14									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 3606; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	ACGCGTCCGCTCTCTATCTGACCTTCCACCTCCCGCGCGCTCTCCGAGAGAGGCGC	60						
QY	61	AGCGCGCTGTGAG	120						
DB	61	AGCGCGCTGTGAG	120						
QY	121	AGGACAAAG	180						
DB	121	AGGACAAAG	180						
QY	181	CACGACGCGTGTGAG	240						

Db 181 CAGCAGCGGTGGCAGAGGCGGGGGGGGGGCTTCTCTCGCCCTGCGATTCAGAGGCTT 240
QY 241 GCTGCTCCCTGCCCCCGGCGCCCGGCATCTCCGCGCGCGGCTTCCCTTACACC 300
Db 241 GCTGCTCCCTGCGCGCGCGCGCGGCATCTCCGCGCGCGGCTTCCCTTACACC 300
QY 301 GGGTGCAGCGCGCGGCGGACCTCCCTCGGATTTTCCGGGCGCGCGGGGGGGCTGCGCTGAGCCT 360
Db 301 GGGTGCAGCGCGCGGCGGACCTCCCTCGGATTTTCCGGGCGCGCGGGGGGGCTGCGCTGAGCCT 360
QY 361 CGGCCCCGCGCTGCGCGCGCGGTGCGGAACTCTTTGCGCGCGCCCGAGCGCGCGCTTCCC 420
Db 361 CGGCCCCGCGCTGCGCGCGCGGTGCGGAACTCTTTGCGCGCGCCCGAGCGCGCGCTTCCC 420
QY 421 CCTTGCGACCGTTTGGCGCGCTGCGCTTCCGCTCCGACATGAAAGATGACCTCTTACAA 480
Db 421 CCTTGCGACCGTTTGGCGCGCTGCGCTTCCGCTCCGACATGAAAGATGACCTCTTACAA 480
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Db 541 GGTGAAGGCTTATCTTCTCTCCATCCCGAGGTATTGATGAATTTGTTTGAAGTGT 600
QY 601 TAGTGCAGAGACTGTGGAAGAAAGTGTGCTGAAGAGAAACCAACAAAGCAAAAGATGAAC 660
Db 601 TAGTGCAGAGACTGTGGAAGAAAGTGTGCTGAAGAGAAACCAACAAAGCAAAAGATGAAC 660
QY 661 ATCTCCCAAGAAAGTACAGAGGTACAGAGTACGAATATGCAAGGAGTGTGTGACAGCT 720
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Db 1021 CCTGAATCAGGAACCCGCACTCAGCTGTCTTTGCTTGGCCCATTTGTACTGCAATGG 1080
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 QY 3601 AAAAAA 3606
 DB 3601 AAAAAA 3606
 RESULT 2
 US-10-618-252-14
 ; Sequence 14, Application US/10618252
 ; Publication No. US20040018542A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanfear, Jeremy
 ; APPLICANT: Rodas, Nicola M.
 ; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
 ; FILE REFERENCE: PC9477B
 ; CURRENT APPLICATION NUMBER: US/10/618,252
 ; PRIOR FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: 9826777.6
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 ; PRIOR APPLICATION NUMBER: 9823882.7
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 ; PRIOR APPLICATION NUMBER: 9811500.9
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 9908247.1
 ; PRIOR FILING DATE: 1999-04-09
 ; PRIOR APPLICATION NUMBER: 9910801.1
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 14
 ; LENGTH: 3606
 ; TYPE: DNA
 ; ORGANISM: Mouse
 US-10-618-252-14
 Query Match 100.0%; Score 3606; DB 7; Length 3606;
 Best Local Similarity 100.0%; Pred No. 0; Indels 0; Gaps 0;
 Matches 3606; Conservative 0; Mismatches 0;

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Qy	2761	GGAAGAGACAGCAATGTGATTTCAAGGCCAGCGCCGCGCCTAG	CAAGAGACAACCTGA	2820
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Db	2821	GAACTGAACGTGAAGGTTGAAGCTGATCTGAAGTGAAGCTGTGAT	CTGCCCCAGCA	2880
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: Publication No. US20040152106A1
:
: GENERAL INFORMATION:
: APPLICANT: ROBERTSON, Harold
: APPLICANT: DENOVAN-WRIGHT, Elleen
: APPLICANT: NOVAMERON, INC.
: TITLE OF INVENTION: GENE NECESSARY FOR STRIATAL FUNCTION
: TITLE OF INVENTION: US$ THERMOF AND
: TITLE OF INVENTION: COMPOUNDS FOR MODULATING SAME
: FILE REFERENCE: 2817,102
: CURRENT APPLICATION NUMBER: US/10/659, 770
: CURRENT FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 09/660, 208
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/217, 765
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: 60/158, 043
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 12
:
: LENGTH: 7618
:
: TYPE: DNA
:
: ORGANISM: mouse
:
: FEATURES:
: NAME/KEY: unsure
: LOCATION: (7075)...(7076)
: OTHER INFORMATION: a or g or c or t/u, unknown or other
US-10-659-770-12

```

Query Match	Similarity	85.0%	Score 3064	DB 7	Length 7618
Best Local	Similarity	99.6%	Pred. No. 0		
Matches 3070	Conservative	1	Mismatches 11	Indels 0	Gaps 0
QY	525	GTTCGACGATGAAAAGGTGAAGGCTTATCTTCTCTCCATCCCGAGTATTAGATGAT	584		
DB	273	GTTTGACGATGAAAAGGTGAAGGCTTATCTTCTCTCCATCCCGAGTATTAGATGAT	332		
QY	585	TTTGTTTCGAAAGGTTAGTGCAGAGCTGTGAAAAAGTGGCTGAAGAGAAAAACA	644		
DB	333	TTTGTTTCGAAAGGTTAGTGCAGAGCTGTGAAAAAGTGGCTGAAGAGAAAAACA	392		
QY	645	AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAGCAGGTACACAGATACGAATATGCAG	704		
DB	393	AAGCAAAAGATGAACCATCTCCCAAGAAAGTCAGCAGGTACACAGATACGAATATGCAG	452		
QY	705	GAGTCGTGTACAGAGCTGAACAAGCTACATATAGAGCAGCGCTGGAACAACGGACGGGACAAC	764		
DB	453	GAGTCGTGTACAGAGCTGAACAAGCTACATATAGAGCAGCGCTGGAACAACGGACGGGACAAC	512		
QY	765	ACCTGCTCCTCTATAGAGCTCAGCAGCATCATCAGATAGCAAAAACCGACGGATTGG	824		
DB	513	ACCTGCTCCTCTATAGAGCTCAGCAGCATCATCAGATAGCAAAAACCGACGGATTGG	572		
QY	825	CACGTACTTCTCTGGAGAGTGCATTAATACCTGTGTGTCTTCAACACCCGGGATGA	884		
DB	573	CACGTACTTCTCTGGAGAGTGCATTAATACCTGTGTGTCTTCAACACCCGGGATGA	632		
QY	885	AGGAAGGCCAACCCCGGCTCATCCCTGCAGGGGCCCATCACCCAGGGTACCAACCATCTCTG	944		
DB	633	AGGAAGGCCAACCCCGGCTCATCCCTGCAGGGGCCCATCACCCAGGGTACCAACCATCTCTG	692		
QY	945	CCTACGTGGCCAAAGCTAGAAAGAGTGTGTGTAGTAAGATATCCTTGGGAGTGAAGCAT	1004		
DB	693	CCTACGTGGCCAAAGCTAGAAAGAGTGTGTGTGTAGTAAGATATCCTTGGGAGTGAAGCAT	752		
QY	1005	TTCTCTGAGGTAATGAGGCTGTGAATCAGAAACCCGCAATCAAGTCTGTCTTTGCTTGCCCA	1064		
DB	753	TTCTCTGAGGTAATGAGGCTGTGAATCAGAAACCCGCAATCAAGTCTGTCTTTGCTTGCCCA	812		
QY	1065	TTGTCACTGCCATTGGAGACTTGAATTGGCATCTTTGAACGTGACGGCACTGCGGGCAAG	1124		

Db	813	TTGTCACTGCCCATTTGGAACTTTGATTTGGCATCTCTGGAATCTGACAGGACCTGGGGCAAG	872
Qy	1125	AGGCGTTTGTGCTTCAGCCCATCAGAGGGTTGGCAACGCCAATCTTGGCTTGGGCTTCCGTA	1184
Db	873	AGGCGTTTGTGCTTCAGCCCATCAGAGGGTTGGCAACGCCAATCTTGGCTTGGGCTTCCGTA	932
Qy	1185	CAATCACACGAGTGCAGAGTGTCTAAGAGTCTTCGCCAAACAGACCGAATCTGAATGACTTCC	1244
Db	933	CAATCACACGAGTGCAGAGTGTGTAGAGGTCTTCGCCAAACAGACCGAATCTGAATGACTTCC	992
Qy	1245	TACTGCAGGTATCAAAAGACATCTACTTTGATTAACATAGTTGGCAATAGACTCTTACTTGAAC	1304
Db	993	TACTGCAGGTATCAAAAGACATCTACTTTGATTAACATAGTTGGCAATAGACTCTTACTTGAAC	1052
Qy	1305	ACATCATGATATATGCAAAAAATCTAGTGAAGCCCGACCGCTCGGCTCTTCCAGGTGG	1364
Db	1053	ACATCATGATATATGCAAAAAATCTAGTGAAGCCCGACCGCTCGGCTCTTCCAGGTGG	1112
Qy	1365	ACCACAAAGACAGAGAGCTGTACTGTGACCTGTGTTGACATTTGGGGAGAGAAAGAGGGGA	1424
Db	1113	ACCACAAAGACAGAGAGCTGTACTGTGACCTGTGTTGACATTTGGGGAGAGAAAGAGGGGA	1172
Qy	1425	AGCCCATCTTCAAGAAAGCAAGAGGATCAGATTTTCCATTGAGAAAGGATTTGGCTGGTC	1484
Db	1173	AGCCCATCTTCAAGAAAGCAAGAGGATCAGATTTTCCATTGAGAAAGGATTTGGCTGGTC	1232
Qy	1485	AAGTGGCAAGAACAGGCGAGTCTTTGAACATTCGCCGATGCTTACGCGAACCTCGCTTTA	1544
Db	1233	AAGTGGCAAGAACAGGCGAGTCTTTGAACATTCGCCGATGCTTACGCGAACCTCGCTTTA	1292
Qy	1545	ACAGGAGGTGGAACCTGTACACAGGCTTACCAAGAGAACATTTGTGTATGCCCCATAG	1604
Db	1293	ACAGGAGGTGGAACCTGTGTACACAGGCTTACCAAGAGAACATTTGTGTATGCCCCATAG	1352
Qy	1605	TGAGCGGAGGCGAGCGTGTATTTGGCCGTGGAGAGATGTTGAACAAAGATCAGCGGTAGCGCT	1664
Db	1353	TGAGCGGAGGCGAGCGTGTATTTGGCCGTGGAGATGTTGAACAAAGATCAGCGGTAGCGCT	1412
Qy	1665	TCTCCAAAGACAGACAGAAACAATTTCAAGATGTTTGTCTGTCTTCTGCGCACTGGCGTTTC	1724
Db	1413	TCTCCAAAGACAGACAGAAACAATTTCAAGATGTTTGTCTGTCTTCTGCGCGCATGGCGTTTC	1472
Qy	1725	ACTGTGCTTACATGTATCCAACAGGATCCGCACTCAGAAATGCATCTTACAGGGTTTACATGG	1784
Db	1473	ACTGTGCTTACATGTATCCAACAGGATCCGCACTCAGAAATGCATCTTACAGGGTTTACATGG	1532
Qy	1785	AGAGGCTTCTCTACACAGCAATCTGCACTCCGAGAGATGGCAAGGCTCATATGGGCTTCA	1844
Db	1533	AGAGGCTTCTCTACACAGCAATCTGCACTCCGAGAGATGGCAAGGCTCATATGGGCTTCA	1592
Qy	1845	ACCTTACAGACAGCAATCTGCGGGGACATCTGAGCTTATCCATTTGACATTTGGTCTCTTCCG	1904
Db	1593	ACCTTACAGACAGCAATCTGCGGGGACATCTGAGCTTATCCATTTGACATTTGGTCTCTTCCG	1652
Qy	1905	AGAACATGTGGCTTGGGATCTTTTGTCTACATGATCCATTCGGTCTTGTGGGACATCTGTT	1964
Db	1653	AGAACATGTGGCTTGGGATCTTTTGTCTACATGATCCATTCGGTCTTGTGGGACATCTGTT	1712
Qy	1965	TTGAACCTTGA AAAATTTGTGCCGTTTATCATGTCTGTGAAGAAAGAACTATGGCGGGTTC	2024
Db	1713	TTGAACCTTGA AAAATTTGTGCCGTTTATCATGTCTGTGAAGAAAGAACTATGGCGGGTTC	1772
Qy	2025	CTTACCAAACTGGAAGATGACATGACGATGAGGACACTGACATGATCCATTACTTCAAA	2084
Db	1773	CTTACCAAACTGGAAGATGACATGACGATGAGGACACTGACATGATCCATTACTTCAAA	1832
Qy	2085	ACAAACAATGGCTCTTCAACAAGCTTCAGCGCAAGAGGCTTGCTAATTCGTGTCTGGCC	2144
Db	1833	ACAAACAATGGCTCTTCAACAAGCTTCAGCGCAAGAGGCTTGCTAATTCGTGTCTGGCC	1892
Qy	2145	ATGACCTTGAACCAAGGGGCTTCAAGTAACAGTACTGTGCAAGATTTGACACACCCCTTGG	2204
Db	1893	ATGACCTTGAACCAAGGGGCTTCAAGTAACAGTACTGTGCAAGATTTGACACACCCCTTGG	1952

QY	2205	CGCGCGCTGTA	CTCCACTCTCCACCA	ATGAGACAA	CAACA	CTTCTCCGACGAGGTGCATATCC	2264
Db	1953	CGCGCGCTGTA	CTCCACTCTCCACCA	ATGAGACAA	CAACA	CTTCTCCGACGAGGTGCATATCC	2012
QY	2265	TTGACGCTGGA	AGGGGCA	CAATATCTTCTCCAC	CTCGTGCACGAGGTTCGAGCAGGTGC		2324
Db	2013	TTGACGCTGGA	AGGGGCA	CAATATCTTCTCCAC	CTCGTGCACGAGGTTCGAGCAGGTGC		2072
QY	2325	TGGAGATCAT	CCGCAAA	AGCCATATCGCACA	CCGACCTCGCCCTTATATCTTTGGGAA	CAGGA	2384
Db	2073	TGGAGATCAT	CCGCAAA	AGCCATATCGCACA	CCGACCTCGCCCTTATATCTTTGGGAA	CAGGA	2132
QY	2385	AGCAGTTTGA	GAGAGATGTAC	ACAGACAGGGT	CGCTGAACCTCCACAA	CCAGTCCCATCCGAG	2444
Db	2133	AGCAGTTTGA	GAGAGATGTAC	ACAGACAGGGT	CGCTGAACCTCCACAA	CCAGTCCCATCCGAG	2192
QY	2445	ACCGTGTCA	TCCGCTTGATGATGAC	CGCTGTGATCTTTTGCTCTGTGAC	CAAACTATGAC		2504
Db	2193	ACCGTGTCA	TCCGCTTGATGATGAC	CGCTGTGATCTTTTGCTCTGTGAC	CAAACTATGAC		2252
QY	2505	CAGTTACAAA	TTTGACAGCGAATGATATATATG	CAAAATTCGTGGCTGAGGGTGA	TGAGA		2564
Db	2253	CAGTTACAAA	TTTGACAGCGAATGATATATATG	CAAAATTCGTGGCTGAGGGTGA	TGAGA		2312
QY	2565	TGAAGAA	GCTGGGCATACAGCCCATTCATATG	TGAGACAGACACAA	CGAGATGAAGTCC		2624
Db	2313	TGAAGAA	GCTGGGCATACAGCCCATTCATATG	TGAGACAGACACAA	CGAGATGAAGTCC		2372
QY	2625	CTCAAGGG	CGAGCTCGGATTTCTAAAGCTGTGGCA	TTCCCTGTATATACACTTGA	CGGC		2684
Db	2373	CTCAAGGG	CGAGCTCGGATTTCTAAAGCTGTGGCA	TTCCCTGTATATACACTTGA	CGGC		2432
QY	2685	AGATTCCTCCCA	CCACACAGAGCCCTCTGTAAAGCC	CTGCAGGGATTA	CTCAATCACTAGTGG		2744
Db	2433	AGATTCCTCCCA	CCACACAGAGCCCTCTGTGTAAAGCC	CTGCAGGGATTA	CTCAATCACTAGTGG		2492
QY	2745	AGAAGGTAA	TTTCGGGGGAAAGAGACAGCAATGTG	GAATTCAGGCCACCGCCGGCGCTTA			2804
Db	2493	AGAAGGTAA	TTTCGGGGGAAAGAGACAGCAATGTG	GAATTCAGGCCACCGCCGGCGCTTA			2552
QY	2805	GCAAGAGCA	CACTGAGAAAGCTGAAAGCTGAAGG	TTGAAACATGATCTGAAAGTGA	AGTCC		2864
Db	2553	GCAAGAGCA	CACTGAGAAAGCTGAAAGCTGAAGG	TTGAAACATGATCTGAAAGTGA	AGTCC		2612
QY	2865	TGATGTC	TGCGCCAGCAACCGACTCAACTCTGTCTGTGACT	TCGTTCTTTTGTTTTCA			2924
Db	2613	TGATGTC	TGCGCCAGCAACCGACTCAACTCTGTCTGTGACT	TCGTTCTTTTGTTTTCA			2672
QY	2925	GGGGTGAAA	CCCCCTGTCAAGAGGTACCGTGCATATC	CATGTGAAGCAGACGACTCC			2984
Db	2673	GGGGTGAAA	CCCCCTGTCAAGAGGTACCGTGCATATC	CATGTGAAGCAGACGACTCC			2732
QY	2985	TGCTTGC	CCGACACACACTCGTGAAGTGAACAC	CCGAGCTCTGCGGTTCAGAGCTCGG			3044
Db	2733	TGCTTGC	CCGACACACACTCGTGAAGTGAACAC	CCGAGCTCTGCGGTTCAGAGCTCGG			2792
QY	3045	CTATCTCCG	TGGCTCCACTCGGAATGCAATTTGCTCC	ACGAGCCAGCACTGCATCG			3104
Db	2793	CTATCTCCG	TGGCTCCACTCGGAATGCAATTTGCTCC	ACGAGCCAGCACTGCATCG			2852
QY	3105	TCGTGAG	GGGGGACAGAACCA	CAGGAAGGTTCTTGCTGCATCTTCC	ATGAAGGTTGTG		3164
Db	2853	TCGTGAG	GGGGGACAGAACCA	CAGGAAGGTTCTTGCTGCATCTTCC	ATGAAGGTTGTG		2912
QY	3165	CCAAGTTCC	TGTTCTGTGTCATGCTGCTGTGCTTGG	TGTGATGTTAGGAATGGACACA			3224
Db	2913	CCAAGTTCC	TGTTCTGTGTCATGCTGCTGTGCTTGG	TGTGATGTTAGGAATGGACACA			2972
QY	3225	CGCCCCCTGT	TTGTGAAGTTTACATGTGAACCTTCTTA	TAGTTTACAGATTTGTGTGCCCCG			3284
Db	2973	CGCCCCCTGT	TTGTGAAGTTTACATGTGAACCTTCTTA	TAGTTTACAGATTTGTGTGCCCCG			3032

QY	3285	GGACACATGTATATGAAGGTCA	CAGTCCACAGGTGACAGAGAAATCCAAACTGTGATTAC	33444
Db	3033	GGACACATGTATATGAAGGTCA <th>CAGTCCACAGGTGACAGAGAAATCCAAACTGTGATTAC</th> <td>30922</td>	CAGTCCACAGGTGACAGAGAAATCCAAACTGTGATTAC	30922
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QY	3405	CTCAGAAAGAAAGCATACCTCTG <th>CCCTCATCCAGGGGACACAGGGTACATCCAGGCATCG</th> <td>34664</td>	CCCTCATCCAGGGGACACAGGGTACATCCAGGCATCG	34664
Db	3153	CTCAGAAAGAAAGCATACCTCTG <th>CCCTCATCCAGGGGACACAGGGTACATCCAGGCATCG</th> <td>32122</td>	CCCTCATCCAGGGGACACAGGGTACATCCAGGCATCG	32122
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QY	3525	ACTGATGCTTCGGGCACTGGCC <th>CAATCCCTTATACAAAGAAATTAATAAGGACATA</th> <td>35844</td>	CAATCCCTTATACAAAGAAATTAATAAGGACATA	35844
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Db	3333	TTAAATTTCTCCACAGCA	CAAA	3354
RESULT 4				
US-10-659-770-11				
Sequence 11, Application US/10659770				
Publication No. US20040152106A1				
GENERAL INFORMATION:				
APPLICANT: ROBERTSON, Harold				
APPLICANT: DENOVAN-WRIGHT, Eileen				
APPLICANT: NOVANEURON, INC.				
TITLE OF INVENTION: GENE NECESSARY FOR STRIATAL FUNCTION,				
TITLE OF INVENTION: USES THEREOF, AND				
TITLE OF INVENTION: COMPOUNDS FOR MODULATING SAME				
FILE REFERENCE: 2817/102				
CURRENT APPLICATION NUMBER: US/10/659,770				
CURRENT FILING DATE: 2003-09-10				
PRIOR APPLICATION NUMBER: 09/680,208				
PRIOR FILING DATE: 2000-10-06				
PRIOR APPLICATION NUMBER: 60/217,765				
PRIOR FILING DATE: 2000-07-12				
PRIOR APPLICATION NUMBER: 60/158,043				
PRIOR FILING DATE: 1999-10-07				
NUMBER OF SEQ ID NOS: 12				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 11				
LENGTH: 7581				
TYPE: DNA				
ORGANISM: unknown				
FEATURE:				
OTHER INFORMATION: CDNA				
FEATURE:				
NAME/KEY: unsure				
LOCATION: 3383, 3384				
OTHER INFORMATION: a or g or c or t/u, unknown, or other				
FEATURE:				
NAME/KEY: unsure				
LOCATION: 3392, 3397				
OTHER INFORMATION: a or g or c or t/u, unknown, or other				
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NAME/KEY: unsure				
LOCATION: 3399, 3401				
OTHER INFORMATION: a or g or c or t/u, unknown, or other				
FEATURE:				
NAME/KEY: unsure				
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OTHER INFORMATION: a or g or c or t/u, unknown, or other				
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NAME/KEY: unsure				
LOCATION:				

[illegible]

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1545 ACGAGGAGGTGGACCTGTACACAGGCTACACACAGAGAACATTTGTGTATGCCATAG 1604
1293 ACGAGGAGGTGGACCTGTACACAGGCTACACACAGAGAACATTTGTGTATGCCATAG 1352
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1353 TGAAGCGAGGAGGCGGATTTGGCGGTGGACAGTGGTGAACAAGATCAGCGGTAGCGCT 1412
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2853 TCTGAGGGGCGACAGACCAACAGAGAGTTCCTTGCTGCATCTCCATGAGGGGTGCG 2912
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3152 CTCAGAAAGAGCACTACCTGCGCCCTCATCCAGGGGACAGAGGTAATCCCAAGCAATCG 3211
3465 GGAACATGAAGCTCTCACTTCAACATGTCCAAGTAATTAACACCTGCCCTCCCTCC 3524
3212 GGAACATGAAGCTCTCACTTCAACATGTCCAAGTAATTAACACCTGCCCTCCCTCC 3271
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RESULT 5
US-10-202-107-1
; Sequence 1, Application US/10202107
; Publication No. US20030096323A1
GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: James, Larry C.
; APPLICANT: Leibel, Lorraine A.
; APPLICANT: Menikoff, Frank S.
; APPLICANT: Strick, Christine A.
; TITLE OF INVENTION: PD510 CELL-BASED ASSAY AND SEQUENCES
; FILE REFERENCE: PC2111ANIS
; CURRENT APPLICATION NUMBER: US/10/202,107
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/308,978
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-202-107-1

Query Match      72.4%; Score 2610.6; DB 5; Length 3219;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 2844; Conservative 0; Mismatches 214; Indels 35; Gaps 7;

QY 525 GTTTGACGATGAAAAGGTGAAAGGCTATCTTCTCCATCCCGAGTATTAGAAAT 584
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QY 585 TTGTTCTGAAAGTGTAGTGACAGACTGTGAAAAGTGTGAAAGAAACCAACA 644
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DB 363 ACCTGCTCCCTATGAGCTCAGAGCATCATCAGATAGCCAAAGCCGAGATTG 422
QY 825 CACTGACTTCTTGGAGAGTGAATATAGCCTGTGTGTTCATACCAACCCGAGATGA 884
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DB 483 AGGAAGCCCAACCCCGGCTCATCCCTGACAGGCGCCATCACCCAGGCTACCATCTCTG 542
QY 945 CCAAGAGGCAAGTCTAGGAAGAGCTGTGTAAGAGATATCTTGGAGATGAGGAT 1004
DB 543 CCAAGAGGCAAGTCTAGGAAGAGCTGTGTAAGAGATATCTTGGAGATGAGGAT 602
QY 1005 TTCTCGAGGTACTGCGCTGGAATCAAGAAACCCGATCCAGTCTGTTCTTTGCTTGCCA 1064
DB 603 TTCTCGAGGTACTGCGCTGGAATCAAGAAACCCGATCCAGTCTGTTCTTTGCTTGCCA 662
QY 1065 TTGTCACTGCTATGGAAGATTGATCTTGAATCTGTACAGGCACTGTGGGCAAG 1124
DB 663 TTGTCACTGCTATGGAAGATTGATCTTGAATCTGTACAGGCACTGTGGGCAAG 722
QY 1125 AGGCGCTTTCGCTCAGCATCAGAGGTTGCAACAGGCAATCTTGTGGGCTTCCGTAG 1184
DB 723 AGGCGCTTTCGCTCAGCATCAGAGGTTGCAACAGGCAATCTTGTGGGCTTCCGTAG 782
QY 1185 CAATACACAGGTGAGGTGTGTAGAGTCTCCGCAAAACAGACCGAACTGAATGACTTCC 1244
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DB 783 CAATACACAGGTGAGGTGTGTAGAGTCTCCGCAACAGACCGAACTGAATGACTTCC 842
QY 1245 TACTGACGTATCAAAAGCATATCTTTGATATACATATGTTGCCATATACCTCTACTTTGAAC 1304
DB 843 TACTGACGTATCAAAAGCATATCTTTGATATACATATGTTGCCATATACCTCTACTTTGAAC 902
QY 1305 ACATCATATATATATCAAAAAATCTAGTAAGCGGACCGGCGGCTCTTCCAGGTG 1364
DB 903 ACATCATATATATATCAAAAAATCTAGTAAGCGGACCGGCGGCTCTTCCAGGTG 962
QY 1365 ACCACAAGAACAGAGCTGTACTCGACCTGTGTAACATTTGGAGAGAGAGAGGGA 1424
DB 963 ACCACAAGAACAGAGCTGTACTCGACCTGTGTAACATTTGGAGAGAGAGAGGGA 1022
QY 1425 AGCCCATCTTCAAGAAACCAAGAGATCATATTTTCCATTTGAAGAAAGGATTTGCTGTGTC 1484
DB 1023 AGCCCGTCTTCAAGAAACCAAGAGATCATATTTTCCATTTGAAGAAAGGATTTGCTGTGTC 1082
QY 1485 AGTGGCAAGAACAGGCGAAGTCTTGAACATTTCCGATGCGGACCGGCTTGA 1544
DB 1083 AGTGGCAAGAACAGGCGAAGTCTTGAACATTTCTGATGCTTACGAGACCGGCTTGA 1142
QY 1545 ACAGGAGGTGACCTGTACACAGGCTACACAGAGAACATTTCTGTATGCCATAG 1604
DB 1143 ACAGGAGGTGACCTGTACACAGGCTTACACAGGAGAACATTTCTGTATGCCATAG 1202
QY 1605 TGAGCGAGGCAAGCTGTATTTGCGTGACAGATGTGAACAGATCAGCGGTAGCGCT 1664
DB 1203 TGAGCGGCGGACCGGTATCGGTGTGTGTCAATGGTTAAAGATCAGCGGACGCGCT 1262
QY 1665 TCTCCAAAGACAGAGAACAACTTCAAGATGTTGCTCTTTCGCGGACCTGCGCTTGC 1724
DB 1263 TCTCCAAAGACAGATGAGAACAACTTCAAGATGTTGCTCTTTCGCGGACCTGCGCTTGC 1322
QY 1725 ACTGTGCTAACATGTACCAAGAGATCCGCACTCAGATGATCTTACAGGTTACCATG 1784
DB 1323 ACTGTGCTAACATGTACCAAGAGATCCGCACTCAGATGATCTTACAGGTTACCATG 1382
QY 1785 AGAAGCTTCTTACCAACAGCATCTGCACTCCAGAGAGTGGCAAGGCTCATGCGCTTCA 1844
DB 1383 AGAAGCTTCTTACCAACAGCATCTGCACTCCAGAGAGTGGCAAGGCTCATGCGCTTCA 1442
QY 1845 ACCTACAGAGCGCATCTGCGGAGACATGAGATATTTCCATTTGACATTTGCTCTTTCG 1904
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DB 1503 AGAACAATGTGGGCTGTGGATCTTTGTACATGATTCATGCGTCTTGTGGGACATCTCTGT 1562
QY 1965 TTGAACCTTGAATAATTTGCGGCTTTTATCATGTCTGTGTAAGAAACATATCGCGGCTTC 2024
DB 1563 TTGAACCTTGAATAATTTGCGGCTTTTATCATGTCTGTGTAAGAAACATATCGCGGCTTC 1622
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DB 1683 ACAAACAATGGGCTTCAACAGACTGAGGCAAGAGGCGCTTAAATTTGCGTGTGCGC 1742
QY 2145 ATGACCTGACCAACAGGCGCTTCAATACAGTACCTGACGAAGTTCAGACACCCCTG 2204
DB 1743 ATGACCTGACCAACAGGCGCTTCAATACAGTACCTGACGAAGTTCAGACACCCCTG 1802
QY 2205 CGGCGCTGTACTCTCACTTCAACATGAGAGCAACCACTTCTCCAGAGGTTCATCC 2264
DB 1803 CTGCGTTTGTACTCTCACTTCAACATGAGAGCAACCACTTCTCCAGAGGTTCATCC 1862
QY 2265 TTGAGCTGAAAGGCAATATCTTCCACCTGAGCTCAGCGAGTACGACAGGTG 2324
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Db	1863	TCAGCTGGAAAGACACAAACATCTTCTCCACCCCTAGCTCCAGCAGATACAGCAGCTGC	1922
Oy	2325	TGGAATCATCCGCAAAAGCCATCATCGCCACCGCCTCGCCCTATATCTTGGGAA	2384
Db	1923	TGGAATCATCCGCAAAAGCCATCATCGCCACCGCCTCGCAGCTGTATCTTGGGAA	1982
Oy	2385	AGCAATTGGAAGAGATGTATCCAGACAGGGTCGTAACTCCACAAACCAATGCCATCGAG	2444
Db	1983	AGCAATTGGAAGAGATGTATCCAGACAGGGTCGTAACTCCACAAACCAATGCCATCGAG	2042
Oy	2445	ACCGGTATCGGCTGTAGATGATCGCTGTGATCTTGTGCTGTGACAAACTATGGC	2504
Db	2043	ACCGGTATCGGCTGTAGATGATCGCTGTGATCTTGTGCTGTGACAAACTATGGC	2102
Oy	2505	CAGTTACAAAATTGACAGCGATGATATATATGAGAAATTCGTGGCTGAGGGTGTATGA	2564
Db	2103	CAGTTACAAAATTGACAGCAATATGATATATATGAGAGTTCTGGGCTGAGGGGATGAGA	2162
Oy	2565	TGAGAGACTGGGCACTACAGCCCATTTCTATGATGACAGAGACAGCGAGATGAATCC	2624
Db	2163	TGAGAGATTGGGGATACAGCCCATCTTATGATGACAGAGACAGCGAGATGAATGCC	2222
Oy	2625	CTCAAGGGCAGCTGGGATTTCTACATATGCTGTGGCCCATTCCTGCTATACACTTGAAGC	2684
Db	2223	CTCAAGGACAGCTTGGATTTCTACATATGCTGTGGCCCATCTCTGCTATACACTTGAAGC	2282
Oy	2685	AGATCCTCCACCCACAGAGCCTCTGTGAAGGCTCGAGGGATTAACCTCATCATGTGGG	2744
Db	2283	AGATCCTCCACCCACAGAGCCTCTGTGAAGGCTCGAGGGATTAACCTCATCATGTGGG	2342
Oy	2745	AGAGGTAAATTCGCGGGAGAGACAGCATATGTGATTTCAAGGCCAGAGCCCGGCGCTTA	2804
Db	2343	AGAGGTAAATTCGAGGGGAGAGACAGCAATGTGATTTCAAGGCCA-----GCACATA	2396
Oy	2805	GCAAGAGACACCTGAGAAAGCTGAACGTGAAGGTTGAAGACATGATCCGAAATGACGTCC	2864
Db	2397	GCAAAAGCACATGTAGAAAGCCGACAGAGAGGTGATGAATGATCTGAGG-----	2448
Oy	2865	TGATGTCTGCCAGCAGACCCGACTCAACTGTCTTCTGTACTTCGTTCTTTTGG-----	2917
Db	2449	TGATGTCTGCCAGCAGACCTGACTCAACTGTCTTCTGTACTTCGTTCTTTTATTTTAT	2508
Oy	2918	-TTTTCAAGGGTGA AAAACCCCTGTCAAGAGTACCGTCCGATATCATATGTAAGCAGA	2976
Db	2509	TTTTTTTACGGGGGTGA AAAACCTCTCTCAGAAAGTACCGTCCGATATCATATGTAAGCAGA	2568
Oy	2977	CGACTCCCTGCTGTGCGGACACACACTCGGAGACATGAGAGAACCGAGCTCTGCGGTTC	3036
Db	2569	TGACTCCCT-----GGCACACCTCGGACCGTGAAGAACCCGGGCTCACCCGTTTCA	2621
Oy	3037	GACGTCCGCTACTCGGTGGCTCACTCACTCCGATGCTATTTGTCTCCAGGCGACGA	3096
Db	2622	GACATCCGCTATTCATATGGCTTCGCTCAACCCCGAATGCCATTTGCTACAGGCGACGA	2681
Oy	3097	CTGCATCTGTGAGAGGGGACAGAGACACAGAGAGATTTCTTCCCTGCATCTCCCATGA	3156
Db	2682	CTGCAGCTGTGAGAGGGGACAGAGACACAGAGAGGTTCTTACTCTGCATCTTCCATGA	2741
Oy	3157	GGGTGTGG---CAAGTTCCTTGCTGTCTGTGCATCTGCTGTGCTTGTGTGGTATGG	3213
Db	2742	GGGTGTGGTTCTGTGTTTCACTCTCAACAGAGATGCTACTCTGTGTGTGGCTTTGTATGA	2801
Oy	3214	AATGGGACACAGCCCTTGTGTTGTGAAGTTTACATGTAACCTCTTATAGGTTAACTGAG	3273
Db	2802	AATGGGACACAGCCCTTGTGTTGTGAAGTTTACATGTAACCTCTTGTAGGTTAACTGAG	2866
Oy	3274	TTTGTGGCTGGGACACATGTATATGAAGTCACTGTCCAGGTGACAGAGAAATCCAAA	3333
Db	2861	TTTCGTAGCTGGGACCCCTGTATATGAAGTTTACAGTCCACAGGTGATAGAGAAATTCAG	2920
Oy	3334	CTGTGATTTACAGGTGCACTACAGGTATGCTCTTCACTATCTGGGGGCACTAGGTG	3393
Db	2921	CTGTATAGTTACAGGTGCACTATATGTTGTTCACTTCACTTTTACCTGGGGGCACTAGAGTGT	2980

QY	3354	AGTCTGCTCCACTCAGAGGAAGCATACCTTGCCCTCATCTCAGGGGACACAGGGTACAT	3453
Db	2981	AGTCAGCTCCACGAGGAAGGAAGATACCTCTGCTCCATCAAGGGGACACAGGGTACAT	3040
QY	3454	CCGAGGCATCGGGGAACTGAAGCTCTCATCTCAACCATGTCAAGATTTAAACACCTC	3513
Db	3041	CCGAGGCATCAGAGAACCTGCAG--CTACCTCAACCATGTCAAGATTTAAACACACC	3098
QY	3514	CCCTCCCCCTCACTGTAGCTTGGGCACTGCGCAATCCTTTATACAAAGAAATATA	3573
Db	3099	CCCATCCCCCTCACTGTAGCTTTGGCAACTTGGCAACCTTCAACAAGAAATATA	3158
QY	3574	AGTAAAGCATTAATTTAAAAAATAAAAA	3606
Db	3159	AGTAAAGGCGTATAATTTCTCCGACAGCAAAA	3191

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RESULT 6
US-10-887-276-1
; Sequence 1, Application US/10687276
; Publication NO. US2005002636a1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: James, Larry C.
; APPLICANT: Leibel, Lorraine A.
; APPLICANT: Menhitl, Frank S.
; APPLICANT: Strick, Christine A.
; TITLE OF INVENTION: PDE10 CELL-BASED ASSAY AND SEQUENCES
; FILE REFERENCE: PC33111A1S
; CURRENT APPLICATION NUMBER: US/10/887,276
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US/10/202,107
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/308,978
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-887-276-1

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Query Match 72.4%; Score 2610.6; DB 8; Length 3219;

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Best Local Similarity  51.58;  Freq: NO. 0;
Matches 2844;  Conservative  0;  Mismatches 214;  Indels  35;  Gaps  7;

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QY	585	TTGTGTTTCGAAAGTTTAGTGCAGAGACTGTGAAAAAGTGTGTAAGAGAAAAACA	644
Db	183	TTGTGTTTCGAAAGTTTAGTGCAGAGACCGTGAAGAGTGTGTAAGAGAAAAACA	242
QY	645	AAGCAAAAAGATGAACCATCTCCCAAGGAAGTCAGCAGGTACCAAGATTCGAATATGCAG	704
Db	243	AAGCAAGAAGATGAACCATCTCTTAAGGAAGTCACAGGTATCACAGAACGAATGCAGG	302
QY	705	GAGTCGTGTACGAGCTGAACAGTACATATAGAGACGCGCTGAGACACGGCGGGGCAAC	764
Db	303	GAGTCGTGTACGAGCTGAACAGCTACATATAGAGACGCGCTGAGACACGGCGGGGCAAC	362
QY	765	ACCTGCTCTCTATAGAGCTACGACAGCATCATCAGGATTCGCCAAMAAGCCGACGGATTTG	824
Db	363	ACCTGCTCTCTATAGAGCTAAGCAGTATCATCAGGATTCGCCAAMAAGCCGACGGATTTG	422
QY	825	CACGTACTCTCTGAGAGAGTGAATAATACCTGTGTGTTTATACACCCGGGATGA	884
Db	423	CACGTACTCTCTGAGAGAGTGAATAATATCTGTGTGTTTACACACACCCGGGATGA	482
QY	885	AGGAAGGCCAACCCCGCTCATCTCCTGACAGGAGCCATCACCCAGAGGTTCACACATCTCTG	944

||||| 483 AGAAGGTCAACCCCTCTCATCTCCGCAAGGCCCATACCCAGGGACACCATCTTCTG 542
||||| 945 CCTACGTGGCCAAAGTCTAGAGAACGTTGTGTAGAGGATATCTTGGGGATGAGCGAT 1004
||||| 543 CCTATGTGGCCAAAGTCTAGAGAACCTCTGTGTAGAGGACATCTTGGGGATGAGCGAT 602
||||| 1005 TTCTCTGAGGTACTGGCCTTGGAAATCAGAAACCCGCATCCAGTCTGTTCTTTGCTTGCCA 1064
||||| 603 TTCCAGAGGCACTGGTCTGAGGTCAAGAAACCGAAATCCAGTCTGTTGCTTCTCTTA 662
||||| 1065 TTGTCACTGTCCATTTGAGAGCTTATTTGGCATCTTTGAACCTGTACAGGCACTGGGGCAAG 1124
||||| 663 TTGTCACTGTCCATTTGAGAGCTTATTTGGCATCTTTGAACCTGTACAGGCACTGGGGCAAG 722
||||| 1125 AGGCTTTGCTGCTCAGCATCAGAGGTTGCAACAGCCAACTTGTCTTGGGGCTTCCGTAG 1184
||||| 723 AGGCTTTGCTGCTCAGCATCAGAGGTTGCAACAGCCAACTTGTCTTGGGGCTTCCGTAG 782
||||| 1185 CAATACACCAAGGTGACAGGTGTAGAGGTCTGCGCAACAGACCGAACTGATGACTTCC 1244
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||||| 1365 ACCACAAGAACAGAGAGCTTACTCGGACCTGTTTGAATTTGGGGAGAGAGAGGGGA 1424
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||||| 1485 AAGTGGCAAGACAGGCGAAGTCTTGAACATTTCCCGATGCTACGCGGACCTCGCTTGA 1544
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||||| 1143 ACAGGAGGTGACCTGTACACAGGCTATACAGGCGAAACATTTCTGTATGCCATAG 1202
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||||| 1323 ACTGTGCTTAACATGTACACAGATCCGCCACTCAGATGATCTACAGGGTTAACATAG 1382
||||| 1785 AGAAGCTTTCCTTACACAGATCTGCACTTCCAGAGGTGCAAGGGCTTCACTGCGCTTCA 1844
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||||| 1845 ACCATACAGACGATCTGCGGGGACATCGAGTATTCACCTTGAACATTTGATGCTTTCG 1904
||||| 1443 ACTTGCAGACGCACTTGCAGGACATCGAGTATTCACCTTGAACATTTGATGCTTTCG 1502
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||||| 1503 AGAATGTGGCTTGGGATCTTTGTCTACATGATCAATCGGTCTTGTGGGACATCTGTT 1562
||||| 1965 TTGAATTTGAAAAATTTGCGGTTTATCATGTCTGTGAAGAAACATATCGGGGGTTC 2024
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||||| Db 1623 CTTACCAACAATGGAAGCATGAGTCAAGGTGCAACCTGACATGATATGCTTCAAA 1682
||||| Qy 2085 ACAACAATGGCTCTTCAACAAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 2144
||||| Db 1683 ACAACAATGGCTCTTCAACAAGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAG 1742
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||||| Qy 2205 CGGCTGTACTTCACTTCAACATGAGAACACCACTTCTCCAGAGGTTGATCCATCC 2264
||||| Db 1803 CTGCTGTGTACTTCACTTCAACATGAGAACACCACTTCTCCAGAGGTTGATCCATCC 1862
||||| Qy 2265 TTGAGCTGGAAGGACCAATATCTTCTCACCTGAGCTTCAAGGAGTACAGAGAGTGC 2324
||||| Db 1863 TCCAGCTGGAAGGACCAACATCTTCTCACCTGAGCTTCAAGGAGTACAGAGAGTGC 1922
||||| Qy 2325 TGAAGATCATCCGCAAAAGCATATGCAACGACCTGCGCTTATACCTTGGGAACAGA 2384
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||||| Qy 2385 AGCATTTGAGAGAGATGTACAGACAGGGTCTGTAAACCTTCCCAACAGTCCCATCG 2444
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||||| Qy 2445 ACCGTTCATCCGCTTGAATGATGATGCTGCTGATCTTTGCTGTGACCAACATATGTC 2504
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||||| Db 2103 CAGTTACAAAATTTGACAGCAATGATATATGCAAAATTTGAGGCTGAGGGGATGAGA 2162
||||| Qy 2565 TGAAGAGCTGGGCAATACAGCCATTTCTATGATGACAGAGACAGAGCAAGAGAGAGTCC 2624
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||||| Db 2283 AGATCTTCCACCAACAGAGCTTGTGTAAGGCTTGAAGGCTTGAAGGATTAACCTCAATCAGTGG 2342
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||||| Qy 2805 GCAAGAGCAACCTGGAAGAGCTGAAGTGAAGGTTGAAGCTGATCTGGAAGTGAAGCTGC 2864
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||||| Qy 2865 TGAATGTGCTGCGCAACAGCTCAACCTGCTTCTGATCTTGTGCTTCTTTTG----- 2917
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||||| Qy 2918 -TTTTCAAGGGGTGAAAAACCCCTGTCAAGAGTACCGTGTGCAATATCAGTGAAGAGA 2976
||||| Db 2509 TTTTAAACGGGGTGAAAACCTCTCAAGAGGTACCGTGTGCAATATCAGTGAAGAGA 2568
||||| Qy 2977 CGACTCCCTGCTTGCAGCAACAGCTTCAACCTGCTTCTGATCTTGTGCTTCTTTTCA 3036
||||| Db 2569 TGAATCTCT-----GCGACACCTGAGACCTGAGCAACCGGGCTTCAACGCTTCA 2621
||||| Qy 3037 GAGTCCGCTACTCCGTGCTTCAACCTGCACTGCACTCGAATGTATTTGCTTCCAGGCGACA 3096
||||| Db 2622 GACATGGCTATTCATGGCTCGGCTGACCCCGAATGCAATTTGTCTACAGGCGAGAA 2681
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QY	3097	CTGCATCTCTCGAAGGGGGGAGAGACCA	CAGAGAGGTTCTTGCTCGATATCTCCCAAGA	3158
Db	2682	CTGGGCTTGGCTGGAGGGGGAGAGACGA	CAGAGAGGGGTTCTTAACTCTGCATCTTCCAAAGA	2741
QY	3157	GGGAGTGG--CCAGTTCCCTGGATTCTGTG	CATGCTCTGCTGGTGGCAATGGTTAGG	3213
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QY	3214	AATGGGACACAGCCGCCCTTGTGTGAAGTT	TATCATGTGACCTTCTTATAGTTAACTGAG	3273
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Db	3041	CCGAGGCACTGAGAACTGCAAG--CTCAC	CTCAACCATGTCTCAAGAAATTAAACACACC	3098
QY	3514	CCCTCCCCCTCACTGTAGCTTTCGGCA	ACTGGCCATATCCCTTTTATCAAGAGAAATTAA	3573
Db	3099	CCCATCCCTCATCTGTAGCTTGTGGCA	ACTTGCACAAACCTTTCACAAAGAAATTTAA	3158
QY	3574	AGTAAGGCATTAATAATTAAAAA	AAAAAAAAAAAA 3606	
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RESULT 7
US-10-440-998-3
? Sequence 3, Application US/10440998
? Publication No. US20030215919A1
? GENERAL INFORMATION:
? APPLICANT: Loughney, Kate
? TITLE OF INVENTION: Phosphodiesterase 8A
? FILE REFERENCE: 27866/35047
? CURRENT APPLICATION NUMBER: US/10/440,998
? CURRENT FILING DATE: 2003-05-19
? PRIOR APPLICATION NUMBER: US/09/686,055
? PRIOR FILING DATE: 2000-10-11
? PRIOR APPLICATION NUMBER: 08/951,648
? PRIOR FILING DATE: 1997-10-16
? NUMBER OF SEQ ID NOS: 48
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 4389
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (3)..(2411)
? US-10-440-998-3

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	Query Match	Similarity	Score	1871.8	DB 6	Length 4389
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	Matches 2065	Conservative	0	Mismatches 322	Indels 0	Gaps 0
Oy	415	CTTCCCGCTTGCGACGTTTGAGCGCTGACCTTCCGACATGAGATGACCTTC	474			
Db	2	CTTGGCCCTCGCGCGCGCGCGCGCTCTCTTCCGCTCCGACATGAGATGACCTTC	61			
Oy	475	TAAACATCGAGTTGCTTCCGAGGCTGACCGAGTGTTCCTCAGCCCCAGTTTGACGGA	534			

Db	62	TAAATAATGCAAGCTGCTTCGGAAGCTGACCGAATGCTTCTTGAGCCCAATTGGACAGA	121
Qy	535	TGAAAAGGTGAAGGCTATCTTTCTCCATCCCAGGTATTGATGTAATTTGTTCTGA	594
Db	122	TGAAAAAGTGAAGGCATATCTTTCTTTCACCCCAGGATTTAGATGTAATTTGATCTGA	181
Qy	595	AAAGTTTATGTCANAGACTGTGGAAAAGTGGCTGTAAGAGGAAAACCAACAAGCAAAAGA	654
Db	182	AAAGTTTATGTCANAGACATGAGAGAAATGGCTAAGAGGAAAGAACAAATCAGAAAGA	241
Qy	655	TGAACCATCTCCCAAGGAGTCAGACAGGTACAGAGATACGATATGACGAGAGTCGTGTA	714
Db	242	TGAATTCGGCTCTTAAGGAGATCAGACAGGTACCAAGATACGATATGACGAGGAGTTGTATA	301
Qy	715	CGAGCTGAACGCTACATATAGACAGCGCTTGACACAGGGCGGGACAAACCATGCTCTCT	774
Db	302	TGAACCTAAACAGCTATATATAGAACAAACGGTTTGACACAGAGAGAAACAACAGCTACTCT	361
Qy	775	CTATAGAGCTCAGCAGCATCATCAGGATATGCCCCAAAAGCCGACGGATTTGACATGTAATT	834
Db	362	CTATAGAACATGACGACATCATTTAAATAATGCAAAAAGCCATGATATTTGACATGTAATT	421
Qy	835	CCTTGAGAGTGCATATAATAGCTGTGTGTGTATATACACCCCGGATGAAAGAGGCCA	894
Db	422	CCTTGAGAGTGCATATAATAGCTGTGTGTGTATATACCGCACCTGGGATTAAGAGAGAAA	481
Qy	895	ACCCCGGCTACCTCTGACAGGAGCCCATCAACCAAGGATACCAATCTCTGCTTATGTGGC	954
Db	482	ACCCCGGCTACCTCTGCTGAGGAGCCATCACTCAAGGAGCAACCGCTCTCTGCTTATGTGGC	541
Qy	955	CAAGCTTATGAGAAAGCTGTGTGTGTATGAGAGATATCCTTGAGGATAGAGATTTCCCTGAGG	1014
Db	542	CAAGTCCAGGAAAAACATGCTATGTAAGAGACATCTTGAGATATAGCAATTTCAAGAGG	601
Qy	1015	TACAGGCTGTGAAATCAAGAAACCCGCAATCCAGCTGTGTTCTTGCTGGCCATGTGTCACTGC	1074
Db	602	TACAGGCTGTGAAATCAAGAAACCTGATACGATCTGTGTTCTTGCTTGATCCAAATTTGTACATGC	661
Qy	1075	CATTGAGACTTGTATGATTTGATGCTTTGAACTGTACAGGACCTGAGGACCAAGAGGCTTCTG	1133
Db	662	AAATTGGTGACTTGTATTTGGTATTTCTGAGCTGTATTCGGCATGAGGACCAAGAGGCTTCTG	721
Qy	1135	CCTCAGCCATCAGAGAGTTTGGACACAGCCAAATCTTGCTTGGGCTTCCGTAGAGAAATACACA	1199
Db	722	TCTTATGTCACAGAGAGTTTGGACACAGCCAAATCTTGCTTGGGCTTCAGTAGCAATATACACA	781
Qy	1195	GATGAGGTTGTATGAGGTTCTGCGCAAAACAGACCGAATGAAATGACTTCTACTCGAGCT	1254
Db	782	GATGAGGTTATGCAAGAGCTTCTGCGCAAAACAGACCGAATGAAATGAACTTCTACTCGAGCT	841
Qy	1255	ATCAAAAGCATATCTTTGATTAACATATGTTGCCATAGACTCTCTACTTGAACATCATGAT	1314
Db	842	ATCAAAAAATATTTTGTATTAACATATGTTGCCATATGATTTCTACTTGAACATCATATGAT	901
Qy	1315	ATATGCAAAAAATCTATGTGAACGCGCACCGCTGGCGCTCTTCCAGGTGAGCCACAAGA	1374
Db	902	ATATGCAAAAAAATCTGTGAATGCGCATCGTTGTGCACTTTTCCAGGTGAGCCATTAAGAA	961
Qy	1375	CAAGGAGCTGTACTCGGACTGTGTTGCACTTGAGGAGAGAAAGAGGGAAGCCCATCTT	1434
Db	962	CAAGGAGTTATTTACAGCCCTTTTGTATTTGGAGAGGAAAAGAGAAAACCTGTCTT	1022
Qy	1435	CNAGNAGACNAGAGATCAGATTTTTCATTTGAGNAGAGATTGCTGTGACATGTGGCAAG	1494
Db	1022	CNAGNAGACNAGAGATNAGATTTTTCATTTGAGNAGAGATTGCTGTGCAAGTGTGCAAG	1081
Qy	1495	AAACAGGCGAAGCTTTGAACATTTCCGATGCTTAAGCGGACCTCTGCTTTAACAGGAGAGT	1554
Db	1082	AAACAGGCGAAGCTCTGAAATTTCCAGATGCTTAAGCACCAAGCTTTTAAACAGAGAAAT	1144
Qy	1555	GGACCTGTATCACAGGCTACACAGAGGAAATTTCTGTGTATGCGCAATGATGAGCGCGAG	1614
Db	1142	AGACTTGTATCACAGGCTACACAGCGGAAATCTCTGTGATGCGCAATGCTGACGCGAGG	1201

QY	1615	CAGCGTATATGGCGTGTGGAGATGGTGAACAGATGACGGGTAGCGCTTCTTCAAGAC	1674
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Db	1202	CAGGTATATAGTGTGGTGGAGATGGTGAACAGATGACGGGTAGCGCTTCTTCAAGAC	1261
QY	1675	AGACGAGAACCACTTCAAGATGTTGGCTCTTCTGGCAGTCGGCTTGCATCTGTCTAA	1734
Db	1262	AGATGAAACCACTTCAAAATGTTGGCGTCTTGTGGCTTATAGCTTACCATCTGTCTAA	1321
QY	1735	CATGTACCAAGATCCGCCACTAGAAATGATCTTACAGGGTTACATGGAGAAAGCTTTC	1794
Db	1322	TATGTATCATGTGAATTTGGCCACTAGATGTGATTTACCGGGTAAAGATGAAAAAGCTGC	1381
QY	1795	CTACCAAGCATCTGCACCTCCGAGGATGGCAAGGCGTCATGCGCTTCAACCTACGAC	1854
Db	1382	CTACCATGCAATTTGTACTTACAGAAAGTGGCAAGGCTCATGTCAATTCACCTTCCCGT	1441
QY	1855	ACGCATCTGCCGGGACATCTGAGCTATTTCACTTTTGACATTTGCTCTTTCGAGAACATGTG	1914
Db	1442	GGCTCTCTGCAAAAGAAATTTGATTTCCACTTTTGACATTTGCTCTTTCGAGAACATGTG	1501
QY	1915	GCCTGGGATCTTGTGTATATGATTCATCGGTCTTGTGGGACATCTCTGTTTGAACTTGA	1974
Db	1502	GCCTGGGATTTTGTGTATATGATTCATCGGTCTCTGTGGGACATCTCTGTTGAGCTTGA	1561
QY	1975	AAATTTGGCCGTTTATCATATGTCTGTGAGAAAGAACTATCCGGGGGTTCCCTTACCAAA	2034
Db	1562	AAAGTTGTGTGTTTATTTATGTCTGTGAGAAAGAACTATCCGGGGGTTCCCTTATCCAA	1621
QY	2035	CTGGAGCATGCAAGTCAAGGTGGGCACTGCATGTATCCATCTTCAAAAACAATATGG	2094
Db	1622	CTGGAGCATGGGTCACTGTAGCACTGCATGTATGCCATCTTCAAGAACATTCACAC	1681
QY	2095	CCTCTTTCACAGACCTCGAGCCGCAAGGCGTGTATTTGCGTGTGTGGCATGACCTTGA	2154
Db	1682	GCTTTTCACAGACCTTGGAGCCCAAGAGCTGTGTTTGGTGTGTATGACCTTGA	1741
QY	2155	CCACAGGGGCTTCAAGTAAACGTACCTGCAGAAAGTTCCACCACTTCCGGCGGCTCTCTA	1801
Db	1742	CCACAGGGGCTTCAAGTAAACGTACCTGCAGAAAGTTCCACCACTTCCGGCGGCTCTCTA	1801
QY	2215	CTTCCACTTCCACCATGGAGCAACCACTTCTCCGAGAGGATGCCATCTTCAAGCTGGA	2274
Db	1802	CTTCCACTTCCACCATGGAGCAACCACTTCTCCGAGCTGTGTCTCATCTTCCAGTTGGA	1861
QY	2275	AGGGGACAATATCTTCTCCACCTGAGTCTCAGCAGATGACGAGTGTCTGAGATCAT	2334
Db	1862	AGGGGACAATATCTTCTCCACCTGAGTCTCAGCAGATGACGAGTGTCTGAGATCAT	1921
QY	2335	CCGCAAGGCATCATCGCACCGACCTTGGCTGTATCTTTGGGAAACAGAAAGCATTTGGA	2394
Db	1922	CCGCAAGGCATCATTTGCCACAGACCTTGTATTACTTTGGGAAACAGAAAGCATTTGGA	1981
QY	2395	GGAGATGTACCGAGACAGGTCGCTGAACCTCCACAAACAGTCCCATGGAGCCGGTAT	2454
Db	1982	AGAGATGTACCGAGACCGGATCTAAACCTTATATATCATCATCAATAGAACCGTGTAT	2041
QY	2455	CGGCTGTATGATGATCGCTGTGATCTTGTGCTGTGTGACAAACTATGAGCATTTACAA	2514
Db	2042	TGGTTGTATGATGATCGCTGTGACCTTGTGTGTGTGTGACAAACTGTGGCCGTACAA	2101
QY	2515	ATTGACAGCGAATGTATATATATGCAAAATCTGGGCTGAGGGGTATGATGAAGAACT	2574
Db	2102	ATTGACAGCGAATGTATATATATGCAAAATCTGGGCTGAGGGGTATGAATGAAGAAAT	2161
QY	2575	GGGCAATACGCCCATCTCTATGATGACAGAACAAAGCAATGAAATGCTTCAAGGCA	2634
Db	2162	GGGCAATACGCCCATCTCTATGATGACAGAACAAAGATGAAATGCTTCAAGGCA	2221
QY	2635	GGTCCGATCTTCAATAGCTGTGGCACTTCCCTGTATACCACTTGAAGCAGATCTCTCC	2694
Db	2222	GCTTGGGTTCTAATAGCTGTGGCACTTCCCTGTATACCACTTGAAGCAGATCTCTCC	2281

Oy		2695	ACCCAGAGCCTTGTGTAAGGCCTGCAGGGATTAACCTCAATCAGTGGAAGATAAT	2754
Db		2282	TCCACGAGCCTTTCTGAAAGCATCAGGATTAATTCTCATGTCGTGGAGAAAGTGAT	2341
Oy		2755	TCGCGGGGAAGAGACACAATATGTGATTTGAGGCCAGGCCCGCGC	2801
Db		2342	TCGAGGGAGAGACTGCAACCTGGATTTCATCCCATCCGTGGCTC	2388
RESULT 8				
US-09-321-801-1				
; Sequence 1, Application US/09321801				
; Patent No. US20020115176A1				
; GENERAL INFORMATION:				
; APPLICANT: Lanfear, Jeremy				
; APPLICANT: Robas, Nicola M.				
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES				
; FILE REFERENCE: PC9477A				
; CURRENT APPLICATION NUMBER: US/09/321,801				
; CURRENT FILING DATE: 1999-05-27				
; EARLIER APPLICATION NUMBER: 9826777.6				
; EARLIER FILING DATE: 1998-12-04				
; EARLIER APPLICATION NUMBER: 9823882.7				
; EARLIER FILING DATE: 1998-10-30				
; EARLIER APPLICATION NUMBER: 9811500.9				
; EARLIER FILING DATE: 1998-05-28				
; EARLIER APPLICATION NUMBER: 9908247.1				
; EARLIER FILING DATE: 1998-04-09				
; EARLIER APPLICATION NUMBER: 9910801.1				
; EARLIER FILING DATE: 1999-05-10				
; NUMBER OF SEQ ID NOS: 19				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 1				
; LENGTH: 2554				
; TYPE: DNA				
; ORGANISM: Human				
US-09-321-801-1				
Query Match	51.5%;	Score 1858.4;	DB 3;	Length 2554;
Best Local Similarity	86.8%;	Pred. No. 0;		
Matches 2045;	Conservative	0;	Mismatches 311;	Indels 0;
Gaps				
Oy		446	TTGGCTCCGACATGGAAGATGACCCCTTAACATGGGAGTTGCTTCGGAAGCTGACC	505
Db		1	TTGGCTCCGACATGGAAGATGACCTTCTAATAATGAGCTGCTTCCGAAAGCTGACC	60
Oy		506	GAGTCTTTCCTCAGCCCAAGTTGACGGATGAAAAGTGAAGGCTTATCTTCTCCAT	565
Db		61	GAGTCTTTCCTCAGCCCAAGTTTGAACATGAAAAAGTAGGCAATCTTCTCTTCAAC	120
Oy		566	CCCCAGTATTAGATGAATTTGTTCTGAAAGTGTAGTGACAGACTGTGGAAAAATGG	625
Db		121	CCCAGTATTAGATGAATTTGTACTGAAAGTGTAGTGACAGACTGTGGAAAAATGG	180
Oy		626	CTGAAGAGAAAAACCAACAAGCAAAGAATGAACATCTTCCACAGGAGTACAGAGTAC	685
Db		181	CTGAAGAGAAAAACAACAATCAAGAATGATAGCTCTTAAAGAAAGTCAGCAGTAC	240
Oy		686	CAGGATTAAGAAATATCAGGAGAGTGTGTACGAGTGAACAGCTATCATAGACAGGCTG	745
Db		241	CAAGATTAAGAAATATCAGGAGAGTGTGTATGAACTTAACAGCTTATTAAGAACAGGTTG	300
Oy		746	GACACGAGCGGAGAACACCACTGCTCTCTATGAGCTCAGCAGCATCATCAGATTAAGC	805
Db		301	GACACGAGAGAGAACACCACTGCTCTCTATGAGCTCAGCAGCATCATTAATAATAGCC	360
Oy		806	ACAAAAGCCGACGATTTGCACTGTACTTCTTGAAGATGCAATATATAGCTGTGTGTG	865
Db		361	ACAAAAGCCGATGATTTGCACTGTATTCTTCTTGAAGATGCAATATATAGCTGTGTATA	420
Oy		866	TTTCATTAACAACCCGGAGATGAAGAAAGCCAAACCCGGGCTCATCCCTGCAGAGGCCATCAC	925
Db		421	TTTCATTAACAACCTGGGATTAAGAAAGAAACCCCGGCTCATCCCTGTGGGCCATCACT	480

QY 926 CAGGGTACCAACATCTGCTGACGTCAGAGTCTAGAGAGACGTTGTTGATAGAGAT 985
 DB 481 CAGGGCACCAACGCTCTGCTTATATGAGTCAGAGAACACTGTTATAGAGAC 540
 QY 986 ATCTTGGGAGATGAGCGATTTCTCGAGGTACTGCGCTGGAATTCAGAAACCCGATCCAG 1045
 DB 541 ATCTTGGAGATGAGAGATTTCCAGAGGTACTGGAATTCAGAGGACTGTATCCAG 600
 QY 1046 TCTGTTCTTTGCTTGGCCATTGTCTACGTGCATTGGAGACTTGTATGGCATCTTGAATCG 1105
 DB 601 TCTGTTCTTTGCTTCAATGTCTCATGCAATTTGGATTTGATTTCTTCAGAGCTG 660
 QY 1106 TACAGGCACTGGGGGAAAGAGGCTTTCGCTCAGCATCAGAGGTTGCAACAGCAT 1165
 DB 661 TATCGGCACTGGGGGAAAGAGGCTTTCGCTTATGTCACAGAGGTTGCAACAGCAAT 720
 QY 1166 CTGCTTGGGCTTCCGTAGCAATATACAGAGTGCAGTGTGTAGAGTCTCCCAACAG 1225
 DB 721 CTGCTTGGGCTTCAGTAGCAATATACAGAGTGCAGTGTGTAGAGGCTTTCCAACAG 780
 QY 1226 ACCGAATGATGATCTTCTTACTGACGATTCAAAGACATCTTTGATTAACATAGTGC 1285
 DB 781 ACAGAAATGAAATGATCTTCTTACTGACGATTCAAACATATTTTGTATTAAGTTGCA 840
 QY 1286 ATAGACTCTTACTGAAACATCATGATATATGCAAAAATCTAGTAAAGCCGACGCG 1345
 DB 841 ATAGATCTTCTTACTGAAACATCATGATATATGCAAAAATCTAGTAAAGCCGATCT 900
 QY 1346 TGCGGCTCTTCCAGAGTGCACCAAGAACAGAGAGTGTACTCGACCTGTTTGAAT 1405
 DB 901 TGTGCACTTTTCCAGAGTGCACCAAGAACAGAGAGTGTATATTCAGACTTTTGAAT 960
 QY 1406 GGGGAGGAGAGAGAGAGAGCCCATCTTCAAGAAACCAAGAGATCAGATTTTCATT 1465
 DB 961 GGAAGAGGAGAGAGAGAGAACTGTCTTCAAGAAACCAAGAGATATTTTCAAT 1020
 QY 1466 GAGAAAGGATTTGCTGTGCAAGTGCAGAGAGAGGAGGATTTGAACCTCCCATGCG 1525
 DB 1021 GAGAAAGGATTTGCTGTGCAAGTGCAGAGAGAGGAGGATTTGAACCTCCCATGCG 1080
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 DB 1081 TATGAGAGACCAACGCTTTTAAACAGAGAGGTGAGCTGTATACAGGCTTACACAGAGAAAC 1140
 QY 1586 ATCTGTGTATGCCATATGATGAGCCGAGGACGCTGATTTGCGTGTGCAATGCTGAAC 1645
 DB 1141 ATCTGTGTATGCCATATGATGAGCCGAGGACGCTGATTTGCGTGTGCAATGCTGAAC 1200
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 DB 1201 AAGATCACCGTATGAGGCTTCTCTTAAACAGATGAAACACTTCAAAATGTTTGCCTG 1260
 QY 1706 TTCTGCGCACTGGCTTGTGCACTGTCTTAAACATGTATCAGAGATCCGCACTCAGAAATGC 1765
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 QY 1766 ATCTACAGGGTTACATGAGAGAGCTTTCTTACACAGATCTGCACTCCGAGAGTGC 1825
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 DB 1381 CAGAGCTTATAGCGGCTTCAACCTTCCCGGCTCTCTGAAAGAAATGAAATATTTCCAC 1440
 QY 1886 TTGTACATTTGCTCTTTCGAGAAACATGTCCTGGGATCTTTGTCTACATGATCCAG 1945
 DB 1441 TTGTACATTTGCTCTTTCGAGAAACATGTCCTGGGATCTTTGTCTACATGATCCAG 1500
 QY 1946 TCTTGTGAGCAATCTGTTTGAACCTTGAAATTTGTGCGTTTATCATGTCGTGAAG 2005
 DB 1501 TCTGTGTGAGCAATCTGCTTGAAGCTTGAAGATTTGTGTGTTTATATGCTGTGAAG 1560

QY 2006 AAGAACTATCGCGGGTCTTACCAACATGGAAGATGACAGGTGGCACACTGC 2065
 DB 1561 AAGAACTATCGCGGGTCTTATACAACTGGAAGATGAGGGTCACTGTAGCACACTGC 1620
 QY 2066 ATGTATGCCATATCTTCAAAACAAATGCGCTCTTCAAGACCTTGAGCGCAAGGCTTG 2125
 DB 1621 ATGTATGCCATATCTTCAAAACAAATGCGCTCTTCAAGACCTTGAGCGCAAGGCTTG 1680
 QY 2126 CTAAATGCGTGTCTGTGCATGACCTTGACCAAGGGGCTTCAATTAAGCTTACCTGCG 2185
 DB 1681 CTAAATGCGTGTCTGTGTGCATGACCTTGACCAAGGGGCTTCAATTAAGCTTACCTGCG 1740
 QY 2186 AAGTTGCAACACCCCTGCGCGCTGTACTCACTTCCACCATGAGAACCAACACTTC 2245
 DB 1741 AAGTTGCAACACCCCTTACACGCTCTTACTCACTTCCACCATGAGAACCAACACTTC 1800
 QY 2246 TCCGACGCTGTCCATCTTCACTGGAAGGGCAATATCTTCCACCTGAGCTCC 2305
 DB 1801 TCCGACGCTGTCCATCTTCACTGGAAGGGCAATATCTTCCACCTGAGCTCC 1860
 QY 2306 AGCGAGTACGAGAGGCTGTGAGATCATCCGCAAGGCATCATGCGACGACCTGCG 2365
 DB 1861 AGCGAGTACGAGAGGCTGTGAGATCATCCGCAAGGCATCATGCGACGACCTTGT 1920
 QY 2366 CTATCTTGGGAAACAGAGAGGATTTGAGAGATGTACAGACAGGGTCTGTAACCTC 2425
 DB 1921 TTATATCTTGGGAAACAGAGAGGATTTGAGAGATGTACAGACAGGGTCTGTAACCTT 1980
 QY 2426 CACAAACAGTCCCATGAGACCGGTCTCATCGCTTGTATGATGATGCTGCTGTATCTTGC 2485
 DB 1981 AATATATCATCATCATAGAGACCGGTCTCATCGCTTGTATGATGATGATGCTGCTGTAT 2040
 QY 2486 TCTGTGACCAAACTATGCGCCAGTTTCAAAATTTGACAGGAAATGATATATGACAAATTC 2545
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 QY 2546 TGGGCTGAGGGTGTATGATGAGATGAGAGAGTGGGCAATACAGCCCATCTTATATGAGACA 2605
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 QY 2606 GACAAAGGATGAGATGCTCTTCAAGGGGCACTCGGATTTCTACATGCTGTGCGCATTTCCC 2665
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 QY 2666 TGCTATACCACTTGAACCAAGATCTCTCCACCCACAGAGCCTCTGCTGAGAGGCTGCAAG 2725
 DB 2221 TGCTATACCACTTGAACCAAGATCTCTCTCCACAGAGCCTCTGCTGAGAGGCTGCAAG 2280
 QY 2726 GATAAATCTCAATCAATGAGGAGAGGATTTGCGGGGAGAGAGACAGCAATGTGATTTCA 2785
 DB 2281 GATAAATCTCAATCAATGAGGAGAGGATTTGCGGGGAGAGAGATGAGAGATGAGATTTCA 2340
 QY 2786 GAGCCAGGCGCGGCGC 2801
 DB 2341 TCCCATCTCGTGGCTC 2356

RESULT 9
 US-10-618-252-1
 ; Sequence 1, Application US/10618252
 ; Publication No. US20040018542A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanfear, Jeremy
 ; APPLICANT: Robas, Nicola M.
 ; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
 ; FILE REFERENCE: PC9477B
 ; CURRENT APPLICATION NUMBER: US/10/618,252
 ; PRIOR FILING DATE: 2003-07-11
 ; PRIOR APPLICATION NUMBER: 9826777.6
 ; PRIOR FILING DATE: 1998-12-04
 ; PRIOR APPLICATION NUMBER: 9823882.7
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 9811500.9

PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 9908247.1
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 9910801.1
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent Ver. 3.2
SEQ ID NO: 1
LENGTH: 2554
TYPE: DNA
ORGANISM: Human
us-10-618-252-1

Query Match 51.5%; Score 1858.4; DB 7; Length 2554;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 2045; Conservative 0; Mismatches 311; Indels 0; Gaps 0;

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DB 61 GAGTGTCTCTGAGCCCGATTGACGATGAAAAAGTGAAAGGCTATCTTCTCCAT 120
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DB 121 CCCAGGATTTAGATGATTTTGTATCTGAAAGTGTAGTGACAGAGAGAAATGG 180
QY 626 CTGAAGAGAAAAACAACAAGAAAAAGATGAACTTCCCAAGAAAGTCAAGAGTAC 685
DB 181 CTGAAGAGAAAAACAACAATCAGAAAGATGATCAGCTCTTAAGAAAGTCAAGAGTAC 240
QY 686 CAGGATACGAATTTGAGAGGAGTGTGTACGAGCTGACGATACAGAGAGAGGCTGTG 745
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DB 301 GACACGAGAGAGAGACAACAACGATCTCTCTATGAACTGAGCAGCATTAATAATAGCC 360
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QY 866 TTCAATACACCCGGGATGGAAGAGCAACCCCGGCTCATCCCTGAGGGGCCCATACCC 925
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DB 1141 ATCTGTGATATGCCATATGATGACCGAGGACCGTGTATTTGGGTGTGAGATGTGAAC 1200
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DB 1201 AAGATCAGCGGATAGGCGCTTCTTAACAGATGAAACCACTTCAAGATGTTTGTCTGC 1260
QY 1706 TTCTGCGCATGCGCTTTGACCTGTGTACATGTACACAGATTCGCACTCAGATGC 1765
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QY 1766 ATCTACAGGATTCATGAGAAAGCTTTCTTACACAGATCTGCACTTCCAGAGGTGG 1825
DB 1321 ATTTACCGGATTCATGAGAAAGCTGTCTTACATTAAGATTTGTACAGAAAGGTGG 1380
QY 1826 CAAAGCTCATGCGGCTTCAACCTACAGACGATGTGCGGGAATCAGAGCTATTTCCAC 1885
DB 1381 CAAAGCTCATGCGGCTTCAACCTTCCGAGCTGTCTGCAAGAAATTTGAATTTATTCAC 1440
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QY 2066 ATGTATGCCATTTCTTAAACAAACAATGCGCTTCTTACAGACTCGAGGCAAAAGGCTTG 2125
DB 1621 ATGTATGCCATTTCTTGAAGAAATACACAGCTTTTACAGACTTTGAGGCAAAAGGCTTG 1680
QY 2126 CTAAATTCGCTGTGTGCAATGACCTGACCAAGGAGGCTTCAAGTAACTGACTCTGAG 2185
DB 1681 CTGAATTCGCTGTGTGTATGATGACCTGACCAAGGAGGCTTCAAGTAACTGACTCTGAG 1740
QY 2186 AAGTTGACCAACCCCTGCGGCGGTGTACTCCACTTCCACATGGAAGCAACCACTTC 2245
DB 1741 AAGTTGACCAACCCCTGACCGGCTTCTTATCTTCACTTCACTGAGAGCAACCACTTC 1800
QY 2246 TCCCAAGCGGTGTCATCTTTCAGCTGGAAGGCAAAATTTCTTCCACCTGAGCTTC 2305
DB 1801 TCCCAAGCTGTGTCTTCTTCACTTTCAGTGAAGGCAAAATTTCTTCCACCTGAGCTTC 1860
QY 2306 AGCAGATACAGAGAGGTGTGAGATCATTCGCAAAAGCATCATCGCACAGACTGCGC 2365
DB 1861 AGTGAATATAGCAGAGGTGTGAGATCATTCGCAAAAGCATCATTCGCAAGACTGCGC 1920
QY 2366 CTATATCTTTGGAAACAGAAAGCAAGTTGAGAGATGTATCAAGACAGGAGTGTGAACTTC 2425

Db 1921 TTAATCTTTGGAAACAGGAAGAGTTGGAGAGATGTACCAACCGGATCACTAAACCTT 1980
Oy 2426 CACAAACGAGTCCATCGAGACCGTGTCAATCGGCTTGATGATGATGCTGTGTATCTTGC 2485
Db 1981 AATATCATCATCATAAGAGACCGTGTAAATGGTTTGAATGATGATGCTGTGTACCTTTGT 2040
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Oy 2606 GACAAAGCAATGAAAGTCCCTCAAGGGCAGCTCGGATTTCAATAGCTGTGGCCATTCCC 2665
Db 2161 GACAAAGAAAGATGAAAGTCCCGCCAGGCCAGCTTGGGTTCTACAAATGCGCTGGCCATTCCC 2220
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Db 2221 TGCTATACCACTTCAACCGAATCCTCCTCCACGAGCCCTTCTTGAAAGCATGACAG 2280
Oy 2726 GATAACCTCAATCAGTGGGAGAGGTAAATTCGCGGGGAGAGAGACAGCAATGTGATTTCA 2785
Db 2281 GATATCTCAGTCACTGGGAGAGAGGTGANTGAGGGGAGAGACAGCACTGATTTCA 2340
Oy 2786 GAGCCAGGCGCGCGC 2801
Db 2341 TCCCATCCGTGGCTC 2356

RESULT 10
US-09-321-801-3
; Sequence 3, Application US/09321801
; Patent No. US20020115176A1
; GENERAL INFORMATION:
; APPLICANT: Robas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321,801
; EARLIER FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; EARLIER FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1.
; SEQ ID NO 3
; LENGTH: 2798
; TYPE: DNA
; ORGANISM: Human
US-09-321-801-3

Query Match 49.6%; Score 1790.2; DB 3; Length 2798;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1981; Conservative 0; Mismatches 318; Indels 0; Gaps 0;
Oy 503 ACCGAGTGTCTCAGCGCCAGTTTGACGATGAAAAAGTGAAGGCTATCTTCTCTC 562
Db 303 ACCGAGTGTCTCAGAGAGCAGGTTTGACAGATGAAAAAGTGAAGGCAATCTTCTCTT 362
Oy 563 CATCCCGAGATTAATGATGAATTTGTTCTGAAAGTGTATGTCAGAGACTGTGAAAAAG 622
Db 363 CACCCCGAGATTAATGATGAATTTGTTCTGAAAGTGTATGTCAGAGACTGTGAAAA 422

Oy 623 TGGCTGAAGAGAAAAACCAAGAAAGAAAGATGAAACCATCTCCAGGAAGTCAGAG 682
Db 423 TGGCTGAAGAGAGAAACAACAAATCAGAGTGAATCAGGCTCCATAGGAAGTCAGAG 482
Oy 683 TACCAAGATACGAATATGACAGGAGTGTGTACGAGCTGAAACAGCTTACATAGAGAGGC 742
Db 483 TACCAAGATACGAATATCAGGAGTGTGTATATGAACTTAAACAGCTTATATGAAACAGG 542
Oy 743 CTGACACAGGCGGGGGAACAACACCTGCTCTCTATGAGCTCAGAGGATCATCAGATA 802
Db 543 TTGACACAGAGAGAGACAAACAGTACTCTCTATGAACTGAGACGATCATTTAAATA 602
Oy 803 GCCACAAAAGCCGACGGAATTTGACCTGTACTCTTGGAGAGTGAATATAGCTGTGT 862
Db 603 GCCACAAAAGCCGAGATTTGACCTGTATTTCTTGGAGAGTGAATATATAGCTGTGT 662
Oy 863 GTTTCATACCAACCCGGAGTGAAGAGCCACCCGGCTCATCTCTGACAGGGCCCATC 922
Db 663 ATATTCAAGCCACCTGGGATTAAGAGAGAAACCCCGCTCATCTCTGCTGGGCCCATC 722
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Db 843 CAGTCTGTTCTTGTGCTTACCAATGTCACTCAATGTGTGACTGATTTGATATTCAG 902
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Db 1383 AACATCTGTGACGCCATGTGACGCGAGGACGCTGATGAGTGTGTGCAAGTGTGTC 1442
Oy 1643 AACCAAGTACAGCGGATGAGGCTTCTCCAAAGACAGCGAACAATTCAGAGTTTGTCT 1702
Db 1443 AACCAAGTACAGTGTGAGGCTTCTCTTAAACAGATGAAACAACTTCAAAATGTTTCC 1502
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Db 1683 CACTTTGACATTTGTCTTTTGAAGAAAGATGCGCTCGGATTTTGTCTACATGATTCAT 1742
Qy 1943 CGGTCTGTGGGACATCTGTTTGAATCTGAAATTTGCGGTTTATCATGTTCTGTG 2002
Db 1743 CGGTCTGTGGGACATCTGCTGTGAGCTTGAAGAAATTTGTCTTTTATGTCTGTG 1802
Qy 2003 AAGAAAGACTATCGCGGGTCTCTTACCAACATGGAAGATGCACTGCGGACAC 2062
Db 1803 AAGAAAGACTATCGCGGGTCTCTTATCAACATGGAAGATGCGGTCATGAGACAC 1862
Qy 2063 TGCATGTATGCTTACTTCAAAACAATGCGCTCTTCAAGACTCGAGCGCAAGGC 2122
Db 1863 TGCATGTATGCTTACTTCAAAACAATGCAACGCTTTTCAAGACTCGGCAAGGA 1922
Qy 2123 CTGCTTAAATGCGGTGTGTGCTGCACTGAGACCAAGGGGCTTCAAGTAAAGCTACTG 2182
Db 1923 CTGCTTAAATGCGGTGTGTGCTGCACTGAGACCAAGGGGCTTCAAGTAAAGCTACTG 1982
Qy 2183 CAGAAATTCGACCAACCCCTGCGGCGCTGTACTTCACTTCAACATGAGCAACCA 2242
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Qy 2243 TTCTTCCAGAGCGGTGTCTTCACTTCACTGAGAGGCAATATTTCTTCCACTCTGAG 2302
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Db 2103 TCCAGAGAGTATGAGAGGCTGTGAGATGATCCGAAAGGCAATCCGCAACGCACTC 2162
Qy 2363 GCCCTTACTTGTGGAAACAGAAAGAGCTGTGAGAGATGTACCAAGAGGCTGCTGAAC 2422
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Qy 2483 TGTCTGTGTGACCAACTATGAGGCAAGTAAACAAATTTGACAGGAAATGATATATGAGAA 2542
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Db 2523 AGGATTAATCTCACTCACTGTGGGAGAAAGTATTTGAGAGGAGAGAGACTGCAACTGAT 2582
Qy 2783 TCAGGCGCAGGCGCGGCGC 2801

Db 2583 TCATCCCATCCGTGCTC 2601
RESULT 11
US-10-618-252-3
Sequence 3, Application US/10618252
Publication No. US20040018542A1
GENERAL INFORMATION:
APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, Nicola M.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC94778
CURRENT APPLICATION NUMBER: US/10/618,252
CURRENT FILING DATE: 2003-07-11
PRIOR APPLICATION NUMBER: 9826777.6
PRIOR FILING DATE: 1998-12-04
PRIOR APPLICATION NUMBER: 9823882.7
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 9811500.9
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 9908247.1
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: 9910801.1
PRIOR FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 3
LENGTH: 2798
TYPE: DNA
ORGANISM: Human
US-10-618-252-3
Query Match 49.6%; Score 1790.2; DB 7; Length 2798;
Best Local Similarity 86.2%; Pred. No. 0;
Matches 1981; Conservative 0; Mismatches 318; Indels 0; Gaps 0;
Qy 503 ACCGATGTTTCTTCAAGCCCGAGTTTGAAGATGAAAGGTGAAGGCTTATCTTCTC 562
Db 303 AGCCAGATGCTCCAGAGACAGGTTTGAAGATGAAAGGTGAAGGCAATATCTTCTCT 362
Qy 563 CATCCCGAGTATTAATGATTAATTTTGTGAAAGTTTATGTCAGAGACTGTGAAAG 622
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Qy 743 CTGACACGGGCGGGGACACCACTGCTCTCTATGAGCTCAGAGCATCATCAGAT 802
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Qy 863 GTGTTCATACACCCGAGATGAAAGAGCCAAACCCCGCTCATCCCTGTGAGGCCCAT 922
Db 663 ATATTCACCGCACCTGAGATTAAGAGAAAGAAACCCCGCTCATCCCTGTGAGGCCCAT 722
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Db 723 ACTCAGGCAACACGCTCTGTGCTTATGTGCGCAATTCAGAGAAACACGCTAGTAA 782
Qy 983 GATATCTTGGGAGTGAAGCATTTCTGAGATCTGAGCTGAGATCAAGAACCCGATC 1042
Db 783 GATATCTTGGAGATGAAGCATTTCTCAAGAGTATGAGCTGAGAACAGGAGCTGTATC 842
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Db 843 CAGTCTGTTCTTTGCTTACCAATGTCACTGCAATTGATGACTGATGTGATTTCTCGAG 902
Qy 1103 CTGTACAGGCACTGGGGCAAAAGAGGCTTCTGCTCAGCCATCAGAGAGTTTGCAAGACC 1162
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Db 1023 CAGACGAACTGAATGACTTCTTCTGACGATTCGAAGACATATTTGATTAATAGTT 1082
Qy 1283 GCCATGACTCTCTACTTGAACATCATGATATATGCAAAAAATTAAGTAAGCCGAC 1342
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Qy 1883 CACTTGAATGTGCTTTTGAAGAACATGTGCGCTGGGATCTTTGTCTACATGTATCAT 1942
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Db 1743 CGGTCTGTGGGACATCTGCTTTGAGCTTGAAGAAAGTGTGTGCTTTTATATGTCTGTG 1802
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Db 1803 AAGAGAACTATCGCGGGTCTTTTATCAACTGGAAGCATGCGGTCTGATACACAC 1862
Qy 2063 TGCATGTATGCAATCTTCAAAACAAACATGCGCTTCTTCAAGACTCTGAGGCGAAAGC 2122
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Qy 2123 CTGCTAATTTGCGTGTGTCATGACCTGACCAAGGAGCTTGAAGTAAAGCTACCTG 2182

Db 1923 CTGCTAATTTGCGTGTGTCATGACCTGACCAAGGAGCTTCAAGTAAAGCTACCTG 1982
Qy 2183 CAGAGTTTGAACCAACCCCTGGCGGCTGTATCTCACTCCACCATGAGCAACAC 2242
Db 1983 CAGAGTTTGAACCACTTGTGACCGCTTCTTACTTCACTTCCACCATGAGCAACAC 2042
Qy 2243 TTCTCCAGAGGTTTCCATCTTTCAGCTGGAAGGCAATATCTTCTCAACCTGAGC 2302
Db 2043 TTCTCCAGAGGTTTCCATCTTTCAGCTTTCAGTTGGAAGGCAATATCTTCTCAACCTGAGC 2102
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Db 2103 TCCAGTGAATATGACAGAGTGTGAGATCATTCGCAAGCCATCATGCGCACCTC 2162
Qy 2363 GCCCTATCTTTGGGAAAGGAGAGTGAAGAGATGTACAGACAGGAGCTGTAAC 2422
Db 2163 GCTTATATCTTTGGAAGAGAGAGTGAAGAGATGTACAGACAGGATCACTTAAC 2222
Qy 2423 CTCCAAACCAAGTCCCATGAGACCGTGTCAATCGGCTTGAATGATGACCTGTGATCTT 2482
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Qy 2543 TTCTGGGCTGAGGAGTGAATGAATGAAGAGTGGGCAATACGCCATCTTATATGAGAC 2602
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Qy 2723 AGGATTAACCTCATCATGTGGGAGAGATTTGGCGGGGAAAGACAGCAATGTGATT 2782
Db 2523 AGGATTAATCTCAGTCAAGTGGGAGAGAGTGAATGAGGGAGAGATGCAACCTGATT 2582
Qy 2783 TCAGGCCAGGCGCGCGC 2801
Db 2583 TCATCCCATCTCGTGGCTC 2601

RESULT 12
US-10-440-998-5
; Sequence 5, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 2786/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67) .. (2403)
US-10-440-998-5
Query Match 49.6%; Score 1787.4; DB 6; Length 3195;

Best Local Similarity 86.6%; Pred. No. 0; Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;

QY 525 GTTTACGGATGAAAAGTGAAGGCGCTATCTTCTCTCCATCCCGAGTATTAGATGAT 584

Db 104 GTTTACGATATATAAAGTGAAGGCGCTATCTTCTCTCCATCCCGAGTATTAGATGAT 163

QY 585 TTGTTCTGAAAAGTGTAGTGAAGAGCTGTGAAAAGTGTGTAAGAGAAAACCAACA 644

Db 164 TTGTTCTGAAAAGTGTAGTGAAGAGAGTGAAGAAATGGCTGAAGAGAAAACCAACA 223

QY 645 AACCAAAAGATGAACCATCTTCCCAAGAAAGTCAAGCGATACCAAGATTAAGATATGCGAG 704

Db 224 AATCAAAAGATGAATCGGCTCTCTAAGAAAGTCAAGCGATACCAAGATTAAGATATGCGAG 283

QY 705 GAGGTGTACAGAGTGAACAGCTACATAGAGAGCGCTGTGACAGCGGGGAGCAACC 764

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QY 765 ACCGTCTCTATAGAGCTCAGAGCATCATAGATAGCCACAAAAGCTGACGATTTG 824

Db 344 AGCTACTCTCTATGAATCAGAGCATCATTAATAATAGCCACAAAAGCTGATTTG 403

QY 825 CACTGTACTCTCTGTGAGAGTGCATATATAGCTGTGTGTGTTCATACACCCGGATGA 884

Db 404 CACTGTATTTCTTGTGAGAGTGCATATATAGCTGTGTATTTCAAGCACCTGGGATTA 463

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QY 1665 TCTCCAAAGACAGAGAAACAATTTCAAGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1724

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RESULT 14
US-10-458-839-2
Sequence 2, Application US/10458839
Publication No. US20030215898A1
GENERAL INFORMATION:
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Hunter, John Joseph
APPLICANT: Williamson, Mark
TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
FILE REFERENCE: 5800-71
CURRENT APPLICATION NUMBER: US/10/458,839
PRIOR FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: US/09/420,190
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 4381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (67)...(2403)
US-10-458-839-2

Query Match 49.6%; Score 1787.4; DB 6; Length 4381;
Best Local Similarity 86.6%; Pred. No. 0;

Matches 1971; Conservative 0; Mismatches 306; Indels 0; Gaps 0;
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DB 104 GTTTACCGATGAAAGGTGAAGGCTTATCTTCTCTCATCCCGAGGATATGATGAT 163
QY 585 TTGTTTGAAGGTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 644
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2505 CAGTTACAAATTTGACAGGCAATGATATATGACGAATTTCTGGGCTGAGGATGAGA 2564
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2565 TGAAGAGCTGGGCAATACAGCCATCTCTATGATGAGACAGACCAAGCAGATGAAGTCC 2624
2144 TGAAGAGATTTGGGAATACAGCCATCTCTATGATGAGACAGACCAAGCAGATGAAGTCC 2203
2625 CTCAAGAGGAGCTCGGATCTTCAATGCTGTGCGCATTTCCCTGCTATACCACTTGAAGC 2684
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2685 AGATCTCCCAACCAAGAGCTCTGTCTGAAGGCTGAGGAGATTAACCTCAATCATGAGG 2744
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RESULT 15
US-10-440-998-1
; Sequence 1, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2298)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (868)..(870)
; OTHER INFORMATION: The amino acid encoded by nucleotides 868-870 is
; OTHER INFORMATION: either Pro or Leu
US-10-440-998-1

Query Match 49.5%; Score 1785; DB 6; Length 2298;
Best Local Similarity 86.5%; Pred. No. 0; Mismatches 306; Indels 0; Gaps 0;
Matches 168; Conservative 1;

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1 TTGACGATGAAAGAGTAAAGGCTATCTTCTCTCAATCCCAAGTATTAAGTAAATT 60
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Search completed: January 12, 2006, 18:44:26
 Job time : 2733 secs

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QY	309	GCGCGCGGAGCTCTCTCGAATTTTCCGGGCGCGCGCGCGGCGCTGCGCTCGGCGCCCG	368
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Qy 1269 TTGATTAACATAGTTGGCATAGACTCTCTTAATTGAACATCATGATATATGCAAAAAATC 1328
Db 1092 TTGATTAACATAGTTGGCATAGACTCTCTTAATTGAACATCATGATATATGCAAAAAATC 1151
Qy 1329 TAGTGAAGCCGACCGCTGCGGCTTCTCAAGTGAACCAAGAAACAGAGGCTGTACT 1388
Db 1152 TAGTGAAGCCGACCGCTGCGGCTTCTCAAGTGAACCAAGAAACAGAGGCTGTACT 1211
Qy 1389 CGGACCTGTTTGAACATTTGGGAGAGAAAGAGGGAGGCCCATCTTCAAGAAAGCAAGG 1448
Db 1212 CGGACCTGTTTGAACATTTGGGAGAGAAAGAGGGAGGCCCATCTTCAAGAAAGCAAGG 1271
Qy 1449 AGATCAGATTTTCAATTGAGAAAGGATTTGCTGTCAAGTGGCAAGAACAGCGAGTCT 1508
Db 1272 AGATCAGATTTTCAATTGAGAAAGGATTTGCTGTCAAGTGGCAAGAACAGCGAGTCT 1331
Qy 1509 TGAACATTTCCGATGCTTACGGGAGACCTTCTGCTTTTAAAGAGAGGTGTGACAG 1568
Db 1332 TGAACATTTCCGATGCTTACGGGAGACCTTCTGCTTTTAAAGAGAGGTGTGACAG 1391
Qy 1569 GCTACACCAAGAGAACATTTCTGTATGCTCCATAGTGAAGGAGGCAAGGATGAGG 1628
Db 1628 GCTACACCAAGAGAACATTTCTGTATGCTCCATAGTGAAGGAGGCAAGGATGAGG

Db 1392 GCTATACCAAGCGGAAACATTTGTGTATGCCCATAGTAGAGCCGCGAGCGTATCGGTG 1451
Qy 1629 TGTGTGACAGATGTGAACAAAGATCAGCGGATAGCGCTTCTCCAAAGACAGACGAACAAT 1688
Db 1452 TGTGTGACAGATGTGAACAAAGATCAGCGGATAGCGCTTCTCCAAAGACAGACGAACAAT 1511
Qy 1689 TCAAGATGTTTGTCTCTTCTGCGACCTGAGCTTGTGACATGTATCAACAGAGA 1748
Db 1512 TCAAGATGTTTGTCTCTTCTGCGCTGAGCTTGTGACATGTATCAACAGAGA 1571
Qy 1749 TCCGCACTCAGATGATCTACAGGGTTACATGGAAGACTTTCTTCAACAGACATCT 1808
Db 1572 TCCGCACTCAGATGATCTACAGGGTTACATGGAAGACTTTCTTCAACAGACATCT 1631
Qy 1809 GCACTCCGAGAGAGGAGGAGGCCCATGCGGTTCAACTTCAAGACAGCATCTGCGGG 1868
Db 1632 GCACTCCGAGAGAGGAGGAGGCCCATGAGCACTTCAACTTCAAGACAGCATCTGCGGG 1691
Qy 1869 ACATGAGCTATTCACATTTTGAACATTTGCTCTTGAAGACATGTGAGCTGAGATCTTTG 1928
Db 1692 ACATGAGCTATTCACATTTTGAACATTTGCTCTTGAAGACATGTGAGCTGAGATCTTTG 1751
Qy 1929 TCTACATGATTCATCGTCTTGTGGGACATCTGTTTGAACCTGAAATTTGCGCTT 1988
Db 1752 TCTACATGATTCATCGTCTTGTGGGACATCTGTTTGAACCTGAAATTTGCGCTT 1811
Qy 1989 TTAATATCTGTGAGAGAGAACTATGCGGGTCTTACCAACATGGAAGATGCGAG 2048
Db 1812 TTAATATCTGTGAGAGAGAACTATGAGCGSWSCTTACCAACATGGAAGATGCGAG 1871
Qy 2049 TCACGGTGGCACATGATGTATGCAATCTTCAAAACAAAGATGCGCTTCTTCAAGACC 2108
Db 1872 TCACGGTGGCCACATGATGTATGCAATCTTCAAAACAAAGATGCGCTTCTTCAAGACC 1931
Qy 2109 TCGAGCGCAAGAGCGCTGTAATGCGGTCTGTGTCATGACTGTGACACAGGGCTTCA 2168
Db 1932 TCGAGCGCAAGAGCGCTGTAATGCGGTCTGTGTCATGACTGTGACACAGGGCTTCA 1991
Qy 2169 GTTAAAGCTATCTGAGAGAGTTGCAACCCCTGGGGGCGGTGATCTCAACTTCACCA 2228
Db 1992 GTTAAAGCTATCTGAGAGAGTTGCAACCCCTGGGGGCGGTGATCTCAACTTCACCA 2051
Qy 2229 TGGAGCAACCACTTCTCCAGACGAGTGTCCATCTTCAAGCTGGAAGGGCAATATCT 2288
Db 2052 TGGAGCAACCACTTCTCCAGACGAGTGTCCATCTTCAAGCTGGAAGGGCAATATCT 2111
Qy 2289 TCTCCACCTTGAAGCTCCAGAGATACAGACAGTGTGAGATCATCCGCAAAAGCATCA 2348
Db 2112 TCTCCACCTTGAAGCTCCAGAGATACAGACAGTGTGAGATCATCCGCAAAAGCATCA 2171
Qy 2349 TCGCACCAGACCTGCGCTTATCTTTGGGAAACAGGAACAGTTGAGAGATGTACAGA 2408
Db 2172 TCGCACCAGACCTGCGCATGTATCTTTGGGAAACAGGAACAGTTGAGAGATGTACAGA 2231
Qy 2409 CAGGTCGCTGAACCTCCACAAACAGTCCCATTCAGAACCGTGTCAATCGGCTTGAATGA 2468
Db 2232 CAGGTCGCTGAACCTCCACAAACAGTCCCATTCAGAACCGGCTGTATCGGCTTGAATGA 2291
Qy 2469 CTGCTGTGATCTTGTCTGTGTACCAATATGAGCGAGTTTGAACAAATTTGACAGCGAATG 2528
Db 2292 CTGCTGTGATCTTGTCTGTGTAGAAATATGAGCGAGTTTGAACAAATTTGACAGCGAATG 2351
Qy 2529 ATATATATGCAAGATTTCTGGGCTGAGGGTATGAGATGAAGAACTGTGGCATACAGCCCA 2588
Db 2352 ATATATATGCAAGATTTCTGGGCTGAGGGGATGAGATGAAGAACTGTGGGATACAGCCCA 2411
Qy 2589 TTCCATATGAGACAGAGACAGAGATGAGTCCCTCAAGGCGAGCTCGGATTTCTACA 2648
Db 2412 TTCCATATATGAGACAGAGACAGAGATGAGTCCCTCAAGGACAGCTTGGATTTCTACA 2471
Qy 2649 ATGCTGTGGCAATTCCTGTGTATACCACTTGAAGCAGATCTTCCACACAGAGCTTC 2708
Db 2472 ATGCTGTGGCAATTCCTGTGTATACCACTTGAAGCAGATCTTCCACACAGAGCTTC 2531


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/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 3640
/ LENGTH: 3397
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-3640

Query Match      5.1%; Score 184; DB 7; Length 3397;
Best Local Similarity 54.8%; Pred. No. 4,4e-34;
Matches 433; Conservative 0; Mismatches 345; Indels 12; Gaps 3;

QY 1968 AACTGAAAATTTGTCCTTTTATCATGTCTGTGAAGAAGATCTACGCGG---GTTC 2024
DB 2120 AACAGAGGTTCTTTCGATGATTTTGAAGTCAAGAAATATTCGAAGAAGCTTG 2179
QY 2025 CTTTACCACAACTGGAAAGCATGCAAGTCAAGGTCACACTGTCATGTATGCAATCTTCAA- 2083
DB 2180 CCTACCACAATTTGAGGCAAGCGCTTTAACAAGGCAAGTGCATGTTTGTCTGTGAAG 2239
QY 2084 -----AACAAACATGGCTCTTTCACAGACTGAGCGCAAGCGCTGAATTTGCGTGC 2138
DB 2240 CAGGCAAGATTCAAGACAGTTGACGATCTGAGACGCTTGATTTGCTGATTTGCCGCTT 2299
QY 2139 TGTGCCATGACCTGACCAACAGGGGCTTGATTAAGCTAACCTGACAGAGTTGACACCC 2198
DB 2300 TAAAGCATATTTGAGCAATCGGTGTGAACAATCATATACAGCGAGAGAGACACC 2359
QY 2199 CCTTGGCGGCGCTGATCTCACTCCACATGAGAGCAACCACTTCTCCAGACGGTGT 2258
DB 2360 CCTTGGCCAGCTGTACTGCTCACTCCACATGAGAGCAACCTTCCAGACGGTGTGA 2419
QY 2255 CCATCTTCAAGCTGGAAGGAGCAATATCTTCCACCTGTAGCTCCAGAGTACGAGAC 2318
DB 2420 TGGTCTTAAACGCCCAAGGCAACCAAGATCTCAGTGGCTTCTCATTTGAAGATATMAA 2479
QY 2319 AGGTGCTGAGATCATCCGCAAAAGCCATCATCGCCACCGACCTGCGCTATCTTTGGGA 2378
DB 2480 CCACATTTGAAATATATCAAGCAAGCAATTTTACCACTGACCTGATCATTTAAGA 2539
QY 2379 ACAGGAAGAGTTGAGAGATGTACCAAGAGGCTGCTGAACCTCCACCAACAGTCCC 2438
DB 2540 GACGAGAGAAATTTTGTGAATTAAGAAAAATTAAGATTCAAGTTTGAAGATCTCTTC 2599
QY 2439 ATCGAGACCGTGTATCGCTGTATGATGATGATGATGATGATGATGATGATGATGATG 2498
DB 2600 AAAAGAGATTGTTTCTGCGCAATGCTGATGATGATGATGATGATGATGATGATGATG 2659
QY 2499 TATGCGCAATTAACAAAATTGACAGCAATGATATATATATGACAAATCTGGGCTGAGG 2558
DB 2660 CCTGCGCTATTCAACAGAGATGACAGAACTGCTGACAGCGAATTTCTTTGATCAAGAG 2719
QY 2559 AT---GAGATGAAGAGCTGGGCATACAGCCCATTCCTATGATGACAGAGACAAAGCGAG 2615
DB 2720 ACAGAGAGAGAAAGAACTTAACATGAGACCGGCTGATCTAATGAACAGGAGAAAGAAA 2779
QY 2616 ATGAAGTCCCTCAAGGAGAGCTGATTTTCAATATGCTGTGCAATCTCCCTGCTATACA 2675
DB 2780 ATAAATATCCAAATATGCAAGTTGGGTTATGAGACCCCATCTGCTTGAAGCTGTATGAG 2839
QY 2676 CTTTGAAGGAGATCTCCACACCAAGAGACTGCTGCTGAAGGCTGACAGAGATTAACCTCA 2735
DB 2840 CCTTGAAGGAGATCTCCACACCAAGAGACTGCTTTCCTGCTGAGTGTGCAAGAAAGAGAG 2899
QY 2736 ATCAGTGGGA 2745
DB 2900 AAAAAATGGCA 2909

RESULT 4
US-11-136-527-2875
/ Sequence 2875, Application US/11136527
/ Publication No. US20050287570A1
/ GENERAL INFORMATION:
```

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/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William M
/ TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ PRIOR APPLICATION NUMBER: 2005-05-25
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 2875
/ LENGTH: 3997
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-2875

Query Match      5.0%; Score 179.2; DB 7; Length 3997;
Best Local Similarity 48.8%; Pred. No. 6,6e-33;
Matches 750; Conservative 5; Mismatches 723; Indels 60; Gaps 8;

QY 1244 CTACTGACGATATCAAAAGCATCTTTGATATACATAGTTGCCATAGACTCTCTACTTGA 1303
DB 1187 CTTCTCCAAAGTGGCAAAAGACCTTTCAACCACTGATGACGTCTGTCTGTCTACAG 1246
QY 1304 CACATCATGATATATGCAAAAATCTAGTGAACGCCGACCGCTGCGCTCTTCCAGGTG 1363
DB 1247 GAGATCATACAGAGGCAAGAACTTCAAGCAAGAGATGTGCTCCGTGTTCTGCTG 1306
QY 1364 GACCAAGAAACAAAGACTGTACTCGACCTGTTGACATTTGGGAGAGAAAGAGGGG 1423
DB 1307 GATCAAAATGAGCTGG-----TTGCCAAGTGTGATGATGGC 1342
QY 1424 AAGCCATCTTCAGAAAGACCAAGAGATCAAGATTTTCATTTGAGAAAGGATTCGTGT 1483
DB 1343 GGTGTATGAGACGATGAGATGATATGATATGATATGATATGATATGATATGATATGAT 1402
QY 1484 CAAGTGGCAAGAAAGGAGAGTCTTGAACATTTCCAGATGCTACGCGGACCTGCTGTTT 1543
DB 1403 CAGTGGGACACAGGCGCAAGTCTTGAACATTTCCAGATGATATGATATGATATGATATG 1462
QY 1544 AACAGGAGTGGACCTGTACACAGGCTTACACCAAGAGAAACATTTCTGTATGCCCCATA 1603
DB 1463 TATGCGGGGTATGAGACAGACAGCTGGCTTCGCAAGCGCAACATTTCTGCTGCTTATC 1522
QY 1604 GTGAGCCGAGGC---AGGTGATTTGGCTGTGACAGATGATGATGATGATGATGATGATG 1660
DB 1523 AAGAACGAGAAACCAAGAGTATCGGTGTGCTGATGATGATGATGATGATGATGATGATG 1582
QY 1661 GCTTCTCCAAAGACAGAGAGAAACCTTCAAGATGTTGCTGTCTTGGCGCACTGGGC 1720
DB 1583 TGTTCAGCAAAATTTGATGAGAGACCTGGCCACAGCTTCTCATATTTATGATGATTTAGC 1642
QY 1721 TTGCACTGTGTTAATGATGATACCAAGATTCGCCCATGAGATGATGATGATGATGATGATG 1780
DB 1643 ATCGCTCACTCTCTCTATTAACAAAAGGTGATGATGATGATGATGATGATGATGATGATG 1702
QY 1781 ATGAGAAAGCTTTCTTACCAAGACATCTGACATTCGAGAGAGTGGCAAGGCTCATAGG 1840
DB 1703 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1762
QY 1841 TTCAACCTAACAGACAGATCTGCGGAGCATGAGCATTTTCACTTTGATGATGATGATGATG 1900
DB 1763 GATGGCATCAACCTGTGGCGGCAATTAATCTCAACTTTGCAACTTCACTTAATCTCTCT 1822
QY 1901 -----TTGAGAAACATGTGGCTGGAGATCTTTGTCTACATGATGATGATGATGATG 1951
DB 1823 CGGTCTGCTGAGAGAGATATCTTATGAGCATCTGAGACATGCTGCAAGACATGAAAC 1882
QY 1952 GAGACATCTGTTTGAACCTTGA-----AAATTTGCGCTTTTATCATGATCTGTGAG 2005
DB 1883 TTCAATCAATTAACAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1942
QY 2006 AAGAACTATCGCGGCTCTTACCAACATGAGAAAGCATGACAGTACAGGTGGACACA----- 2061
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Db      1943  AAAGCTACCGGATCCGCCATACCAACGATGACGCTTCTGCTCTCACTT 2002
Qy      2062  --CTGATGATATGCAATCTTCAAAAACAATGAGCTTTTCAAGAGCTCGAGCGCAA 2119
Db      2003  TGTCTCTGCTTACAAAGATCTGAGCTCTCCAACTACCTGAGAGACATGAGATCTTT 2062
Qy      2120  GGCCTGTAATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2179
Db      2063  GGTGTATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2122
Qy      2180  CTGCAAGATTTGACCAACCCCTGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2233
Db      2123  CAGTGCGCTCGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2182
Qy      2234  CAACACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2293
Db      2183  AGGACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2242
Qy      2294  ACCCTGAGCTCCAGAGATGACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2353
Db      2243  CACTTCTCGGAGAGATCATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2302
Qy      2354  ACCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2413
Db      2303  ACRGACMTGGCACACCACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2359
Qy      2414  TGGCTGAACCTCCAGACAGATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2473
Db      2360  GGTATGACCGAACAACAAGACACACAGCTTCTTATGCTCTCTTATGACCTCC 2419
Qy      2474  TGTGATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2533
Db      2420  TGTGACCTCTGCAACAAGCAAGAGCTGGAACACACAGAAAGATGGGAGCTGATC 2479
Qy      2534  TATGCAAAATCTGGCTGAGGTGATGATGATGAAGAGCTGGGCTATACAGCCATCTC 2593
Db      2480  TCAAAAGATTTCTTCTCCAGAGAGCTTGGAGAGAGCCATGGGCAACGCACTGAG 2539
Qy      2594  ATGATGACAGAGACAGAGATGAGTCCCTCAAGGGAGCTGGATCTCAATGCT 2653
Db      2540  ATGATGATCGGAGAGAG--GCTTATCTCTGAACTTCAAGTCAAGCTTATGAGCAC 2596
Qy      2654  GTGGCAATTCCTGCTATACCACTTGAAGAGATCTCCCAACCAAGAGCTGCTGCT 2713
Db      2597  ATGCCAATGCCATCTCAAGCTGTTCAAGACCTGTTCCCAAGGACAGAGCTGAT 2656
Qy      2714  AAGGCTGCAAGGATTAACCTCAATCACTGAGGAGAGGT 2751
Db      2657  GAAAGGCTGCTCAATCTGAGCACTGAGCAAGGT 2694

RESULT 5
US-10-511-657-3
; Sequence 3, Application US/10511657
; Publication No. US2006003915A1
; GENERAL INFORMATION:
; APPLICANT: Lynkeus Biotech GmbH
; TITLE OF INVENTION: Means and Methods for the Specific Modulation of Target Genes in
; TITLE OF INVENTION: and the Eye and Methods for their Identification
; FILE REFERENCE: LY01A04/P-MO
; CURRENT APPLICATION NUMBER: US/10/511,657
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: EP02008761.5
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/431,173
; PRIOR FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3231
; TYPE: DNA
; ORGANISM: homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2586)
; OTHER INFORMATION: Homo sapiens phosphodiesterase 6B, cGMP-specific, rod, beta (cong
; OTHER INFORMATION: initial stationary night blindness 3, autosomal dominant)
US-10-511-657-3

Query Match      4.1%   Score 148.8; DB 6; Length 3231;
Beet Local Similarity 52.0%; Pred. No. 1.1e-25;
Matches 435; Conservative 0; Mismatches 362; Indels 39; Gaps 3;

Qy      1980  TGTGCGTTTATCATGCTGCTGGAAGAACTATCGCGGCTTCTTACCAACAATGGA 2039
Db      1640  TGTGCGGTTCTGTTCTTCAACAGCAAGGATACCGAGATCACTACCAACTGGC 1699
Qy      2040  AGCATGACATCAGGTGGGACATGCTGATGATGCTTCAAAACAAC-----AATG 2093
Db      1700  GCCACGGCTTCAACCTGGCCGACAGATGTTCAACCTGCTCATGACCGCAACTGAAGA 1759
Qy      2094  GCTCTTTCACAGACCTGAGAGGCAAGGCTGTAATGCGTCTGCTGCTGCTGCTGCTG 2153
Db      1760  GCTACTTACAGGACCTGAGGCTTGGCAGATGTAACGCGGCTGCTGCTGCTGCTGCTG 1819
Qy      2154  ACCAGAGGCTTCACTAGTAACAGCTACTGAGAGATTGCAACCCCTGGGCGCTGT 2213
Db      1820  ACCACCGGCGACCAACAACCTGTAACAGATGATGCCAGAACCCCTGGCTAAGCTCC 1879
Qy      2214  ACTGCACTTCAACCATGAGCAACCACTTCTCCAGAGGCTGCTGCTGCTGCTGCTG 2273
Db      1880  ACGGCTCTCGATTTTGGAGCGGCAACCTGAGATTGGGAAGTTCCCTGCTCGGAAG 1939
Qy      2274  AAGGCACAATCTTCTTCCACCTGAGCTCCAGAGATGAGAGAGGCTGAGATCA 2333
Db      1940  AGACCTGAACTTCAACAGAACTGAACTGAACTGGCGGAGACAGAGACGTTATCCTTA 1999
Qy      2334  TCCGAAAGCCATCATGCGCACCGACTGCTGCTTACTTCTTGGGAAACAGAAAGCTTGG 2393
Db      2000  TGAACATGCGCAATCATGCGCACGAGCTGCTGCTGCTTCAAGAAAGAGAGATTTTC 2059
Qy      2394  AGAGATGTACAGACAGAGGCTGTAACCTTCCACACCA----- 2433
Db      2060  AGAAGATGCTGATGATGTCACAAAGTACAGAGACAGAAAGCTGGTGAATCTGT 2119
Qy      2434  -----GTCCATGCAACCGTGTATGCTGCTGATGATGATGATGATGATGATGATG 2483
Db      2120  CCTGGAAGACGACCCGGAAGAGATGCTATGCGCAATGATGAGAGCTGCACTGT 2179
Qy      2484  GCTCTGTACCAAACTATGCGCAATTAACAAATTTGACAGCATATATATATGCAAT 2543
Db      2180  CTGCAATCAACAAGCCCTGGAAGTTCAGAGCAAGGTGCACTTCTGCTGCTGCTGAGT 2239
Qy      2544  TCTGGGCTGAGGATGA---TGAGATGAGAAAGCTGGGCAATACAGCCCATCTTATGATG 2600
Db      2240  TCTGGGAGCAAGTGACTTGAAGAGCAGTCTGATGATGAGCAGCCCATCTTATGATG 2299
Qy      2601  ACAAGACAAAGGAGATGAGTCTCTCAAGGCAAGCTGCAATCTCAATGCTGTCGCA 2660
Db      2300  ACCGAAACAAGGGGCGGAGCTCCCAAGCTGCAAGTGGGCTTCAATGCACTTCTGTGCA 2359
Qy      2661  TTCCCTGCTATACCACTTGAAGCAATCTTCCCAACCAAGAGCTTCTGCTGCAAGGCT 2720
Db      2360  CATTCGTATACAAAGAGTCTCTGTTTCCAGAAAGATCTGCTCCATGTTTGAACGAC 2419
Qy      2721  GAGAGATTAACCTCAATCACTGAGAGAGATTAATTCGCGGGAAGAGACAGCAATG 2776
Db      2420  TGAAGAACTATGAGAAAGTGAAGGCTGCTGATGATGATGAGGCCAAAGTG 2475

RESULT 6
US-10-750-185-46027/c
; Sequence 46027, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:

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; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46027
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Bovine 19866880431658
US-10-750-185-46027

Query Match 4.1%; Score 146.2; DB 6; Length 2163;
Best Local Similarity 87.4%; Pred. No. 4.1e-25;
Matches 160; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 2260 CATCTTCAAGCTGGAAGGCGACAATATCTTCCACCCCTGAGCTCCAGGATAGAGCA 2319
DB 1275 CTTCCTTAAGTTGGAAGGCGACAACATCTTCTCCACCCCTGAGCTCCAGGATATGAGCA 1216
QY 2320 GGTGCTGAGATCATCCGCAAGCCATCATCGCCACCGACTCGCCCTTACTTTGGGAA 2379
DB 1215 GGTGCTTGAATCATCCGCAAGCCATCATCGCCACCGACTCGCTGTACTTTGGGAA 1156
QY 2380 CAGGAAGCATTTGAGAGATGTACCAAGAGGTCGCTGAACTTCACACCAAGTCCCA 2439
DB 1155 CCGGAAGCATGTTGAGAGATGTACCAAGAGTGTACCAAGTGTGCTGAACTTAATTAACCAATACCA 1096
QY 2440 TCG 2442
DB 1095 TAG 1093

RESULT 7
US-10-750-623-46027/c
; Sequence 46027, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46027
; LENGTH: 2163
; TYPE: DNA
; ORGANISM: Bovine 19866880431658
US-10-750-623-46027

Query Match 4.1%; Score 146.2; DB 6; Length 2163;
Best Local Similarity 87.4%; Pred. No. 4.1e-25;
Matches 160; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

CY 2260 CATCTTCAAGCTGGAAGGCGACAATATCTTCTCCACCCCTGAGCTCCAGGATAGAGCA 2319
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DB 1275 CTTCCTTAAGTTGGAAGGCGACAACATCTTCTCCACCCCTGAGCTCCAGGATATGAGCA 1216
QY 2320 GGTGCTGAGATCATCCGCAAGCCATCATCGCCACCGACTCGCCCTTACTTTGGGAA 2379
DB 1215 GGTGCTTGAATCATCCGCAAGCCATCATCGCCACCGACTCGCTGTACTTTGGGAA 1156
QY 2380 CAGGAAGCATTTGAGAGATGTACCAAGAGGTCGCTGAACTTCACACCAAGTCCCA 2439
DB 1155 CCGGAAGCATGTTGAGAGATGTACCAAGAGTGTACCAAGTGTGCTGAACTTAATTAACCAATACCA 1096
QY 2440 TCG 2442
DB 1095 TAG 1093

RESULT 8
US-10-750-185-46028
; Sequence 46028, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46028
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Bovine 19866880722444
US-10-750-185-46028

Query Match 2.0%; Score 72.8; DB 6; Length 764;
Best Local Similarity 87.0%; Pred. No. 9.7e-08;
Matches 80; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1960 CTGTTTGAAGTTGAAAAATGTGCGGTTTATCATGTCTGTGAAGAACTATCGGCG 2019
DB 673 CAGCTTGAGCTGGAAGAGTTGTGCGGTTTCATCATGTCTGTGAAGAACTATCGGCG 732
QY 2020 GGTTCCTTACCAACAATGGAAGCATGCACTCA 2051
DB 733 GGTTCCTTACCAACAATGGAAGCATGCGGTGA 764

RESULT 9
US-10-750-623-46028
; Sequence 46028, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
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; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46028
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Bovine 1986680722444
US-10-750-623-46028

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Query Match	2.0%;	Score 72.8;	DB 6;	Length 764;
Best Local Similarity	87.0%;	Pred. No. 9.7e-08;		
Matches 80;	Conservative 0;	Mismatches 12;	Indels 0;	Gaps 0;

QY 1960 CHTGTTTGAACCTGAAAATTTGTCGCTTTATATAGTCGTGAAGAACTACCGCG 2015

Nb 673 CACGCTTCGAGCTGAGAAAGTGTGCGCTTTCATCATGTCGTGAAGAACTACCGCG 732

Qy	2020	GGTTCCTTACCAACTGGAAGCATGCAGTCA	205
Db	733	GGTTCCTTACCAACTGGAAGCATGCAGTCA	764

RESULT 10
US-11-075-185-35

Query Match	1.6%	Score 58.8	DB 7	Length 10968
Best Local Similarity	47.8%	Pred. No. 0.00057		
Matches 171; Conservative	0	Mismatches 187	Indels 0	Gaps 0

QY 57 GCGAGCGGCGGCTGGAGGAAGAGGCGGCGCGAGTCTGGCGGCGGCGGAG 116

Db 8467 GCGGCGAGCGAGCGGAGTGCACACGCGACCGCGTCTGAGCGCGCAGCGGCG 852

QY 117 GAGGAGCAAGAGGAGCTCCCTTGAAGCGTCCCCCAGGCAAGTAGTCACCCGAGCAAGC 176

Db 8527 GCCGGGCGCGAGCTGCGGAACTTTTCGCTGTGCGCCGCGCCGCGCGCGCGAGGTGTGCGC 858

QY 177 GTGGCAGCAGGGGTGGCAGCGCGGGGCGCGCGCTTCTCTCGCTCGGATTCAAG 236
8587 CTCGACGGCGGCTACGCGTGGCTGGCGCGCGCAGGCGCTACGCGTACGCGCCGGCGTTCCAG 864
Db

QY 237 GCTTGTCCTCCCTGCAGCGGCGGGGCGGCCCATCTCCGCGCGCCGCGCTTCCCTAC 296
| | | | |
Db 8647 GCAGTCGCGAGAGTGTGCGCGCGCGGCAACAACGCTGTACGCGCGGGATCGCGCTGCCGACC 870

Qy 297 ACCCGGATGACGCGCGGAGACTCTCTCGAATTTCCGGGCGCGCGCGCGGCTGCCCC 356
Db 8707 GCGGTGCGGACACGCGCGAGACTTCGGATTCATCCGCGCGCTGCTCGACGCGGTCTG 876

```

RESULT 11
US-11-075-185-1
Sequence 1, Application US/11075185
Publication No. US20050266434A1
GENERAL INFORMATION:
APPLICANT: REEVES, CHRISTOPHER D
APPLICANT: JULIEN, BRYAN
APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBERUTICINS
FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: US 60/568,290
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 78869
TYPE: DNA
ORGANISM: Sorangium cellulosum
US-11-075-185-1

```

Query Match	1.6%;	Score 58.8;	DB 7;	Length 78869;
Best Local Similarity	47.8%;	Pred. No. 0.0015;		
Matches 171; Conservative	0;	Mismatches 187;	Indels 0;	Gaps 0;

[illegible]

QY 117 GAGGAGGACAAAGAGGACGCTCCCTTGAAGGTCCGCCAGGACAGTAGTACCGGACAGCTG 1/6

Db 23794 GCCGGGGCGGACGTGGCGGACCTTTGGGTGGCGCGCGCGCGGCGGCGGACGATGTGGCG 2385

177 GTGGCAGCAGCGGTGGCAGCGCGCGCGCGCGCTCTTCTCTGCGCTGCGGATTCAG 236
 23854 CTCACGCGCGGCTACCGCTGGCTGGCGGCGGCGGCGGCTACGGGCTACGGCGCGCTTCAG 2391

	GCTTGGCAGG	TGTGCACCAATCGTCGCCAACC	CATTCCAAACAATTTTGGAATTAAGA	AATAAACCATCTTACTGATG	298
Oy	237	GCTTAGCTGCTCC	CCCCCCCAGCACATCTCCAGCGAGCACT	TTTTTTTAC	296
Ddb	23914	GCCCTGCGGAGGT	GTGGCGCGCGGACGACGCTGTAAGCGGAGTCCGCGTCGGAC		23916

[illegible]

QY	Db
357	GCCTTCGACCCCGGCTCTGCGCGCGCGGTGCGCGAACCTCTTTGGCGGCCCCGACAGGCGCGCG 414
24034	CACCTCTTGTGTCGCGCGGTGCCCGCAGAGGAGAGCGTCCGACGACGACAAAGTGCTGC 24091

```

RESULT 12
US-10-453-372-659/C
; Sequence 659, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446

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/ PRIOR FILING DATE: 2001-03-19
 / PRIOR APPLICATION NUMBER: 60/199476
 / PRIOR FILING DATE: 2000-03-25
 / PRIOR APPLICATION NUMBER: 09/863776
 / PRIOR FILING DATE: 2001-05-23
 / PRIOR APPLICATION NUMBER: 60/208263
 / PRIOR FILING DATE: 2000-05-31
 / PRIOR APPLICATION NUMBER: 09/939398
 / PRIOR FILING DATE: 2001-06-24
 / PRIOR APPLICATION NUMBER: 60/227800
 / PRIOR FILING DATE: 2000-08-25
 / Remaining Prior Application data removed - See File Wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 1609
 / SOFTWARE: CuroSeqList version 0.1
 / SEQ ID NO 659
 / LENGTH: 4607
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (237)..(3125)
 US-10-453-372-659

Query Match 1.6%; Score 58; DB 6; Length 4607;
 Best Local Similarity 52.0%; Pred. No. 0.00072;
 Matches 153; Conservative 0; Mismatches 140; Indels 1; Gaps 1;

QY 120 GAGGACAGAGGAGGAGTCCCTTGAGGCTCCCCAGGAGTACTACCCGACAGGGGTG 179
 DB 345 GGGAGATCAGCCCTGCTGCGCGCGGAGATGCTGAGAGCCGACAGACAGACAGACAGA 286
 QY 180 GAGGACAGGAGGAGGAGTCCCTTGAGGCTCCCCAGGAGTACTACCCGACAGGGGTG 239
 DB 285 GAGGACAGGAGGAGGAGTCCCTTGAGGCTCCCCAGGAGTACTACCCGACAGGGGTG 227
 QY 240 TGCTGCTCCCTGCG 299
 DB 226 GGCCTCG 167
 QY 300 CGGAGGAGGAGGAGGAGTCCCTTGAGGCTCCCCAGGAGTACTACCCGACAGGGGTG 359
 DB 166 GTCTTGGCG 107
 QY 360 TCGGCG 413
 DB 106 CCG 53

RESULT 13
 US-11-052-554A-520
 / Sequence 520, Application US/11052554A
 / Publication No. US2005028866A1
 / GENERAL INFORMATION:
 / APPLICANT: Sachdeva, et al.
 / TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
 / FILE REFERENCE: 30853/40359A
 / CURRENT APPLICATION NUMBER: US/11/052,554A
 / CURRENT FILING DATE: 2005-02-07
 / PRIOR APPLICATION NUMBER: US 60/589,227
 / PRIOR FILING DATE: 2004-07-20
 / PRIOR APPLICATION NUMBER: IN 173/DEL/2004
 / PRIOR FILING DATE: 2004-02-06
 / NUMBER OF SEQ ID NOS: 763
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 520
 / LENGTH: 3990
 / TYPE: DNA
 / ORGANISM: Mycobacterium tuberculosis H37Rv
 US-11-052-554A-520

Query Match 1.6%; Score 57.8; DB 7; Length 3990;
 Best Local Similarity 50.4%; Pred. No. 0.00076;

Matches 193; Conservative 0; Mismatches 187; Indels 3; Gaps 2;
 QY 52 GAGAGGCGCAGCGCGCGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 111
 DB 2880 GGGCGGTGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2939
 QY 112 CGAGAGAGAGGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 171
 DB 2940 CAACGCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2999
 QY 172 CAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 229
 DB 3000 CAACGCCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3059
 QY 230 ATTCAAGGCTTGTCTCTCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 289
 DB 3060 GGGGCG 3119
 QY 290 CCCCTACACCGG-GGTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
 DB 3120 TGCCAGCGCGCGGAAACGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3179
 QY 349 CTGCGCTGAGCTTGGCG 408
 DB 3180 CGGCG 3239
 QY 409 CGCGCGCTTCCCTTGGCGCGCG 431
 DB 3240 CAAGGCGCTTCTCGGACCGACG 3262

RESULT 14
 US-11-136-527-2572/c
 / Sequence 2572, Application US/11136527
 / Publication No. US20050287570A1
 / GENERAL INFORMATION:
 / APPLICANT: Wyeth
 / APPLICANT: Mounts, William M
 / TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
 / FILE REFERENCE: 031896-041000 (AM101086)
 / CURRENT APPLICATION NUMBER: US/11/136,527
 / CURRENT FILING DATE: 2005-05-25
 / PRIOR APPLICATION NUMBER: US 60/574,294
 / PRIOR FILING DATE: 2005-05-26
 / NUMBER OF SEQ ID NOS: 362830
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 2572
 / LENGTH: 6269
 / TYPE: DNA
 / ORGANISM: Rattus norvegicus
 US-11-136-527-2572

Query Match 1.6%; Score 57.8; DB 7; Length 6269;
 Best Local Similarity 47.0%; Pred. No. 0.00092;
 Matches 212; Conservative 0; Mismatches 237; Indels 2; Gaps 1;

QY 9 GCTCTCATCTGCTCTTCAACCTCCCGCGCGCGCTCCCGAGAAAGGAGGAGGAGGAGGAG 68
 DB 717 GCTTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 658
 QY 69 CTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 128
 DB 657 AGGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 598
 QY 129 AGGAGGCTCTTGAAGGCTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 186
 DB 597 CGGCGCGCGAGAGATCTCTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 538
 QY 187 CGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246
 DB 537 CGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 478
 QY 247 CCTGCG 306

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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:48:45 ; Search time 81 Seconds
(without alignments)
4317.846 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206
Sequence: 1 MEDGSPNNASCPRRLTECPFL.....GGPAPSKSTPBKLNKVED 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: _Genesegp_21:.*
2: genesegp1980s:.*
3: genesegp1990s:.*
4: genesegp2000s:.*
5: genesegp2001s:.*
6: genesegp2002s:.*
7: genesegp2003as:.*
8: genesegp2003bs:.*
9: genesegp2004s:.*
9: genesegp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4206	100.0	796	3	AAV53940
2	4198	99.8	796	8	ADT92234
3	4123	98.0	794	3	AAAB26855
4	4123	98.0	794	8	ADT92235
5	4080	97.0	779	8	ADT92238
6	4078.5	97.0	797	8	ADT92217
7	4072	96.8	790	8	ADT92236
8	4012.5	95.4	795	8	ADT92219
9	4004	95.2	789	3	AAAB26854
10	4004	95.2	789	8	ADT92233
11	3997	95.0	788	3	AAAB26856
12	3997	95.0	788	8	ADT92237
13	3997	95.0	803	2	AAV13935
14	3997	95.0	803	4	AAAB28257
15	3997	95.0	803	7	AAE39535
16	3997	95.0	803	8	ADM34018
17	3993	94.9	789	3	AAV53935
18	3951.5	93.9	779	6	ABR42040
19	3880	92.2	806	4	AAAM51617
20	3878	92.2	779	2	AAV13936
21	3878	92.2	779	3	AAAB26853
22	3878	92.2	779	4	AAAB28258
23	3878	92.2	779	4	AAAB73486
24	3878	92.2	779	7	AAE39536

25	3878	92.2	779	8	ADM34020	Adm34020 Human pho
26	3878	92.2	779	8	ADO36626	Ado36626 Human pho
27	3878	92.2	779	8	ADR46243	Adr46243 Human pho
28	3878	92.2	779	8	ADT92232	Adt92232 Human PDE
29	3878	92.2	779	9	AEAB92222	Aeab92222 Human mod
30	3873	92.1	766	2	AAV13934	Aav13934 Human pho
31	3873	92.1	766	4	AAAB28256	Aab28256 Human pho
32	3873	92.1	766	7	AAE39534	Aae39534 Human pho
33	3873	92.1	766	8	ADM34016	Adm34016 Human pho
34	3867	91.9	791	3	AAV53936	Aav53936 A human p
35	3815	90.7	759	3	AAV53972	Aav53972 Amino acil
36	3815	90.7	767	3	AAV53963	Aav53963 Formula V
37	3808	90.5	754	3	AAV53961	Aav53961 Formula V
38	3798.5	90.3	758	3	AAV53962	Aav53962 Formula V
39	3796	90.3	774	3	AAV57306	Aav57306 Rat phosp
40	3790	90.1	749	3	AAV53959	Aav53959 Formula I
41	3790	90.1	750	3	AAV53960	Aav53960 Formula I
42	1726	41.0	329	9	ADY50217	Ady50217 Human PDB
43	1726	41.0	329	9	ADZ46773	Adz46773 Human PDB
44	1710	40.7	339	8	ADR46245	Adr46245 Human pho
45	1692	40.2	327	8	ADR46247	Adr46247 Human pho

ALIGNMENTS

RESULT 1
AAV53940
ID AAV53940 standard; protein; 796 AA.
XX

AC AAV53940;
XX

DT 13-MAR-2000 (first entry)
XX

DE A murine phosphodiesterase enzyme designated PDE11.
XX

KW Phosphodiesterase enzyme; PDE11; cGMP; GMP; male erectile process;
XX

KW sexual dysfunction; PDE11 imbalance.
XX

OS Mus sp.
XX

PN EP967284-A1.
XX

PD 29-DEC-1999.
XX

PF 21-MAY-1999; 99EP-00303985.
XX

PR 28-MAY-1998; 98GB-00011500.
XX

PR 30-OCT-1998; 98GB-00023882.
XX

PR 04-DEC-1998; 98GB-00026777.
XX

PR 09-APR-1999; 99GB-00008247.
XX

PR 10-MAY-1999; 99GB-00010801.
XX

PA (PF1Z) PRIZER LTD.
XX

PA (PF1Z) PFIZER INC.
XX

PI Lanfear J, Robas NM;
XX

PI WPI; 2000-064614/06.
XX

DR N-PSDB; AAZ26971.
XX

XX Novel polypeptides and polynucleotides used to identify agents which modulate phosphodiesterase activity.

XX Example 8; Page 70-74; 158p; English.

CC The present sequence represents a murine phosphodiesterase enzyme, designated PDE11. PDE11 sequences from human and rat are also disclosed. PDE11 is found in the striatum and corpus cavernosum. PDE11 is believed to catalyze the conversion of cGMP to GMP. As cGMP is the messenger in the male erectile process, inhibiting the activity of PDE11 is likely to increase the concentration of cGMP and so enhance the male erectile process. The PDE11 enzymes are used in assays for identifying agents

CC which can affect PDE11 activity or expression. They are also used to
 CC screen for agents useful in the treatment of sexual dysfunction. The
 CC identified agent can be used in a pharmaceutical compositions to treat a
 CC disease or condition associated with PDE11. A PDE11 gene or expression
 CC product can be used to prepare a medicament for the treatment or
 CC modulation of disturbances associated with a PDE11 imbalance. The gene or
 CC expression product can also be used to screen for modulators of PDE11
 CC activity or expression

XX Sequence 796 AA;

Query Match 100.0%; Score 4206; DB 3; Length 796;

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEDGSSNNA	CFRRIT	TECFL	SPSL	TD	DEK	KAY	LSL	HP	QV	LD	EP	VS	ES	VS	AE	TV	E	K	M	K	R	K	60	
DB	1	MEDGSSNNA	CFRRRL	TECP	LSPL	TD	DEK	KAY	LSL	HP	QV	LD	EP	VS	ES	VS	AE	TV	E	K	M	K	R	K	60	
QY	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
DB	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
QY	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
DB	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
QY	121	GFALY	FL	GE	CN	NS	LC	VP	IP	PG	ME	GO	PR	LI	PA	GP	IT	Q	T	T	I	S	A	V	180	
DB	121	GFALY	FL	GE	CN	NS	LC	VP	IP	PG	ME	GO	PR	LI	PA	GP	IT	Q	T	T	I	S	A	V	180	
QY	181	ERF	PR	GT	GL	ES	GT	RI	Q	S	V	L	C	P	I	V	A	I	G	L	I	G	I	L	E	240
DB	181	ERF	PR	GT	GL	ES	GT	RI	Q	S	V	L	C	P	I	V	A	I	G	L	I	G	I	L	E	240
QY	241	SVAI	H	Q	V	O	V	C	R	G	L	A	K	O	T	E	L	N	D	F	L	D	V	S	K	300
DB	241	SVAI	H	Q	V	O	V	C	R	G	L	A	K	O	T	E	L	N	D	F	L	D	V	S	K	300
QY	301	QV	D	H	K	N	K	E	L	Y	S	D	L	P	D	I	G	E	K	E	K	P	I	F	K	360
DB	301	QV	D	H	K	N	K	E	L	Y	S	D	L	P	D	I	G	E	K	E	K	P	I	F	K	360
QY	361	R	N	R	E	V	D	L	Y	G	T	T	N	I	L	C	M	P	I	V	S	R	G	S	V	420
DB	361	R	N	R	E	V	D	L	Y	G	T	T	N	I	L	C	M	P	I	V	S	R	G	S	V	420
QY	421	A	L	H	C	A	N	M	T	H	R	I	H	S	E	C	I	R	V	T	M	E	K	S	Y	480
DB	421	A	L	H	C	A	N	M	T	H	R	I	H	S	E	C	I	R	V	T	M	E	K	S	Y	480
QY	481	P	E	N	N	M	P	G	I	F	V	M	I	R	S	C	G	T	S	C	F	E	L	E	K	540
DB	481	P	E	N	N	M	P	G	I	F	V	M	I	R	S	C	G	T	S	C	F	E	L	E	K	540
QY	541	L	O	N	N	G	L	F	T	D	L	E	R	K	G	L	L	A	C	H	D	D	H	R	G	600
DB	541	L	O	N	N	G	L	F	T	D	L	E	R	K	G	L	L	A	C	H	D	D	H	R	G	600
QY	601	S	T	L	O	E	G	N	H	I	F	S	T	L	S	S	E	B	O	V	L	E	I	R	K	660
DB	601	S	T	L	O	E	G	N	H	I	F	S	T	L	S	S	E	B	O	V	L	E	I	R	K	660
QY	661	H	R	D	R	I	G	L	M	T	A	C	D	S	V	T	K	L	M	P	V	T	K	L	M	720
DB	661	H	R	D	R	I	G	L	M	T	A	C	D	S	V	T	K	L	M	P	V	T	K	L	M	720
QY	721	E	V	P	O	G	O	L	G	R	Y	N	A	I	P	C	T	T	L	T	O	I	L	P	T	780
DB	721	E	V	P	O	G	O	L	G	R	Y	N	A	I	P	C	T	T	L	T	O	I	L	P	T	780
QY	781	A	P	S	K	S	T	P	R	K	L	N	K	V	E	D	796									
DB	781	A	P	S	K	S	T	P	R	K	L	N	K	V	E	D	796									

RESULT 2

QY	ADT92234	ID	ADT92234	standard; protein; 796 AA.																						
XX	AC	ADT92234;																								
XX	DT	13-JAN-2005	(first entry)																							
XX	DE	Mouse PDE10A2 isoform sequence.																								
XX	KM	PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;																								
XX	OS	neuroprotective; gene therapy; transgenic; enzyme; PDE10A2; mouse.																								
XX	PN	Mus musculus.																								
XX	PD	W02004090126-A2.																								
XX	PF	21-OCT-2004.																								
XX	PR	30-MAR-2004; 2004WO-US009878.																								
XX	PR	03-APR-2003; 2003US-0459603P.																								
XX	PA	(MEMO-) MEMORY PHARM CORP.																								
XX	PI	Wang D, Bugaj-Gaweda B;																								
XX	PI	WPI; 2004-748763/73.																								
XX	PT	New isolated polynucleotide comprising a polynucleotide sequence coding																								
XX	PT	for a mammalian phosphodiesterase 10A7, or its mutation, useful for																								
XX	PS	treating or preventing memory, psychiatric or cognitive disorders.																								
XX	PS	Disclosure; SEQ ID NO 19; 93pp; English.																								
XX	CC	The invention relates polynucleotide sequences coding for mammalian																								
XX	CC	phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for																								
XX	CC	identifying an agent that modulates the expression or activity of a																								
XX	CC	phosphodiesterase in transfected host cells is provided which involves																								
XX	CC	measuring amounts of cAMP or cGMP produced in the presence of the agent.																								
XX	CC	The agent inhibits the expression or activity of the phosphodiesterase.																								
XX	CC	The polynucleotides are useful in diagnostic assays and for screening																								
XX	CC	modulators, specifically inhibitors of PDE10A7. They are also useful for																								
XX	CC	treating or preventing memory, psychiatric or cognitive disorders.																								
XX	CC	Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms																								
XX	CC	used in a comparison study with the murine and rat PDE10A7 sequences.																								
XX	SQ	Sequence 796 AA;																								
QY	Query Match	99.8%; Score 4198; DB 8; Length 796;																								
QY	Best Local Similarity	99.9%; Pred. No. 0;																								
QY	Matches	795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;																								
QY	1	MEDGSSNNA	CFRRIT	TECFL	SPSL	TD	DEK	KAY	LSL	HP	QV	LD	EP	VS	ES	VS	AE	TV	E	K	M	K	R	K	60	
DB	1	MEDGSSNNA	CFRRRL	TECP	LSPL	TD	DEK	KAY	LSL	HP	QV	LD	EP	VS	ES	VS	AE	TV	E	K	M	K	R	K	60	
QY	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
DB	61	TKKAD	EP	SP	KE	VS	R	Y	Q	D	T	N	M	Q	V	Y	E	L	N	S	Y	I	E	O	120	
QY	121	GFALY	FL	GE	CN	NS	LC	VP	IP	PG	ME	GO	PR	LI	PA	GP	IT	Q	T	T	I	S	A	V	180	
DB	121	GFALY	FL	GE	CN	NS	LC	VP	IP	PG	ME	GO	PR	LI	PA	GP	IT	Q	T	T	I	S	A	V	180	
QY	181	ERF	PR	GT	GL	ES	GT	RI	Q	S	V	L	C	P	I	V	A	I	G	L	I	G	I	L	E	240
DB	181	ERF	PR	GT	GL	ES	GT	RI	Q	S	V	L	C	P	I	V	A	I	G	L	I	G	I	L	E	240
QY	241	SVAI	H	Q	V	O	V	C	R	G	L	A	K	O	T	E	L	N	D	F	L	D	V	S	K	300
DB	241	SVAI	H	Q	V	O	V	C	R	G	L	A	K	O	T	E	L	N	D	F	L	D	V	S	K	300
QY	301	QV	D	H	K	N	K	E	L	Y	S	D	L	P	D	I	G	E	K	E	K	P	I	F	K	360
DB	301	QV	D	H	K	N	K	E	L	Y	S	D	L	P	D	I	G	E	K	E	K	P	I	F	K	360

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Db      |||
301 QVDHKKELYSDFIGEEKSKPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYDP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSVIGVQVWNKISGSAFSGKTENNPFQAFVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSVIGVQVWNKISGSAFSGKTENNPFQAFVFCAL 420
Qy      421 ALHCANMYHRIHSECTIYVYMEKLSYHSICTSEWQGLMRNLPARICRDIELFFPDIG 480
Db      421 ALHCANMYHRIHSECTIYVYMEKLSYHSICTSEWQGLMRNLPARICRDIELFFPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRVRPYHNMKKAIVVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRVRPYHNMKKAIVVAHCMYAI 540
Qy      541 LQNNNGLPFTDLERKGLLIACLDHDLHRGFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Db      541 LQNNNGLPFTDLERKGLLIACLDHDLHRGFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Qy      601 SILOEGHNI FSTLSSEYEOVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Db      601 SILOEGHNI FSTLSSEYEOVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Qy      661 HDRVYIGLMTACDLCSTVKLMPVTKL TANDIYAEFWAGDEMKKLGIOPIPMDDKXD 720
Db      661 HDRVYIGLMTACDLCSTVKLMPVTKL TANDIYAEFWAGDEMKKLGIOPIPMDDKXD 720
Qy      721 EYPOGQLGFYNAVALPCYTTLTQILPPTBPLKACRDNINQWEKVI RGETAMWISGPGP 780
Db      721 EYPOGQLGFYNAVALPCYTTLTQILPPTBPLKACRDNINQWEKVI RGETAMWISGPGP 780
Qy      781 APSKSTPEKLANVKVED 796
Db      781 APSKSTPEKLANVKVED 796

RESULT 3
AAB26855
ID AAB26855 standard; protein; 794 AA.
XX
AC AAB26855;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human phosphodiesterase 10 (PDE10) amino acid sequence 3.
XX
KM Phosphodiesterase 10; PDE10; human.
XX
OS Homo sapiens.
XX
PN JP2000224992-A.
XX
PD 15-AUG-2000.
XX
PF 11-MAY-1999; 99JP-00129343.
XX
PR 30-NOV-1998; 98JP-00338861.
XX
PA (TANA) TANABE SEIYAKU CO.
XX
PI; 2000-605129/58.
XX
DR N-PSDB; AAA09591.
XX
PT Novel phosphodiesterase and its gene for research on complex mechanism of
XX intracellular information transfer.
XX
PS Disclosure; Page 20-23; 29pp; Japanese.
XX
CC Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
XX proteins AAB26853-826856. Phosphodiesterase 10 and its gene are useful
XX for research on the complex mechanism of intracellular information
XX transfer. The invention includes a recombinant vector containing a PDE10
XX gene, and a cell transformed with the vector. Sequences AAA09593-A09606

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CC represent PCR primers used in the isolation of the PDE10 polynucleotide
CC sequences of the invention
XX
SQ Sequence 794 AA;
XX
Query Match 98.0%; Score 4123; DB 3; Length 794;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

Qy      1 MEDGSSNNAFCRRLTBCEPLSLTDEKVAKYLSTHPQVLDFEVSVAETVEKMLRK 60
Db      1 MEDGSSNNAFCRRLTBCEPLSLTDEKVAKYLSTHPQVLDFEVSVAETVEKMLRK 60
Qy      61 TNKADBPSPKVSXYOQTNMGVYELNSYIEORLDTGSDNHLHLLYELSSIIIRATYAD 120
Db      61 TNKADBPSPKVSXYOQTNMGVYELNSYIEORLDTGSDNHLHLLYELSSIIIRATYAD 120
Qy      61 NKKADESPPEKVSXYOQTNMGVYELNSYIEORLDTGSDNHLHLLYELSSIIIRATYAD 120
Db      61 NKKADESPPEKVSXYOQTNMGVYELNSYIEORLDTGSDNHLHLLYELSSIIIRATYAD 120
Qy      121 GFALYFLGECNNSLCVFIPPGMKEGQPLIPAGPITQGTISAAVAKSKTLLVEDIIGD 180
Db      121 GFALYFLGECNNSLCVFIPPGMKEGQPLIPAGPITQGTISAAVAKSKTLLVEDIIGD 180
Qy      181 ERFPGGTGIESGTRIQSVYICLPYTAIGDLIGILELYRMWGEARCLSHQEVATNLAWA 240
Db      181 ERFPGGTGIESGTRIQSVYICLPYTAIGDLIGILELYRMWGEARCLSHQEVATNLAWA 240
Qy      241 SVAIHQVQCGRLAQOTELNDLQVSKYFPDNIYVAIDSLHEIMYAKNLVNAQCALF 300
Db      241 SVAIHQVQCGRLAQOTELNDLQVSKYFPDNIYVAIDSLHEIMYAKNLVNAQCALF 300
Qy      241 SVAIHQVQCGRLAQOTELNDLQVSKYFPDNIYVAIDSLHEIMYAKNLVNAQCALF 300
Db      241 SVAIHQVQCGRLAQOTELNDLQVSKYFPDNIYVAIDSLHEIMYAKNLVNAQCALF 300
Qy      301 QVDHKKELYSDFIGEEKSKPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYDP 360
Db      301 QVDHKKELYSDFIGEEKSKPIFKTKERFSIEKCIQAQVARTGEVLNIPDAYDP 360
Qy      361 RFRREVDLYTGYTTNNILCMPIVSRGSVIGVQVWNKISGSAFSGKTENNPFQAFVFCAL 420
Db      361 RFRREVDLYTGYTTNNILCMPIVSRGSVIGVQVWNKISGSAFSGKTENNPFQAFVFCAL 420
Qy      421 ALHCANMYHRIHSECTIYVYMEKLSYHSICTSEWQGLMRNLPARICRDIELFFPDIG 480
Db      421 ALHCANMYHRIHSECTIYVYMEKLSYHSICTSEWQGLMRNLPARICRDIELFFPDIG 480
Qy      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRVRPYHNMKKAIVVAHCMYAI 540
Db      481 PENNMWPGIFVYMIHRSCTSCFELEKLCRFIMSVKQYRVRPYHNMKKAIVVAHCMYAI 540
Qy      541 LQNNNGLPFTDLERKGLLIACLDHDLHRGFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Db      541 LQNNNGLPFTDLERKGLLIACLDHDLHRGFSNSYLQKFDHPLAALYSTSTMEQHHSQTV 600
Qy      601 SILOEGHNI FSTLSSEYEOVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Db      601 SILOEGHNI FSTLSSEYEOVLEIRKAI IATDLALYGNRKQLEEMVQTSGLNHNS 660
Qy      661 HDRVYIGLMTACDLCSTVKLMPVTKL TANDIYAEFWAGDEMKKLGIOPIPMDDKXD 720
Db      661 HDRVYIGLMTACDLCSTVKLMPVTKL TANDIYAEFWAGDEMKKLGIOPIPMDDKXD 720
Qy      721 EYPOGQLGFYNAVALPCYTTLTQILPPTBPLKACRDNINQWEKVI RGETAMWISGPGP 780
Db      721 EYPOGQLGFYNAVALPCYTTLTQILPPTBPLKACRDNINQWEKVI RGETAMWISGPGP 780
Qy      781 APSKSTPEKLANVKVED 796
Db      779 ATSKSTSEKPTRKVD 794

RESULT 4
ADT92235
ID ADT92235 standard; protein; 794 AA.
XX
AC ADT92235;
XX
DT 13-JAN-2005 (first entry)

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XX Rat PDE10A2 isoform sequence.
 XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; noctropic;
 XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A2; rat.
 XX Rattus norvegicus.
 XX WO2004090126-A2.
 XX 21-OCT-2004.
 XX 30-MAR-2004; 2004MO-US009878.
 XX 03-APR-2003; 2003US-0459603P.
 XX (MEMO-) MEMORY PHARM CORP.
 XX Wang D, Bugaj-Gaweda B;
 XX WPI; 2004-748763/73.
 XX New isolated polynucleotide comprising a polynucleotide sequence coding
 XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
 XX treating or preventing memory, psychiatric or cognitive disorders.
 XX Disclosure; SEQ ID NO 20; 93pp; English.
 XX The invention relates polynucleotide sequences coding for mammalian
 XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
 XX identifying an agent that modulates the expression or activity of a
 XX phosphodiesterase in transfected host cells is provided which involves
 XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
 XX The agent inhibits the expression or activity of the phosphodiesterase.
 XX The polynucleotides are useful in diagnostic assays and for screening
 XX modulators, specifically inhibitors of PDE10A7. They are also useful for
 XX treating or preventing memory, psychiatric or cognitive disorders.
 XX Sequences AD792232-AD792238 represent various mammalian PDE10A isoforms
 XX used in a comparison study with the murine and rat PDE10A7 sequences.
 XX Sequence 794 AA;
 XX
 XX Query Match 98.0%; Score 4123; DB 8; Length 794;
 XX Best Local Similarity 98.4%; Pred No. 0;
 XX Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
 QY 1 MEDGSPNNASCRRRLTECFSPSLTDEKVKAYLSLHPQVLDFFVSBSVAETVEKMLKK 60
 DB 1 MEDGSPNNASCRRRLTECFSPSLTDEKVKAYLSLHPQVLDFFVSBSVAETVEKMLKK 60
 QY 61 TNKADSPSPKVSRYODTNMGQVYELNSYEQRLDTGSDNHLLEYLSITIRATAD 120
 DB 61 TNKADSPSPKVSRYODTNMGQVYELNSYEQRLDTGSDNHLLEYLSITIRATAD 120
 QY 121 GPALYFLGSCNNSLCVFTPPGKMEGPRILPAGPTTQGTTSAYVAKSKRTLLVEDILGD 180
 DB 121 GPALYFLGSCNNSLCVFTPPGKMEGPRILPAGPTTQGTTSAYVAKSKRTLLVEDILGD 180
 QY 181 ERFPRTGLSGSTRIQSVLCPIVTAIGDLIGILEYRHMGEAFCLSHQEVATNLAWA 240
 DB 181 ERFPRTGLSGSTRIQSVLCPIVTAIGDLIGILEYRHMGEAFCLSHQEVATNLAWA 240
 QY 241 SVAIHQOVQCRGLAQTELDNLDVSKTYFNNIYALISLLEHIMTYANLVNARCALF 300
 DB 241 SVAIHQOVQCRGLAQTELDNLDVSKTYFNNIYALISLLEHIMTYANLVNARCALF 300
 QY 301 QVDHKNKELYSPLPIGEEKKEKPIFKKTKEIRFSIKGIAGOVARTGVNLIPAYADP 360
 DB 301 QVDHKNKELYSPLPIGEEKKEKPIFKKTKEIRFSIKGIAGOVARTGVNLIPAYADP 360
 QY 361 RPNREVDLYTGTNNILCMPIVSRGSLGVVQVMNKISGSAFSKTDENNFMFAVFCAL 420
 DB 361 RPNREVDLYTGTNNILCMPIVSRGSLGVVQVMNKISGSAFSKTDENNFMFAVFCAL 420

QY 421 ALHCANMYRIRHSECIYRYVMEKLSYHSICTSEMOGIAMFNLPARICRDIELFHPDIG 480
 DB 421 ALHCANMYRIRHSECIYRYVMEKLSYHSICTSEMOGIAMFNLPARICRDIELFHPDIG 480
 QY 481 PFENMMPGIFVYMIHRSCTGSCFELEKLCRFIMSVKKNRYRVPYNNWKAATVAHGMVAI 540
 DB 481 PFENMMPGIFVYMIHRSCTGSCFELEKLCRFIMSVKKNRYRVPYNNWKAATVAHGMVAI 540
 QY 541 LQNNNGFTDLEERGLALACCHDLDRGFNSNYQKFDHPLAALYSTBOHHSQTV 600
 DB 541 LQNNNGFTDLEERGLALACCHDLDRGFNSNYQKFDHPLAALYSTBOHHSQTV 600
 QY 601 SILOEGNIFSTLSSSEYEQVLEIRKAIATDIALYFGNRKOLEMYQTSILNHNOS 660
 DB 601 SILOEGNIFSTLSSSEYEQVLEIRKAIATDIALYFGNRKOLEMYQTSILNHNOS 660
 QY 661 HRDRVIGLMTACDLCSTYKLMPTVTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720
 DB 661 HRDRVIGLMTACDLCSTYKLMPTVTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDKD 720
 QY 721 EYPOGQLAFYNAVAIPCTTTLTQILPTEPILKACRDLNOMEKVIRGEETAMTSGGP 780
 DB 721 EYPOGQLAFYNAVAIPCTTTLTQILPTEPILKACRDLNOMEKVIRGEETAMTSGGP 780
 QY 781 APSKSTPEKLNMYVED 796
 DB 779 ATSKSTSEKPTRKVD 794
 XX
 XX RESULT 5
 XX AD792238
 XX ID AD792238 standard; protein; 779 AA.
 XX
 XX AD792238;
 XX
 XX 13-JAN-2005 (first entry)
 XX
 XX Mouse PDE10A-b isoform sequence.
 XX
 XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; noctropic;
 XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A-b; mouse.
 XX Mus musculus.
 XX WO2004090126-A2.
 XX 21-OCT-2004.
 XX 30-MAR-2004; 2004MO-US009878.
 XX 03-APR-2003; 2003US-0459603P.
 XX (MEMO-) MEMORY PHARM CORP.
 XX Wang D, Bugaj-Gaweda B;
 XX WPI; 2004-748763/73.
 XX New isolated polynucleotide comprising a polynucleotide sequence coding
 XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
 XX treating or preventing memory, psychiatric or cognitive disorders.
 XX Disclosure; SEQ ID NO 23; 93pp; English.
 XX The invention relates polynucleotide sequences coding for mammalian
 XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
 XX identifying an agent that modulates the expression or activity of a
 XX phosphodiesterase in transfected host cells is provided which involves
 XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
 XX The agent inhibits the expression or activity of the phosphodiesterase.
 XX The polynucleotides are useful in diagnostic assays and for screening
 XX modulators, specifically inhibitors of PDE10A7. They are also useful for

treating or preventing memory, psychiatric or cognitive disorders.
 CC Sequences ADT92217-ADT92218 represent various mammalian PDE10A isoforms
 CC used in a comparison study with the murine and rat PDE10A7 sequences.

Sequence 779 AA;

Query Match 97.0%; Score 4080; DB 8; Length 779;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LTDEKAVATLSLHPQVLDSEVSASAEVTEKMLKRTKAKADEPSPKEVSRYODTNMGG 83
 DB 7 LTDEKAVATLSLHPQVLDSEVSASAEVTEKMLKRTKAKADEPSPKEVSRYODTNMGG 66
 QY 84 VVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKADGAFALYFGEENSLCVFIPGAK 143
 DB 67 VVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKADGAFALYFGEENSLCVFIPGAK 126
 QY 144 EGOPLIPAGPTTGGTTISAYAKSKRTLLVEDILGDERPPRGTEGSTRIGSVLCPLI 203
 DB 127 EGOPLIPAGPTTGGTTISAYAKSKRTLLVEDILGDERPPRGTEGSTRIGSVLCPLI 186
 QY 204 VTAIGDLIGILEYRHWGKAFLSHQEVATNLAWSVAIHQVOYCRGLAKOTELNDEL 263
 DB 187 VTAIGDLIGILEYRHWGKAFLSHQEVATNLAWSVAIHQVOYCRGLAKOTELNDEL 246
 QY 264 LDVSKTYFNNIYADSLLEHIMIYAKNLVNAADRCALFOVDHKNKELYSDFDIEGEKEG 323
 DB 247 LDVSKTYFNNIYADSLLEHIMIYAKNLVNAADRCALFOVDHKNKELYSDFDIEGEKEG 306
 QY 324 PIFPKTKEIRFSIEKGIAGQVARTGVLNPDVADPRFREVDLYGTGTYTRNILLCPYV 383
 DB 307 PIFPKTKEIRFSIEKGIAGQVARTGVLNPDVADPRFREVDLYGTGTYTRNILLCPYV 366
 QY 384 SRGSVIGVQVMWVKISGSAFASKTDENNNPKMAFVCAALHCAWYHRIHSECIYATWE 443
 DB 367 SRGSVIGVQVMWVKISGSAFASKTDENNNPKMAFVCAALHCAWYHRIHSECIYATWE 426
 QY 444 KLSYHSICTSEEWQGLMRFNLPARICRDIELFFHFDIGPEENMPPGIFVYMIHRSCTGSCP 503
 DB 427 KLSYHSICTSEEWQGLMRFNLPARICRDIELFFHFDIGPEENMPPGIFVYMIHRSCTGSCP 486
 QY 504 ELEKLCRFIMSVKKNYRRVYHNWKAIVYAHCMYAILQNNNGLFIDLERKGLILICLCH 563
 DB 487 ELEKLCRFIMSVKKNYRRVYHNWKAIVYAHCMYAILQNNNGLFIDLERKGLILICLCH 546
 QY 564 DLDRHGRPSNSYLQKTFHPLAALYSTSTMEQHHSQTVSIIQLEGHNFSTLSSEYBOVL 623
 DB 547 DLDRHGRPSNSYLQKTFHPLAALYSTSTMEQHHSQTVSIIQLEGHNFSTLSSEYBOVL 606
 QY 624 EIIIRKAIATDLDLAFGNRKOLEEMVOTGSLNHNOSHRDVIGLMMTACDLSVTGLMP 683
 DB 607 EIIIRKAIATDLDLAFGNRKOLEEMVOTGSLNHNOSHRDVIGLMMTACDLSVTGLMP 666
 QY 684 VTFLTANDIYAEFWAEGDEMKKLGIOPIPMWDRDKDEVPOGOLGFYNAVALPCYTTLTQ 743
 DB 667 VTFLTANDIYAEFWAEGDEMKKLGIOPIPMWDRDKDEVPOGOLGFYNAVALPCYTTLTQ 726
 QY 744 ILPPTPEPLAACDNLNOMKEVIRGETTAMWISGPGAPSKSTPEKANVAYED 796
 DB 727 ILPPTPEPLAACDNLNOMKEVIRGETTAMWISGPGAPSKSTPEKANVAYED 779

RESULT 6
 ADT92217 standard; protein; 797 AA.

XX ADT92217;
 XX AC ADT92217;
 XX DT 13-JAN-2005 (first entry)
 DE Murine phosphodiesterase 10A7 (PDE10A7).
 XX

KW PDE10A7, phosphodiesterase 10A7; phosphodiesterase; nootropic;
 KW neuroprotective; gene therapy; transgenic; mouse; enzyme.

OS Mus musculus.

PN WO2004090126-A2.

XX 21-OCT-2004.

XX 30-MAR-2004; 2004WO-US009878.

XX 03-APR-2003; 2003US-0459603P.

XX (MEMO-) MEMORY PHARM CORP.

XX Wang D, Bugaj-Gaweda B;

XX WPI; 2004-748763/73.

XX N-PSDB; ADT92216.

PT New isolated polynucleotide comprising a polynucleotide sequence coding
 for a mammalian phosphodiesterase 10A7, or its mutation, useful for
 treating or preventing memory, psychiatric or cognitive disorders.

PS Claim 2; SEQ ID NO 2; 93pp; English.

The invention relates polynucleotide sequences coding for mammalian
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
 CC identifying an agent that modulates the expression or activity of a
 CC phosphodiesterase in transfected host cells is provided which involves
 CC measuring amounts of cAMP or cGMP produced in the presence of the agent.
 CC The agent inhibits the expression or activity of the phosphodiesterase.
 CC The polynucleotides are useful in diagnostic assays and for screening for
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for
 CC treating or preventing memory, psychiatric or cognitive disorders. The
 CC present sequence represents a mouse PDE10A7 enzyme.

Sequence 797 AA;

Query Match 97.0%; Score 4078.5; DB 8; Length 797;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 776; Conservative 3; Mismatches 6; Indels 7; Gaps 1;

QY 12 FRRLTECFSPS-----LTDEKAVATLSLHPQVLDSEVSASAEVTEKMLKRTKNA 64
 DB 6 FQQAQLCFGRPPSPSATTOGLTDEKAVATLSLHPQVLDSEVSASAEVTEKMLKRTKNA 65
 QY 65 KQSPSPKEVSRYODTNMGGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKADGAFAL 124
 DB 66 KQSPSPKEVSRYODTNMGGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKADGAFAL 125
 QY 125 YFAGEENSLCVFIPPGMEGGRLLIPAGITGGTTISAYVAKSKRTLLVEDILGDERFP 184
 DB 126 YFAGEENSLCVFIPPGMEGGRLLIPAGITGGTTISAYVAKSKRTLLVEDILGDERFP 185
 QY 185 RGTGLESSTRIGSVLCPLIYTAIGDLIGILEYRHWGKAFLSHQEVATNLAWSVAI 244
 DB 186 RGTGLESSTRIGSVLCPLIYTAIGDLIGILEYRHWGKAFLSHQEVATNLAWSVAI 245
 QY 245 HQVOYCRGLAKOTELNDELIDVSKTYFEDNIVADSLLEHIMIYAKNLVNAADRCALFOVDH 304
 DB 246 HQVOYCRGLAKOTELNDELIDVSKTYFEDNIVADSLLEHIMIYAKNLVNAADRCALFOVDH 305
 QY 305 KNEKELYSDFDIEGEKEGKPIFKTKEIRFSIEKGIAGQVARTGVLNPDVADPRFNR 364
 DB 306 KNEKELYSDFDIEGEKEGKPIFKTKEIRFSIEKGIAGQVARTGVLNPDVADPRFNR 365
 QY 365 EVDLYGTGTYTRNILLCPYISRGSVIGVQVMWVKISGSAFASKTDENNNPKMAFVCAALHLC 424
 DB 366 EVDLYGTGTYTRNILLCPYISRGSVIGVQVMWVKISGSAFASKTDENNNPKMAFVCAALHLC 425
 QY 425 ANMYHRIHSECIYRATMEKLSYHSICTSEEWQGLMRFNLPARICRDIELFFHFDIGPEEN 484

Db 426 ANMYRIRHSECTYRVNTEKLSYHSICTSEEWQGLMRPNLPARICRDIELFHFDIGPFEN 485
QY 445 MWPGIFVYVNIHSSCGTSCPELEKLCRFIMS YKKVKNRRVYVNHMKAVYVAHCMYALLONN 544
Db 446 MWPGIFVYVNIHSSCGTSCPELEKLCRFIMS YKKVKNRRVYVNHMKAVYVAHCMYALLONN 545
QY 545 NGLFPLDERKGLLIACLDHGRGFSNSYLQKFDPHPLAALYSTSTMEQHHFSQTVSLIQ 604
Db 546 NGLFPLDERKGLLIACLDHGRGFSNSYLQKFDPHPLAALYSTSTMEQHHFSQTVSLIQ 605
QY 605 LEGHNI PSTLSSESEYBOVLEIRKAI IATD LALYFGNRKQLEBMYQTGSLNLHNSHRDR 664
Db 606 LEGHNI PSTLSSESEYBOVLEIRKAI IATD LALYFGNRKQLEBMYQTGSLNLHNSHRDR 665
QY 665 VTGLMWTACDLCSYTKLMPVTKL TANDIYAEFMAEGDEMKKLGIOPIPMMDSDKDEVPQ 724
Db 666 VTGLMWTACDLCSYTKLMPVTKL TANDIYAEFMAEGDEMKKLGIOPIPMMDSDKDEVPQ 725
QY 725 GOLGFYNAVAIPCYTTLTQILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSK 784
Db 726 GOLGFYNAVAIPCYTTLTQILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSK 785
QY 785 STPEKLANVKVED 796
Db 786 STPEKLANVKVD 797
RESULT 7
ADT92236
ID ADT92236 standard; protein; 790 AA.
XX ADT92236;
XX 13-JAN-2005 (first entry)
DT 13-JAN-2005 (first entry)
DE Mouse PDE10A3 isoform sequence.
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
KW neuroprotective; gene therapy; transgenic; enzyme; PDE10A3; mouse.
XX Mus musculus.
OS WO2004090126-A2.
XX PN 21-OCT-2004.
XX PD 30-MAR-2004; 2004WO-US009878.
XX PF 03-APR-2003; 2003US-0459603P.
XX PR (MEMO-) MEMORY PHARM CORP.
XX PA Wang D, Bugaj-Gaweda B;
XX PI WPI; 2004-748763/73.
XX PS New isolated polynucleotide comprising a polynucleotide sequence coding
PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for
PT treating or preventing memory, psychiatric or cognitive disorders.
XX Die closure; SEQ ID NO 21; 93pp; English.
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms
XX used in a comparison study with the murine and rat PDE10A7 sequences.

XX SQ Sequence 790 AA;
Query Match 96.8%; Score 4072; DB 8; Length 790;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 772; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 24 LTDEKVAKYLISLPVNDLDFEVSASAEVTEKMLRKTKNAKDEBSPKESRYODTNMQG 83
Db 18 LTDEKVAKYLISLPVNDLDFEVSASAEVTEKMLRKTKNAKDEBSPKESRYODTNMQG 77
QY 84 VYELNSYIEORLDTGDNHLLLYELSSIIRIATKADFPALYFLGECNNSLCVFIPGMK 143
Db 78 VYELNSYIEORLDTGDNHLLLYELSSIIRIATKADFPALYFLGECNNSLCVFIPGMK 137
QY 144 EGQPLRIAGPTQGTTSIAYAVASRKTLVEDLIDGRFRFGTCLSEGTPIQSULCPI 203
Db 138 EGQPLRIAGPTQGTTSIAYAVASRKTLVEDLIDGRFRFGTCLSEGTPIQSULCPI 197
QY 204 VTAIGDLIGIELYRHWGKEAFCLSHQEVATANLAMA5VAIHQVQVCRGLAKQTELANDFL 263
Db 198 VTAIGDLIGIELYRHWGKEAFCLSHQEVATANLAMA5VAIHQVQVCRGLAKQTELANDFL 257
QY 264 LDVSKTYPDNIVAIDSLEHIMYAKNLVNADRCALFQVDHKNKELYSDFDIGEKEGK 323
Db 258 LDVSKTYPDNIVAIDSLEHIMYAKNLVNADRCALFQVDHKNKELYSDFDIGEKEGK 317
QY 324 PIFPKTKETIRSEIEKGIAGQVARTGEVNTIPDAVADPFENREVDLYTGYTTRNLICMFIY 383
Db 318 PIFPKTKETIRSEIEKGIAGQVARTGEVNTIPDAVADPFENREVDLYTGYTTRNLICMFIY 377
QY 384 SRGSIVGVQWVNIKSGAFSKTDENNKMPFAVECALALHCCANNMYRIRHSECTRYVME 443
Db 378 SRGSIVGVQWVNIKSGAFSKTDENNKMPFAVECALALHCCANNMYRIRHSECTRYVME 437
QY 444 KLSYHSICTSEEWQGLMRPNLPARICRDIELFHFDIGFENMWPGIFVYVNIHRSCTSCF 503
Db 438 KLSYHSICTSEEWQGLMRPNLPARICRDIELFHFDIGFENMWPGIFVYVNIHRSCTSCF 497
QY 504 ELEKLCRFIMS YKKVKNRRVYVNHMKAVYVAHCMYALLONNGLFTDLERKGLLIACLCCH 563
Db 498 ELEKLCRFIMS YKKVKNRRVYVNHMKAVYVAHCMYALLONNGLFTDLERKGLLIACLCCH 557
QY 564 DLDHRGFSNSYLQKFDPHPLAALYSTSTMEQHHFSQTVSLIQLEGHNI PSTLSSESEYBOVL 623
Db 558 DLDHRGFSNSYLQKFDPHPLAALYSTSTMEQHHFSQTVSLIQLEGHNI PSTLSSESEYBOVL 617
QY 624 EIRKAI IATD LALYFGNRKQLEBMYQTGSLNLHNSHRDVI GLMWTACDLCSYTKLMP 683
Db 618 EIRKAI IATD LALYFGNRKQLEBMYQTGSLNLHNSHRDVI GLMWTACDLCSYTKLMP 677
QY 684 VTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQGOGLFYNAVAIPCTTTLTQ 743
Db 678 VTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDRKDEVPQGOGLFYNAVAIPCTTTLTQ 737
QY 744 ILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSKSTPEKLANVKVED 796
Db 738 ILPTEPEPLKACRDNLNQMEKVI RGEETAMWISGPGAPSKSTPEKLANVKVED 790
RESULT 8
ADT92219
ID ADT92219 standard; protein; 795 AA.
XX ADT92219;
XX 13-JAN-2005 (first entry)
DT 13-JAN-2005 (first entry)
DE Rat phosphodiesterase 10A7 (PDE10A7).
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; nootropic;
KW neuroprotective; gene therapy; transgenic; rat; enzyme.
XX

OS Rattus norvegicus.
 XX PN WO2004090126-A2.
 XX 21-OCT-2004.
 PD 30-MAR-2004; 2004MO-US009878.
 XX PF 03-APR-2003; 2003US-0453603P.
 XX PR (MEMO-) MEMORY PHARM CORP.
 XX PA Wang D, Bugaj-Gaweda B;
 XX PI WPI; 2004-748763/73.
 XX DR N-PSDB; ADT92218.
 DR New isolated polynucleotide comprising a polynucleotide sequence coding
 PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for
 PT treating or preventing memory, psychiatric or cognitive disorders.
 XX Claim 3; SEQ ID NO 4; 93pp; English.
 XX The invention relates polynucleotide sequences coding for mammalian
 CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
 CC identifying an agent that modulates the expression or activity of a
 CC phosphodiesterase in transfected host cells is provided which involves
 CC measuring amounts of cAMP or cGMP produced in the presence of the agent.
 CC The agent inhibits the expression or activity of the phosphodiesterase.
 CC The polynucleotides are useful in diagnostic assays and for screening
 CC modulators, specifically inhibitors of PDE10A7. They are also useful for
 CC treating or preventing memory, psychiatric or cognitive disorders. The
 CC present sequence represents a rat PDE10A7 enzyme.
 XX Sequence 795 AA;
 XX
 Query Match 95.4%; Score 4012.5; DB 8; Length 795;
 Best Local Similarity 96.7%; Pred. No. 0;
 Matches 767; Conservative 5; Mismatches 12; Indels 9; Gaps 3;
 QY 11 CRRRLTEC--FLSPS-----LTDEKRYAVLSLHPVLDEFVSSESVAETVEKMLKRRKTK 63
 DB 5 CFQOALCGPSPSANTRGLTDEKRYAVLSLHPVLDEFVSSESVAETVEKMLKRRKTK 64
 QY 64 AKDEPSPKESRYQDTNMOGVYELNSYIEQRDLDTGDMNLLLYELSSIIIRATKADGFA 123
 DB 65 AEBEPSPKESRYQDTNMOGVYELNSYIEQRDLDTGDMNLLLYELSSIIIRATKADGFA 124
 QY 124 LYFLGECNNSLCVFIIPGMKEGQPRLLIPAGPIQTGTTISAVYAKSRKTLIVEDIIGDERF 183
 DB 125 LYFLGECNNSLCVFTPPGMKEGQPRLLIPAGPIQTGTTISAVYAKSRKTLIVEDIIGDERF 184
 QY 184 PRGTGIESGRIOSVCLPIVTAIGDLIGLEIRYHMGKAPCLSHOEVTATLAAVSA 243
 DB 185 PRGTGIESGRIOSVCLPIVTAIGDLIGLEIRYHMGKAPCLSHOEVTATLAAVSA 244
 QY 244 IHVOVCRGLAKOTELNDFLDVSKTYPDNIVAIDSLHEIMITYAKVLVNAADCALFOVD 303
 DB 245 IHVOVCRGLAKOTELNDFLDVSKTYPDNIVAIDSLHEIMITYAKVLVNAADCALFOVD 304
 QY 304 HKNKEIYSDLFDIGEEKGKPIFKTKTKEIRFSIEKGIAGVANTGEVLANIPDAVADPRFN 363
 DB 305 HKNKEIYSDLFDIGEEKGKPVFKTKTKEIRFSIEKGIAGVANTGEVLANIPDAVADPRFN 364
 QY 364 REVDLTYGTYTRNILLCPYISRGSVIGVOMNKKISSASKTDENNPKMPAFCALALH 423
 DB 365 REVDLTYGTYTRNILLCPYISRGSVIGVOMNKKISSASKTDENNPKMPAFCALALH 424
 QY 424 CANNYHRIHSECTIYRYMEKLSYHSICTSEENQGLARFNLPAICDIELFFHDIGPFE 483
 DB 425 CANNYHRIHSECTIYRYMEKLSYHSICTSEENQGLARFNLPAICDIELFFHDIGPFE 484
 QY 484 NMMPGIFVYMIHRSCTSCPELEKLCRFIMS VKKNYRVDPHYNMKHAVTVAHCMTAILON 543

DB 485 NMMPGIFVYMIHRSCTSCPELEKLCRFIMS VKKNYRVDPHYNMKHAVTVAHCMTAILON 544
 QY 544 NNGLFTELRKGLLIACLDHIDHRGFSNSYIQKRDHPALAYSTSTMEQHHFSCQVSTL 603
 DB 545 NNGLFTELRKGLLIACLDHIDHRGFSNSYIQKRDHPALAYSTSTMEQHHFSCQVSTL 604
 QY 604 QLEGHNISTSSSEYEOVLTEIRKAITATDLALYFGNRKOLEMYQSGSLNHNQSHRD 663
 DB 605 QLEGHNISTSSSEYEOVLTEIRKAITATDLALYFGNRKOLEMYQSGSLNHNQSHRD 664
 QY 664 RYIGLMMTACDLCSTYTKLMPYTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDXDEV 723
 DB 665 RYIGLMMTACDLCSTYTKLMPYTKLTANDIYAEFMAEGDEMKKLGIOPIPMMDRDXDEV 724
 QY 724 OGQIGFYNAVALPCYTTTLTQIIPTEPPLKACRDNLNOMEKVIIRGBETAMISGQAPAS 783
 DB 725 OGQIGFYNAVALPCYTTTLTQIIPTEPPLKACRDNLNOMEKVIIRGBETAMIS--GPATS 782
 QY 784 KSTPEKLVKVED 796
 DB 783 KSTSEKPYRKVD 795
 RESULT 9
 AAB26854
 ID AAB26854 standard; protein; 789 AA.
 XX AAB26854;
 AC 29-JAN-2001 (first entry)
 DT Human phosphodiesterase 10 (PDE10) amino acid sequence 2.
 DE Human phosphodiesterase 10 (PDE10) amino acid sequence 2.
 XX
 KM Phosphodiesterase 10; PDE10; human.
 XX Homo sapiens.
 OS JP2000224992-A.
 XX 15-AUG-2000.
 PD 11-MAY-1999; 99JP-00129343.
 PF 30-NOV-1998; 98JP-00338861.
 PR (TANA) TANABE SEIYAKU CO.
 PA
 XX WPI; 2000-605129/58.
 DR N-PSDB; AAA09590.
 DR Novel phosphodiesterase and its gene for research on complex mechanism of
 PT intracellular information transfer.
 PT Disclosure; Page 16-19; 29pp; Japanese.
 PS
 XX Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10)
 CC proteins AAB26853-B26856. Phosphodiesterase 10 and its gene are useful
 CC for research on the complex mechanism of intracellular information
 CC transfer. The invention includes a recombinant vector containing a PDE10
 CC gene, and a cell transformed with the vector. Sequences AAA09593-A09606
 CC represent PCR primers used in the isolation of the PDE10 polynucleotide
 CC sequences of the invention
 XX
 SO Sequence 789 AA;
 Query Match 95.2%; Score 4004; DB 3; Length 789;
 Best Local Similarity 95.6%; Pred. No. 0;
 Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
 QY 1 MEDGSPNNASCPRRLTECFASPSLTDEKRYAVLSLHPVLDEFVSSESVAETVEKMLKRR 60
 DB 1 MEDGSPNNASCPRRLTECFASPSLTDEKRYAVLSLHPVLDEFVSSESVAETVEKMLKRR 60


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QY 61 TNKADSPKSVSRVYODTNMGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
PR 61 NKSDESAPKSVSRVYODTNMGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
XX ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
PA (MEMO-) MEMORY PHARM CORP.
XX
XX Wang D, Bugaj-Gaweda B,
XX WPI: 2004-748763/73.
XX
XX New isolated polynucleotide comprising a polynucleotide sequence coding
XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX
XX Disclosure: SEQ ID NO 18; 93pp: English.
XX
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms
XX used in a comparison study with the murine and rat PDE10A7 sequences.
XX
XX Sequence 789 AA:
SQ

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PF 30-MAR-2004; 2004WO-US009878.
XX
XX 03-APR-2003; 2003US-0459603P.
XX
XX (MEMO-) MEMORY PHARM CORP.
XX
XX Wang D, Bugaj-Gaweda B,
XX WPI: 2004-748763/73.
XX
XX New isolated polynucleotide comprising a polynucleotide sequence coding
XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX
XX Disclosure: SEQ ID NO 18; 93pp: English.
XX
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms
XX used in a comparison study with the murine and rat PDE10A7 sequences.
XX
XX Sequence 789 AA:
SQ

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Query Match 95.2%; Score 4004; DB 8; Length 789;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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QY 481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVRYNNMKAVTVVAHGMVAI 540
DB 481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVRYNNMKAVTVVAHGMVAI 540
QY 541 LQNNNGLTDLERKGLLIACLDHLDHGFNSYIQKDPHPLAALYSTSTMEQHHFSQTV 600
DB 541 LQNNHTLFTDLERKGLLIACLDHLDHGFNSYIQKDPHPLAALYSTSTMEQHHFSQTV 600
QY 601 SLIQEGHNIFSTLSSEYEOVLIIIRKAIITDIALYFNGRKOLEBMYQTSLSLNNHNS 660
DB 601 SLIQEGHNIFSTLSSEYEOVLIIIRKAIITDIALYFNGRKOLEBMYQTSLSLNNHNS 660
QY 661 HRDRIYGLMTACDLCVTKLMPVTKLTANDIYAEFMAEDMKKLGIOPIPMMDRDKKD 720
DB 661 HRDRIYGLMTACDLCVTKLMPVTKLTANDIYAEFMAEDMKKLGIOPIPMMDRDKKD 720
QY 721 EYPOGQLGFYNAVAIPCTYTTLTQIIPTEPLKACRDNIQWEEKYIRGETAMTISGPBP 780
DB 721 EYPOGQLGFYNAVAIPCTYTTLTQIIPTEPLKACRDNIQWEEKYIRGETAMTISGPBP 780
QY 781 APSKSTPE 788
DB 781 AOKAAASE 788

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RESULT 10
ADT92233
ID ADT92233 standard; protein; 789 AA.

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XX ADT92233;
XX
XX 13-JAN-2005 (first entry)
XX
XX Human PDE10A2 isoform sequence.
XX
XX PDE10A7; phosphodiesterase 10A7; phosphodiesterase; noctropic;
XX neuroprotective; gene therapy; transgenic; enzyme; PDE10A2; human.
XX
XX Homo sapiens.
XX
XX WO2004090126-A2.
XX
XX 21-OCT-2004.
XX
XX

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PF 30-MAR-2004; 2004WO-US009878.
XX
XX 03-APR-2003; 2003US-0459603P.
XX
XX (MEMO-) MEMORY PHARM CORP.
XX
XX Wang D, Bugaj-Gaweda B,
XX WPI: 2004-748763/73.
XX
XX New isolated polynucleotide comprising a polynucleotide sequence coding
XX for a mammalian phosphodiesterase 10A7, or its mutation, useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX
XX Disclosure: SEQ ID NO 18; 93pp: English.
XX
XX The invention relates polynucleotide sequences coding for mammalian
XX phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
XX identifying an agent that modulates the expression or activity of a
XX phosphodiesterase in transfected host cells is provided which involves
XX measuring amounts of cAMP or cGMP produced in the presence of the agent.
XX The agent inhibits the expression or activity of the phosphodiesterase.
XX The polynucleotides are useful in diagnostic assays and for screening
XX modulators, specifically inhibitors of PDE10A7. They are also useful for
XX treating or preventing memory, psychiatric or cognitive disorders.
XX Sequences ADT92232-ADT92238 represent various mammalian PDE10A isoforms
XX used in a comparison study with the murine and rat PDE10A7 sequences.
XX
XX Sequence 789 AA:
SQ

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Query Match 95.2%; Score 4004; DB 8; Length 789;
Best Local Similarity 95.6%; Pred. No. 0;
Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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QY 1 MEDGSPNNASCFRRRLTECFLSPLTDEKVKAYLSLHPQVLDHFVSSEVAETVEKMLRK 60
DB 1 MEDGSPNNASCFRRRLTECFLSPLTDEKVKAYLSLHPQVLDHFVSSEVAETVEKMLRK 60
QY 61 TNKADSPKSVSRVYODTNMGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
DB 61 NKSDESAPKSVSRVYODTNMGVYVELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
QY 121 GFALYFLGECNNSLCVFIPGMEKEGPRLIPAGPIITQGTISAVYAKSRKTLVIEDIIGD 180
DB 121 GFALYFLGECNNSLCVFIPGMEKEGPRLIPAGPIITQGTISAVYAKSRKTLVIEDIIGD 180
QY 181 BRPFGTGLBEGSTRIQSVLCPIYTAIGDLIGILEYHHMGKEAFCLSHQEVATNLMWA 240
DB 181 BRPFGTGLBEGSTRIQSVLCPIYTAIGDLIGILEYHHMGKEAFCLSHQEVATNLMWA 240
QY 241 SVAIHQOVOCRGIAKQTELANDFLDVSRTYFDNIYAIDSLLEHIMIYAKNLVNADRCALF 300
DB 241 SVAIHQOVOCRGIAKQTELANDFLDVSRTYFDNIYAIDSLLEHIMIYAKNLVNADRCALF 300
QY 301 QVDHKNKELYSDDLPIGEEKGKPIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADP 360
DB 301 QVDHKNKELYSDDLPIGEEKGKPIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADP 360
QY 361 RPNREVDLYGTGTTNNILCMPIVSRGSYIGVQWVNKISGSAFSTKDNNFMFAVFCAL 420
DB 361 RPNREVDLYGTGTTNNILCMPIVSRGSYIGVQWVNKISGSAFSTKDNNFMFAVFCAL 420
QY 421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIG 480
DB 421 ALHCANMYHRIHSECIYRVMEKLSYHSICTSEMOGLMRFNLPARICRDIELFHPDIG 480
QY 481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVRYNNMKAVTVVAHGMVAI 540
DB 481 PFENMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQYRRVRYNNMKAVTVVAHGMVAI 540
QY 541 LQNNNGLTDLERKGLLIACLDHLDHGFNSYIQKDPHPLAALYSTSTMEQHHFSQTV 600
DB 541 LQNNHTLFTDLERKGLLIACLDHLDHGFNSYIQKDPHPLAALYSTSTMEQHHFSQTV 600

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QY 601 SLLQEGHNIFSTLSSSEYEOVLIRKAIITDIALYFGNRKQLEEMVQTSGLNHNOS 660
 DB 601 SLLQEGHNIFSTLSSSEYEOVLIRKAIITDIALYFGNRKQLEEMVQTSGLNHNOS 660
 QY 661 HDRVYIGLMTACDLCSTYKLMPTVLTANDIYAEFMAGDEMKLGIOPIPMMDRDXD 720
 DB 661 HDRVYIGLMTACDLCSTYKLMPTVLTANDIYAEFMAGDEMKLGIOPIPMMDRDXD 720
 QY 721 EYPOGOLGFYNAVAIPCYTTTLTQILPTEPPLKACRDNLNOMEKVI RGEETAMWISGPGP 780
 DB 721 EYPOGOLGFYNAVAIPCYTTTLTQILPTEPPLKACRDNLNOMEKVI RGEETAMWISGPGP 780
 QY 781 APSKSTPE 788
 DB 781 AOKAAASE 788

RESULT 11
 AAB26856
 ID AAB26856 standard; protein; 788 AA.
 AC AAB26856;
 DT 29-JAN-2001 (first entry)
 DE Human phosphodiesterase 10 (PDE10) amino acid sequence 4.
 KM Phosphodiesterase 10; PDE10; human.
 OS Homo sapiens.
 PN JP2000224992-A.
 XX 15-AUG-2000.
 XX 11-MAY-1999; 99JP-00129343.
 XX PR 30-NOV-1996; 98JP-00338861.
 XX (TANABE SEIYAKU CO.
 XX WPI; 2000-605129/58.
 XX Novel phosphodiesterase and its gene for research on complex mechanism of intracellular information transfer.
 XX Disclosure; Page 24-27; 29pp; Japanese.
 CC Sequences AAA09589-A09592 encode human phosphodiesterase 10 (PDE10) protein AAB26853-B26856. Phosphodiesterase 10 and its gene are useful for research on the complex mechanism of intracellular information transfer. The invention includes a recombinant vector containing a PDE10 gene, and a cell transformed with the vector. Sequences AAA09593-A09606 represent PCR primers used in the isolation of the PDE10 polynucleotide sequences of the invention
 CC XX
 SQ Sequence 788 AA;

Query Match 95.0%; Score 3997; DB 3; Length 788;
 Best Local Similarity 98.3%; Pred. No. 0;
 Matches 760; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 24 LTDEKTKAVYSLHPQVLDVFSSVSATVEKWLKRTNKAKDBSPKESRYODTNMOG 83
 DB 18 LTDEKTKAVYSLHPQVLDVFSSVSATVEKWLKRTNKAKDBSPKESRYODTNMOG 77
 QY 84 VVYELNSYIEQRDLDTGDNHLLYLELSSIRIATKADGPAALYFGECCNSLICYFTIPGMK 143
 DB 78 VVYELNSYIEQRDLDTGDNHLLYLELSSIRIATKADGPAALYFGECCNSLICYFTIPGMK 137
 QY 144 EGGPRLIPAGPITGCTTISAYVAKSRKTLVLEDIGDERFPFGTGLSGSTRIGSVLCPLT 203

DB 138 EGGPRLIPAGPITGCTTISAYVAKSRKTLVLEDIGDERFPFGTGLSGSTRIGSVLCPLT 197
 QY 204 VTAIDDLIGILELYHMGKEAFCLSHOYATNTLMA5AITHQOVQCGLAQTBLNDL 263
 DB 198 VTAIDDLIGILELYHMGKEAFCLSHOYATNTLMA5AITHQOVQCGLAQTBLNDL 257
 QY 264 LDVSKTYEPDNIYAIISLLEHIMIYAKNLVNADRCALFOVDHNGKELYSDFDIGEKEK 323
 DB 258 LDVSKTYEPDNIYAIISLLEHIMIYAKNLVNADRCALFOVDHNGKELYSDFDIGEKEK 317
 QY 324 PIFKTKTEIRFSIEKGIAGOVARTGEVLNIPDAVADPRENREVDLYGTNTNIIICMPIV 383
 DB 318 PIFKTKTEIRFSIEKGIAGOVARTGEVLNIPDAVADPRENREVDLYGTNTNIIICMPIV 377
 QY 384 SRGSYIGVQVWYVKISGSASFSTDENFMFAVFCALALHCANMTHRIHSECIYRYTME 443
 DB 378 SRGSYIGVQVWYVKISGSASFSTDENFMFAVFCALALHCANMTHRIHSECIYRYTME 437
 QY 444 KLSYHSICTSEEMOGIMRPNLPARICRDIELFHPDIPPENNMPGIFVYMIHRSCTSGCF 503
 DB 438 KLSYHSICTSEEMOGIMRPNLPARICRDIELFHPDIPPENNMPGIFVYMIHRSCTSGCF 497
 QY 504 BLEKLCRFIMSYKQYRVRPYHNWKAIVTAHCMTAIIQNNNGLFTDLERKGLLAQLCH 563
 DB 498 BLEKLCRFIMSYKQYRVRPYHNWKAIVTAHCMTAIIQNNNGLFTDLERKGLLAQLCH 557
 QY 564 DLDHGRFSNSYIQKDPHPLAALYSTTMEQHHPSQTVSILQLEGNHIFSTLSSSEYEOVL 623
 DB 558 DLDHGRFSNSYIQKDPHPLAALYSTTMEQHHPSQTVSILQLEGNHIFSTLSSSEYEOVL 617
 QY 624 EIIIRKAIITDIALYFGNRKQLEEMVQTSGLNHNOSHRDRIYGLMNTACDLCSTYKLM 683
 DB 618 EIIIRKAIITDIALYFGNRKQLEEMVQTSGLNHNOSHRDRIYGLMNTACDLCSTYKLM 677
 QY 684 YTKLFTANDIYAEFMAGDEMKLGIOPIPMMDRDXDEVPQOLGFYNAVAIPCYTTTLTQ 743
 DB 678 YTKLFTANDIYAEFMAGDEMKLGIOPIPMMDRDXDEVPQOLGFYNAVAIPCYTTTLTQ 737
 QY 744 ILPTEPPLKACRDNLNOMEKVI RGEETAMWISGPGPAPSKSTPEKLANKVED 796
 DB 738 ILPTEPPLKACRDNLNOMEKVI RGEETAMWIS--GPATSKSTSEKPTRKVD 788

RESULT 12
 ADT92237
 ID ADT92237 standard; protein; 788 AA.
 XX
 AC ADT92237;
 DT 13-JAN-2005 (first entry)
 DE Rat PDE10A3 isoform sequence.
 KM PDE10A7, phosphodiesterase 10A7; phosphodiesterase; nootropic; neuroprotective; gene therapy; transgenic; enzyme; PDE10A3; rat.
 OS Rattus norvegicus.
 PN WO2004090126-A2.
 XX 21-OCT-2004.
 XX 30-MAR-2004; 2004WO-US009878.
 XX PR 03-APR-2003; 2003US-0459603P.
 XX (MEMO-) MEMORY PHARM CORP.
 XX Wang D, Bugaj-Gaweda B;
 WPI; 2004-748763/73.
 New isolated polynucleotide comprising a polynucleotide sequence coding

PT for a mammalian phosphodiesterase 10A7, or its mutation, useful for
PT treating or preventing memory, psychiatric or cognitive disorders.

PS Disclosure: SEQ ID NO 22; 93pp; English.

CC The invention relates polynucleotide sequences coding for mammalian
CC phosphodiesterase 10A7 (PDE10A7), or its mutation. A method for
CC identifying an agent that modulates the expression or activity of a
CC phosphodiesterase in transfected host cells is provided which involves
CC measuring amounts of cAMP or cGMP produced in the presence of the agent.
CC The agent inhibits the expression or activity of the phosphodiesterase.
CC The polynucleotides are useful in diagnostic assays and for screening
CC modulators, specifically inhibitors of PDE10A7. They are also useful for
CC treating or preventing memory, psychiatric or cognitive disorders.
CC Sequences AD792323-AD792328 represent various mammalian PDE10A isoforms
CC used in a comparison study with the murine and rat PDE10A7 sequences.

XX Sequence 788 AA;

Query Match 95.0%; Score 3997; DB 8; Length 788;

Best Local Similarity 98.3%; Pred. No. 0; Mismatches 8; Indels 2; Gaps 1;
Matches 760; Conservative 3;

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24 LTDEKVKAYLSLHPVLDSESVSAETVEKMLKRTKAKDESPKESVRYODTNMG 83
18 LTDEKVKAYLSLHPVLDSESVSAETVEKMLKRTKAKDESPKESVRYODTNMG 77
84 VYELNSYIEQRLDTGGDNHLLYELSSIIIRIATADGALYFLGECNNSLCVPIPGMK 143
78 VYELNSYIEQRLDTGGDNHLLYELSSIIIRIATADGALYFLGECNNSLCVPIPGMK 137
144 EGQPLIPAGPIITGGTISAVYAKSKRTLLVEDIDGDERFPFGTGESGTRIQSVLCPI 203
138 EGQPLIPAGPIITGGTISAVYAKSKRTLLVEDIDGDERFPFGTGESGTRIQSVLCPI 197
204 VTAIGDLIGILELYHMKCAFCLSHOEVAATNLAMASVAIHQVQCRGLAQTELDNFL 263
198 VTAIGDLIGILELYHMKCAFCLSHOEVAATNLAMASVAIHQVQCRGLAQTELDNFL 257
264 LDVSKTYPDNIYATLSLHEIMITYAKNLVNAADRCALFOVDHKNKELYSLEPIGSEKSK 323
258 LDVSKTYPDNIYATLSLHEIMITYAKNLVNAADRCALFOVDHKNKELYSLEPIGSEKSK 317
324 PFPKTKELRFSIEKGIAGVARGEVLANI PDYAVDPRNRREVDLYGTGTNTIICMPIV 383
318 PFPKTKELRFSIEKGIAGVARGEVLANI PDYAVDPRNRREVDLYGTGTNTIICMPIV 377
384 SRGSYIGVQVWVKISGSAFSTKDENSEPMAFVFCALALHCAAMYHRIHSECIYRTME 443
378 SRGSYIGVQVWVKISGSAFSTKDENSEPMAFVFCALALHCAAMYHRIHSECIYRTME 437
444 KLSYHSICTSEWQGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIRHSCGTSCF 503
438 KLSYHSICTSEWQGLMRFNLPARICRDIELFHPDIGPENMPGIFVYMIRHSCGTSCF 497
504 ELEKICRPTMSYKKNYRRVRYNPMKAVTVAHCMATLIDNNNGLFTDLERKLLAACCH 563
498 ELEKICRPTMSYKKNYRRVRYNPMKAVTVAHCMATLIDNNNGLFTDLERKLLAACCH 557
564 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSILQLEGNIFSTLSSSEYQVL 623
558 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSILQLEGNIFSTLSSSEYQVL 617
624 EIRRAIATATDALYFGNKKOLEMYQTSGLNLHNSHRDRIYGLMTRACDLCSTYKMP 683
618 EIRRAIATATDALYFGNKKOLEMYQTSGLNLHNSHRDRIYGLMTRACDLCSTYKMP 677
664 VTKLANTIVAEFMAEGEMKGLGIOPIMMDRDRDEVPOGOLGRYNAVAPCTTLLTLO 743
678 VTKLANTIVAEFMAEGEMKGLGIOPIMMDRDRDEVPOGOLGRYNAVAPCTTLLTLO 737
744 ILPTEPLLKACRDNLNQWEKVIKGEETAMWISGPGAPSKSTPEKLVNKVD 796

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DB 738 ILPTEPLLKACRDNLNQWEKVIKGEETAMWIS--GPATSKSTSEKPYRKVVD 788

RESULT 13

AA13935 standard; protein; 803 AA.

AA13935;

14-JUL-1999 (first entry)

Human phosphodiesterase, PDE8.

Phosphodiesterase 8; PDE8; human; cyclic nucleotide pathway; therapy;

intracellular cyclic nucleotide level modulation; cAMP; cGMP.

Homo sapiens.

W09919495-A1.

22-APR-1999.

16-OCT-1998; 98WO-US021956.

16-OCT-1997; 97US-00951648.

(ICOS-) ICOS CORP.

Loughney K;

WPI; 1999-277645/23.

N-PEDB; AAX36711.

New isolated phosphodiesterase genes and polypeptides for identifying

specific binding partners.

Claim 3; Page 50-55; 80pp; English.

This sequence is the human phosphodiesterase 8 (PDE8) of the invention.
The phosphodiesterase genes and polypeptides are used to develop products
for treating conditions in which cyclic nucleotide pathways are aberrant
and for modulation of intracellular cyclic nucleotide levels. The PDE8
CC polypeptides exhibit high affinity for hydrolysis of both cAMP and cGMP
CC but relatively low sensitivity to enzyme inhibitors specific for other
CC PDE families. The PDE8A polypeptides and polynucleotides can be used for
CC identifying their specific binding partners. The products can provide
CC approaches for treating conditions in which cyclic nucleotide pathways
CC are aberrant as well as conditions in which modulation of intracellular
CC cAMP and/or cGMP levels in certain cell types is desirable

Sequence 803 AA;

Query Match 95.0%; Score 3997; DB 2; Length 803;

Best Local Similarity 95.4%; Pred. No. 0; Mismatches 17; Indels 0; Gaps 0;
Matches 752; Conservative 19;

```

1 MEDGSPNNASCFRRITLTCGFLSPSLTDEKVKAYLSLHPVLDSESVSAETVEKMLRK 60
15 MEDGSPNNASCFRRITLTCGFLSPSLTDEKVKAYLSLHPVLDSESVSAETVEKMLRK 74
61 TNKAKDESPKESVRYODTNMGVYELNSYIEQRLDTGGDNHLLYELSSIIIRIATRAD 120
75 NTKSEDESPKESVRYODTNMGVYELNSYIEQRLDTGGDNHLLYELSSIIIRIATRAD 134
121 GPALYFLGECNNSLCVPIPGMKSGQPLIPAGPIITGGTISAVYAKSKRTLLVEDIDGD 180
135 GPALYFLGECNNSLCVPIPGMKSGQPLIPAGPIITGGTISAVYAKSKRTLLVEDIDGD 194
181 ERFPRGTLSEGTITQSVLCPIYTAIGDLIGILELYHMKCAFCLSHOEVAATNLAMA 240
195 ERFPRGTLSEGTITQSVLCPIYTAIGDLIGILELYHMKCAFCLSHOEVAATNLAMA 254
241 SVAIHQVQCRGLAQTELDNFLDVSKTYPDNIYATLSLHEIMITYAKNLVNAADRCALF 300

```

DB 255 SVAIHQVOCGLAQOTELNDPLDVSKTYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 314
QY 301 QVDHKNKELYSDFDIEGEEKGKPIFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYADP 360
DB 315 QVDHKNKELYSDFDIEGEEKGKPVFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYADP 374
QY 361 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 420
DB 375 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 434
QY 421 ALHCANMTHRIHSHSECTIYVYVMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDIG 480
DB 435 ALHCANMTHRIHSHSECTIYVYVMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDIG 494
QY 481 PFENMMPGIFVYVMIHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHCMYAI 540
DB 495 PFENMMPGIFVYVMIHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHCMYAI 554
QY 541 LQNNNGLFPTDLERKGLLIACLDHLDHGFNSYLOKPHPLAALYSTSTMEQHHSQTV 600
DB 555 LQNNHTLFTDLERKGLLIACLDHLDHGFNSYLOKPHPLAALYSTSTMEQHHSQTV 614
QY 601 SILOLEGNHIFSTLSSSEYEOVLEIRKAIITADLALYGNRKOLEMYQTSGLNHNOS 660
DB 615 SILOLEGNHIFSTLSSSEYEOVLEIRKAIITADLALYGNRKOLEMYQTSGLNHNOS 674
QY 661 HRDRIYGLMMTACDLCSTYTKLMPVTKLITANDIYAEFMAEGDEMKKGIQIPIMMDRDKD 720
DB 675 HRDRIYGLMMTACDLCSTYTKLMPVTKLITANDIYAEFMAEGDEMKKGIQIPIMMDRDKD 734
QY 721 EYVQGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINOMEKVI RGETAMWISGPGP 780
DB 735 EYVQGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINOMEKVI RGETAMWISGPGP 794
QY 781 APSKSTPE 788
DB 795 AQAQAASE 802

RESULT 14
ID AAB28257 standard; protein; 803 AA.
XX AAB28257;
AC 13-FEB-2001 (first entry)
DT Human phosphodiesterase 8A1 PDB8A1.
DE Human phosphodiesterase 8A1; chromosome 6p26-27.
OS Homo sapiens.
XX US6133007-A.
PN 17-OCT-2000.
PD 16-OCT-1998; 98US-00174437.
PF 16-OCT-1997; 97US-00951648.
PR 16-OCT-1997; 97US-00951648.
PA (ICOS-) ICOS CORP.
XX Loughney K;
PI MPI; 2001-006138/01.
XX N-PSDB; AAC63696.
XX New phosphodiesterase 8A (PDB8A) polypeptides useful in the
PT systematic analysis of the structure and function of PDB8, and for
PT identifying molecules with which PDB8A will interact.

PS Claim 2; Col 39-44; 37pp; English.
XX The present sequence is human phosphodiesterase 8A1 (PDB8A1).
CC Phosphodiesterases hydrolyse 3', 5' cyclic nucleotides to their
CC respective nucleoside 5' monophosphates. The present sequence is a splice
CC variant of PDB8 (AAB28257). This sequence may be used in the systematic
CC analysis of the structure and function of PDB8, and for the
CC identification of molecules with which PDB8 will interact. The coding
CC sequence for the present protein may be used in hybridisation assays to
CC detect the capacity of cells to express PDB8, and as a basis for
CC diagnostic methods useful for identifying a genetic alteration in a PDB8
CC locus that underlies a disease state or states. The human PDB8 gene has
CC been localised to chromosome 6p26-27
XX
SQ Sequence 803 AA;
Query Match 95.0%; Score 3997; DB 4; Length 803;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
QY 1 MEDGSPNNASCRRRLTECFSLSPSLTDEKVKAYLSLHPVQLDFEVSASAEVETKMKRK 60
DB 15 MEDGSPNNASCRRRLTECFSLSPSLTDEKVKAYLSLHPVQLDFEVSASAEVETKMKRK 74
QY 61 TYKADDESPKESVSRVODTNMGVYVELNSYTEORLDGTGDGHLLLYELSSIIIRIATKAD 120
DB 75 NKSSEDESPKESVSRVODTNMGVYVELNSYTEORLDGTGDGHLLLYELSSIIIRIATKAD 134
QY 121 GPALYFLGECNNLSLCPFIIPGMEKQPRILPAGPIITGGTISAVYAKSRKTLVLEDIIGD 180
DB 135 GPALYFLGECNNLSLCPFIIPGMEKQPRILPAGPIITGGTISAVYAKSRKTLVLEDIIGD 194
QY 181 ERFPRGTGIESGTRIQSVLCPIVTAIGDLGILBYLHNMGKAACLSHQEVATNTLMA 240
DB 195 ERFPRGTGIESGTRIQSVLCPIVTAIGDLGILBYLHNMGKAACLSHQEVATNTLMA 254
QY 241 SVAIHQVOCGLAQOTELNDPLDVSKTYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 300
DB 255 SVAIHQVOCGLAQOTELNDPLDVSKTYFDNIYAIDSLHIMIYAKNLVNAIDRCALF 314
QY 301 QVDHKNKELYSDFDIEGEEKGKPIFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYADP 360
DB 315 QVDHKNKELYSDFDIEGEEKGKPVFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAYADP 374
QY 361 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 420
DB 375 RFRREVDLYGTYYTNNILCMPIVSRGSGVIGVQVWVKISGSAFSKTDENNPFKFAVFCAL 434
QY 421 ALHCANMTHRIHSHSECTIYVYVMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDIG 480
DB 435 ALHCANMTHRIHSHSECTIYVYVMEKLSYHSICTSEEMQGLMRNLPARICRDIELFHPDIG 494
QY 481 PFENMMPGIFVYVMIHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHCMYAI 540
DB 495 PFENMMPGIFVYVMIHRSCTSCFELEKLCRFIMSVKQNRARVPYHNMKKAIVVAHCMYAI 554
QY 541 LQNNNGLFPTDLERKGLLIACLDHLDHGFNSYLOKPHPLAALYSTSTMEQHHSQTV 600
DB 555 LQNNHTLFTDLERKGLLIACLDHLDHGFNSYLOKPHPLAALYSTSTMEQHHSQTV 614
QY 601 SILOLEGNHIFSTLSSSEYEOVLEIRKAIITADLALYGNRKOLEMYQTSGLNHNOS 660
DB 615 SILOLEGNHIFSTLSSSEYEOVLEIRKAIITADLALYGNRKOLEMYQTSGLNHNOS 674
QY 661 HRDRIYGLMMTACDLCSTYTKLMPVTKLITANDIYAEFMAEGDEMKKGIQIPIMMDRDKD 720
DB 675 HRDRIYGLMMTACDLCSTYTKLMPVTKLITANDIYAEFMAEGDEMKKGIQIPIMMDRDKD 734
QY 721 EYVQGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINOMEKVI RGETAMWISGPGP 780
DB 735 EYVQGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINOMEKVI RGETAMWISGPGP 794
QY 781 APSKSTPE 788

Db 795 AQAASE 802

RESULT 15
AAE39535
AAE39535 standard; protein; 803 AA.

AC AAE39535;

DT 18-DEC-2003 (first entry)

DE Human phosphodiesterase 8 (PDE8) A2 splice variant, PB66a.

XX Phosphodiesterase 8; PDE8; human; enzyme.

XX Homo sapiens.

PN US656087-B1.

PD 20-MAY-2003.

PP 11-OCT-2000; 2000US-00686055.

PR 16-OCT-1997; 97US-00951648.

PR 16-OCT-1998; 98US-00174437.

PA (ICOS-) ICOS CORP.

PI Loughney K;

DR MPI; 2003-719642/68.

DR N-PSDB; AAD59989.

PT Identifying a specific binding partner of phosphodiesterase 8 (PDE8)

PS Claim 1; Col 39-44; 37pp; English.

CC The invention relates to a method for identifying a specific binding
CC partner of phosphodiesterase 8 (PDE8). The method is useful for
CC identifying a specific binding partner of PDE8, which inhibits or
CC enhances activity of PDE8. The binding partners of PDE8 are useful for
CC purification, detection or quantification of PDE8 products in fluid and
CC tissue samples using immunological procedures. Modulators of PDE8
CC activity are useful in treating a wide range of diseases and
CC physiological conditions in which PDE8 activity is known to be involved.
CC The present sequence is human PDE8 A2 splice variant protein

XX Sequence 803 AA;

Query Match 95.0%; Score 3997; DB 7; Length 803;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEDGSSNNAACRRRLTECTLSPSLTDEKAKAYLSLHPQLDFPVSSESAETVEKMLKRX 60
DB 15 MEDGSSNNAACRRRLTECTLSPSLTDEKAKAYLSLHPQLDFPVSSESAETVEKMLKRX 74
QY 61 TYKADDEPSPKESRYODTNMGOVYELNSYIEORLDTGSDNHLLEYLSIIIRIATKAD 120
DB 75 NKSSEDESAFKSVSRKODTNMGOVYELNSYIEORLDTGSDNHLLEYLSIIIRIATKAD 134
QY 121 GFALYFLGECNNSLCVFIIPGMEQGPRLIPAGPITOGTTISAYVAKSRKTLVVEDILGD 180
DB 135 GFALYFLGECNNSLCVFIIPGMEQGPRLIPAGPITOGTTISAYVAKSRKTLVVEDILGD 194
QY 181 ERFPRGTGLSEGTIRIQSVCLPIVTAIGLLIGILEYRWMGEARCLSHQEVATANTLAMA 240
DB 195 ERFPRGTGLSEGTIRIQSVCLPIVTAIGLLIGILEYRWMGEARCLSHQEVATANTLAMA 254
QY 241 SVAIHQVQVCRGLAKQTEINDFLIDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAIRCALF 300

Db 255 SVAIHQVQVCRGLAKQTEINDFLIDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAIRCALF 314
QY 301 QVDHKNKELYSDDLPIGSEKGGKPIFKTKTKIIRFSIEKGIAGQVARTGEVANIIPAYADP 360
DB 315 QVDHKNKELYSDDLPIGSEKGGKPVFKTKTKIIRFSIEKGIAGQVARTGEVANIIPAYADP 374
QY 361 RPNREVDLYTGTATNIIICMPIVSRGSVIGVQVQWVKISGSAFSTKDENNPFMAVPCAL 420
DB 375 RPNREVDLYTGTATNIIICMPIVSRGSVIGVQVQWVKISGSAFSTKDENNPFMAVPCAL 434
QY 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEMQGLMERNLPAICRDIIEHFPIG 480
DB 435 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEEMQGLMERNLPAICRDIIEHFPIG 494
QY 481 PFENMMPGIFVYMIHRSCTSCFELBKICRPIMSYKRYRVPYNNMGAATVAHCAVAI 540
DB 495 PFENMMPGIFVYMIHRSCTSCFELBKICRPIMSYKRYRVPYNNMGAATVAHCAVAI 554
QY 541 LONNGLFTDLERKGLIACLDLDRHGFNSYLOKFDHPLAALYSTTMEQHHFSQTV 600
DB 555 LONNGLFTDLERKGLIACLDLDRHGFNSYLOKFDHPLAALYSTTMEQHHFSQTV 614
QY 601 SILOLEGHNIFSTLSSSEYEQVLEIIRKAIATDLALYFGNRKQLEMYQTGSLNLHNS 660
DB 615 SILOLEGHNIFSTLSSSEYEQVLEIIRKAIATDLALYFGNRKQLEMYQTGSLNLHNS 674
QY 661 HRDRIYGLMTRACDLCSTYKLMPTVKLTANDIYAFMAEGDEMKLGIOPIPMMDRDKRD 720
DB 675 HRDRIYGLMTRACDLCSTYKLMPTVKLTANDIYAFMAEGDEMKLGIOPIPMMDRDKRD 734
QY 721 EYPOGQLGFYNAVAIPCTTTLTQILPTEBPLLKACRDNLNOMEKVIIRGEETAMWISGFP 780
DB 735 EYPOGQLGFYNAVAIPCTTTLTQILPTEBPLLKACRDNLNOMEKVIIRGEETAMWISGFP 794
QY 781 APSKSTPE 788
DB 795 AQAASE 802

Search completed: January 10, 2006, 13:53:59
Job time : 85 secs

Db 357 IFBEPYDGDABRLSGKEPIPMWDRQQAHLMPQM 391

RESULT 2

A48719 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine

N:Alternate names: PDB5A1

C:Species: Bos primigenius taurus (cattle)

C:Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999

A:Accession: A48719; A35807

R:McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecsek, A.; Seger, D.; Le Trong, H.; Colbr J. Biol. Chem. 268, 22863-22873, 1993

A:Title: The structure of a bovine lung cGMP-binding, cGMP-specific phosphodiesterase de A:Reference number: A48719; PMID:94043054; PMID:8226796

A:Accession: A48719

A:Molecule type: mRNA

A:Residues: 1-875 <MCA>

A:Cross-references: UNIPARC:UPI000014645D; GB:L16545

A:Experimental source: lung

R:Thomas, M.K.; Francis, S.H.; Corbin, J.D.

J. Biol. Chem. 265, 14971-14978, 1990

A:Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding A:Reference number: A35807; MUID:90368672; PMID:2168396

A:Accession: A35807

A:Molecule type: protein

A:Residues: 90-101 <THO>

A:Cross-references: UNIPARC:UPI000017289B

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodie C:Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydro F:602-825/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

F:92/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict

Query Match 21.8%; Score 918; DB 1; Length 875;

Best Local Similarity 30.2%; Pred. No. 2.6e-60;

Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

10 SCFRRLTSCPLSPSLTDE-----KYKAY---LSLHPVLDL-----FVSESVSAE 51

68 SC-----SCPLDPSPPAESVGTPTTRKTSABEPDRPLRFYIKSGVSLSDKKE 122

52 TVEKWLKRTNKADESPKEVSRVODTNMGVVELNSYIBORLDTGDNHLLEYLS 111

123 QMPLTSPFPDNDGQCSR-----LLELVMDISHLDTVALCHKIFLHNG 168

112 IIRIRTKADGFLYLYLGECNNSLCVFIIPGMEGQRLIPAGPIVQGT----- 160

169 LI-----SADRYSLFLVCESSNDKFLI-----SRLEF---DVAEGSTLEBASNNCIRL 213

161 -----ISAVVAKSRKTLVEDILGDERFPRGTGLESGRIGSVLCPIYTAIGDILGLE 215

214 EWNKGI VGHVNAAFGEPLNKDAVEDPRFAEVDQITGYTQSILCMPIKNHEEVAVQA 273

216 LY--RHMGKEAFCLSHOEVAATNLMASVAIHQVQCRGLAKQTEINDELVDVSKTYPDN 273

274 AINKSGNGGTETDEKOPFAVLAFCGIVLHNAQYETSLLENKRNQVLDLASLIFRE 333

274 IVATISLLEHMITAKNLVNAIDRCALFOVDHAKKELYSDFPIGEEKGKPLFKTKTEIR 333

334 QQSLEVIIKKIAATIIISFQVQKCTIFIVDEDCSSFSFVFMECEBELEKSSDTLTREND 393

334 FS-IEKGIAQVAFARGEVLTNPDAVADPRF---NREVLDYGTATRNILCMPIVS--RGS 387

394 ARIRVMTAQVKNTEPLNIPDVSKDKRFPWTNENNGINQOCIRSLCTIYIKGKKKK 453

388 VIQVQVQVNTKISGS-----AFSKTDENNFKMAVFCALALHCAVMYHRIHSECIYRVTM 442

454 VIQGVQVQVNTKISGS-----AFSKTDENNFKMAVFCALALHCAVMYHRIHSECIYRVTM 442

454 VIQGVQVQVNTKISGS-----AFSKTDENNFKMAVFCALALHCAVMYHRIHSECIYRVTM 442

443 EKLSTHSTCTSEEWQGLKRFNLPARI-----CRDIELFHPIDIGFFENMPPGIFVTMI 494

514 EYLSYHSAEAEETRELQ--SLAAVVPBQAQTLKITDPSFSDLELDTALCTIRMPFD 571

455 HRSCTSCBELEKLCRFIMSVKQYR--VPYINWKAIVAVAHQVALLQNN--NGLFTDL 551

Db 572 LNLVQNFQMKHEVLCKWILTSVKKYYRKVAVYHNRBAFNTAQCFMALKAGKIQKRLTDL 631

552 ERKGLITLCLCHDDPHRFNSYLOKPRHPLAALYSTMTMEOHHSQVSLTQLEGHNIF 611

632 EIALLLAALSHDLDRHRVNNSYIQSRSHPLAQLYCHSIMHHHFDQCLMINSFGNQL 691

612 STLSSEYEOVLEIRKAIITADLALYFGRNKOLEMYQTSGLMLNQHSHRDVIGLMMT 671

632 SGLSIEEKTKTLIKIQAIIITDIALYIKRGEFFELIMKQFNLEDPHOKELFLAMLMT 751

672 ACDLCSTKMPVTKLTANDIYAEFMAEGD-EMKKLGIGIPIPMWDRDRDEVQGLGFR 730

752 ACDLSAIRKPMPIQORIAELVATEFFDQDRERKEINIEPADLNMREKKNKIPSMQVGF 811

731 NAVAIPCTTITQLIPTEPRLTKACRDNLNWEKVIQREETAMTSG 777

812 DAICQLVLEALTHVSEDCFPILDCGRKRRQKQALAEQEKTL-ING 857

Db

RESULT 3

UN0106 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human

N:Alternate names: PDB5A1

C:Species: Homo sapiens (man)

C:Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004

A:Accession: UN0106

R:Stacey, P.; Rulien, S.; Dapling, A.; Phillips, S.C.

Biochem. Biophys. Res. Commun. 247, 249-254, 1998

A:Title: Molecular cloning and expression of human cGMP-binding cGMP-specific phosphodie A:Reference number: UN0106; MUID:98308101; PMID:9642111

A:Accession: UN0106

A:Molecule type: mRNA

A:Residues: 1-875 <STA>

A:Cross-references: UNIPROT:O76074; UNIPARC:UPI000003406D; GB:AJ004865; NID:93355605; PII C:GeneID:8

A:Gene: GDB:PDB5A

A:Cross-references: GDB:9032947

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodie C:Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydro F:612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

F:102/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predict

Query Match 21.7%; Score 912.5; DB 1; Length 875;

Best Local Similarity 31.2%; Pred. No. 6.8e-60;

Matches 238; Conservative 136; Mismatches 321; Indels 69; Gaps 18;

61 TNKADBPSPKESVRY--QDTNMQGVVELNSYIBORLDTGDNHLLEYLSIIRIATK 118

126 SDSEKKEQMPLTPRPFHDEBDGQCSRLLELVMDISHLDTVALCHKIFLHIGLI-----S 181

119 ADGFLYLYLGECNNSLCVFIIPGMEGQRLIPAGPIVQGT-----IS 162

182 ADRYSLFLVCESSNDKFLI-----SRLEF---DVAEGSTLEEVSNNCIRLENKGI 230

183 AYVAKSRKTLVEDILGDERFPRGTGLESGRIGSVLCPIYTAIGDILGLELY--BHW 220

221 CHVALGEPPLNKDAVEDPRFAEVDQITGYTQSILCMPIKNHEEVAVQAALINKSG 290

221 GKEAFCLSHOEVAATNLMASVAIHQVQCRGLAKQTEINDELVDVSKTYPDNVAIDSL 280

221 NGGFTETDEKOPFAVLAFCGIVLHNAQYETSLLENKRNQVLDLASLIFREQSLEYI 350

291 LEHMITAKNLVNAIDRCALFOVDHAKKELYSDFPIGEEKGKPLFKTKTEIRFS-IEKG 339

351 LKKIAATIIISFQVQKCTIFIVDEDCSSFSFVFMECEBELEKSSDTLTREDAKINYM 410

340 IAGVAFARGEVLTNPDAVADPRENREVLDYGTAT--RNILCMPIVS--RGSYIGVQ 393

411 YAOVKNTEPLNIPDVSKDKRFPPTT--NTGANNQOCIRSLCTIYIKGKKKVIYGCQ 469

394 MNKISGSA-----FSKTDENNFKMAVFCALALHCAVMYHRIHSECIYRVTMKLSYH 448

Db 470 LVNKRRENTGKPKPRNRDEQFLNFAVIFCGSIGIQTONTQYVEAVERAMAKONTLEVLN 529
Qy 449 SICTSBEMOGLMRFNLPARI-----CRDIELFHFDIGFPENMWPGIFFVYMIHRSCT 500
Db 530 ASAABETRELDQ--SLAAVVPVSAQTLKITDPSFSDLSDETALCTIRMTFDLNLVON 587
Qy 501 SCFPELKLGRFIMSVYKKNRR--VPYNNMGAVTVAMCMYAIL-----QNNGLFTDLERK 554
Db 588 PQMKKEVLCRWILSVYKKNRVAAVYNNMRAFNTAQCMFAALKAGKIQNK---LTDLETL 644
Qy 555 GLLIICLCCHDLDRGFSNSYLQKFDHPFLAALYSTSMEOHFSQTVSIILQEGHNIFFSTL 614
Db 645 ALLIINALSHDLDRKGVNNYSYIQSEHPLAQLYCHSIMEHHNFDQCLMILNSFGNQLSGL 704
Qy 615 SSSSEYQVLEIIRKAIATDLALYFGNRKQLEBMYQTGSLNLHNSHRDVIGLMTACD 674
Db 705 SJBEVKTTLKIKQAILATDLALYIKRGGEFPELLIKNQFNLEDPHQKELFLAMLTACD 764
Qy 675 LCSVTKLMPVTULTANDIYAEFMAEGD-EMKLGIGIPIPMDBDKRDVPOQGLGFYNAV 733
Db 765 LSAITPMPDIOORIMELVATEFPDQDRKRKEINTIEPTDLNNEKNKXKIPSMQVGFDAI 824
Qy 734 ALPCVTTLTQILPPTPEPLKACRDNLQMKVIRGSETAMWISG 777
Db 825 CQLYEAHTVSEDCFPFLDGCRRKQKQALLAEQOE-KMLING 867

RESULT 4

A40981
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
N:Alternate names: cGMP-dependent phosphodiesterase
C:Species: Bos primigenius taurus (cattle)
C:Date: 26-Aug-1999 #sequence revision 26-Aug-1999 #text change 09-Jul-2004
C:Accession: A40981, B36112; A36112; B26650; A60179; C26650
R:Sommeburg, W.K.; Mulaney, P.J.; Beavo, J.A.
J: Biol. Chem. 266, 17655-17661, 1991
A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase
A:Reference number: A40981; MUID:91373395; PMID:1654333
A:Accession: A40981
A:Molecule type: mRNA
A:Residues: 1-921 <SON>
A:Cross-references: UNIPROT:P14099; UNIPARC:UPI0000127BB; GB:M73512; NID:g162829; PION:
R:Le Trong, H.; Beier, N.; Sommeburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Cha
Biochemistry 29, 10280-10288, 1990
A:Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiesterase
A:Reference number: A36112; MUID:91104948; PMID:2176866
A:Accession: B36112
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 592-921 <LEFT>
A:Cross-references: UNIPARC:UPI0000172895
A:Accession: A36112
A:Molecule type: protein
A:Residues: 1-203, 'D', 634-794, 808-868 <CH>
A:Cross-references: UNIPARC:UPI0000172895
R:Charotomeau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A:Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterases
A:Reference number: A26650; MUID:87092242; PMID:3025833
A:Accession: B26650
A:Molecule type: protein
A:Residues: 613-632, 'L', 634-794, 808-868 <CH>
A:Cross-references: UNIPARC:UPI0000172897; UNIPARC:UPI0000172898
A:Experimental source: heart
R:Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Muraashima, S.; Manganuel
Second Messengers Phosphoproteins 13, 87-98, 1991
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-st
A:Reference number: A60179; MUID:92065414; PMID:1659635
A:Accession: A60179
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 311-803, 'DV', 806-921 <TAN>
A:Cross-references: UNIPARC:UPI0000172899

A>Note: part of this sequence was confirmed by protein sequencing
C:Comment: This protein is not glycosylated.
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-
C:Keywords: acetylated amino end; alternative splicing; cAMP binding; cGMP binding; homoc
F:635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNBP>
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 21.6%; Score 909; DB 1; Length 921;
Best Local Similarity 31.1%; Pred. No. 1.3e-59;
Matches 254; Conservative 142; Mismatches 306; Indels 114; Gaps 27;

Qy 16 TFCPLSPSLTDE--KYKAVLSIHPQLDFVSEVSAAETVEK-----LKRKTNKADEPS 69
Db 122 TQVAVIPLVDKAGAAVAVILVHCGQLSD--NEMSLQAVEGHTVALKRVQALQORESS 179
Qy 70 -----PKESVRYODTNMGQVYELNSYTEQRLDTGSDNHL-----LYELSS---- 111
Db 180 VAPKATQNPPEBAADQ-----KGVAVY-----TNQDKRIQLCGELYDLDASSLQ 225
Qy 112 -----IIRATKADGPAALYFLGECNNSL--CVPIPMKREGGPRLLPAGPIQTGTTISAVY 165
Db 226 LKVLQYLQDETQASRCCLLVSEDMQLSCKVIQDKVLEESISF-----PLTTGRL--GVY 279
Qy 166 AKSRKTLVVEDIIGDERFPRGTGLS--GTRIQSYVLCPIYV-AIGDLIGILELYRMWK 222
Db 280 VEDKKSIGLQDLTSRDM-----QQLQSMGCEVQAMLCVPIRATVDQVVALACAFNKG 335
Qy 223 EAFCLSHQEVATANLMAVSAIHQVQCRGLAKQTELN-----DPLDVSKTYFPDNIYAI 277
Db 336 DLFTQDDEHVIOHCFFHYTSTVLST-----LAFQKQKLCCECOALLQVAKULFTHLIDV 390
Qy 278 DSLIHIMTYAKLVNADRCALFOVDHKKELXSLDFDGEKEKPIFKTKKEIRFSIE 337
Db 391 SVLDEITTEANLSNAELCSVFLD--QNELVAKVPD-----GAVDESEIIRHPAD 442
Qy 338 KGIAGQVARTGEVNLIPDAYADPRFNRKYDLYGTYTRNIIICMPTYSRS--SVIYQVMYN 396
Db 443 QGIAGVARTTQGLINIPDAYAHPFLRYGVGDBDGTGRTNIIICFPIKNEQVYIGVAVELN 502
Qy 397 KISGAFSKTDENNPFMAVFCALALHCANMYHRIHSECIYRVTEKLSYHSICTSEW 456
Db 503 KINGPWFSKFEDDLATAFSIGISIAHSLYKVAEQYRSHLANEMMYHMKVSDDEY 562
Qy 457 QGLMRPNLPARICRDIELFHPDIP-----FENMFGIVVMYIHRSCGS 501
Db 563 TKLMDHGIDPVAAIISNFASFYTPRSRPEDDTSMALISMLDMM--NFINNKKIDCPT- 618
Qy 502 CRELEKLCRFIMSVYKKNRVVPYNNMGAVTVAMCMYAILQNN--NNGLFITDLERKGLIA 559
Db 619 -----LAPFCILNVKKGYPDPYNNMMAFVSHPFCILYKULELTNYLEDNEIFALFIS 672
Qy 560 CLCHDLDRGFSNSYLQKFDHPFLAALYST--STMEQHFSQTVSIILQEGHNIFFSTLSS 617
Db 673 CMCHDLDRHGTNNSPGVASKSVLAALYSSEGSMEHHRHAQALAIINTGNCNIFDHSRK 732
Qy 618 EYEQVLEIIRKAIATDLALYFGNRKQLEBMYQTGSLNLHNSHRDVIGLMTADLCS 677
Db 733 DYQRMIDLRDRIILATDLAHNLRIFFDLOKMAEVG--YDRTNQSHSLCLMLTSCDLSLD 791
Qy 678 VTKLMPVTULTANDIYAEFMAEGDEKKLGIDPIPMDBDKRDVPOQGLGFYNAVAIPC 737
Db 792 QTKGMFTTKIKIABLYKEFSQGDLEKANGNPRMMDKKA-YIRBLQISFMEHIMMPI 850
Qy 738 YTTLTQILPPTPEPLKACRDNLQMKV-----IRG 768
Db 851 YKLLQDLFPKAAELRYVAVSNREHWTKVSHKFTIRG 886

RESULT 5

JC2486
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat
N:Alternate names: cGMP-dependent phosphodiesterase
C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004

C/Accession: UC2486

C/Ryan, Q.; Paeklin, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein, Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994

A>Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.

A/Reference number: UC2486; MUID:95110334; PMID:7811274

A/Accession: JC2486

A/Molecule type: mRNA

A/Residues: 1-928 <YAN>

A/Cross-references: UNIPROT:001062; UNIPARC:UP10000127BEC; GB:U21101; NID:9706929; PIDN: A/Experimental source: brain

A/Experimental source: brain

C/Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-C/Key words: alternative splicing; cAMP binding; cGMP binding; homodimer; phosphoprotein; P/643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homolog (cNPDp F109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #atatus predicted

Query Match 21.3%; Score 897; DB 1; Length 928;

Best Local Similarity 30.2%; Pred. No. 1,1e-58;

Matches 248; Conservative 152; Mismatches 292; Indels 130; Gaps 27;

16 TECTLSPSLTDE--KVKAYLSLHPQVLDEPVSSEVSAETVERK---LKR-----59

134 TQVAVLPFLDKETGTVAALVILVHCGQLSD--SEEQSLQVVEKHALVALQFVALQGRRE 191

60 -----KTKKADDESPKESRYQDTNMQ--GVWYELNS-----YIERDQTGGDNH 103

192 AVQNTSADPSBDQDEKGYTAHDKRIQLCGELYDLDTSLQLKVLARLQ--ETQATHC 249

104 LLLVELSSIIIRATKADGAFALYPLGECNNSLCVFIPGMEKGEQRLIPAGITQGTISA 163

250 CLLVSENNLQSLCKVIGEKV--LGE-----EVSFPLTMGRLL--G 285

164 VYAKSRKTLVEDILGDERFPRGTGLESSTRIQSVLCPIVT-AIGDLIGILELYRMHGK 222

286 QVEDKQCIQKDLITSDVDQQLQWNL--GCELRAMLGVPISRATDQVALACAFNKLGG 343

223 EAF-----CLSHQ--EVAATNLMASVAIHQVQVCRGLAQGTLENDPLDVSTYIF 271

344 DFFDEDEDERAIQHCCHYGYTGLTSLAFQK--DQKKECEQA-----LIQVAKNLF 392

272 DNIVAIIDSLBHMIVYAKNLVNAIDRCALFOVDHKKKELYSDFPIGEEKGKPIFKTKKE 331

393 THLDVSVLLDEBITREARNLSNAELCSYFLD--QNELVAVCFD-----GGVDDSEYE 444

332 IRFSIEKGIAGQVARTGEVLNIPDAYADPRNREVDLYGTNTNIIICMPIVSRG--SVIG 390

445 IRIPADQIAGHAVATTGQILNIPDAYAHPLFYRGVDDSTGTRTNIIICFPKINQENYIG 504

391 VVQWYNTKSSGAFSEKTDENNFRMAVFCALALHCANNMTHRIHSECIYRYMETLSTHST 450

505 VAEIVNKKNGPWFSPKFEDELATAFSIYGISIAHSLYKKNVBAQYRSHLANNEMMYHMK 564

451 CTSEMQQLMFPNIPARICRDIELFHPDIG-----PENMMPGIFVYMIH 495

565 VSDDEYTLGLHDGIQPVVAIDSNFANFTYTRSRSLPEDDTSAIIISMLQDM---NFINNYK 621

496 RSCGTSCPELEKLCRFIMSVKKNYRRVRYNMKKAIVTAHGMVAILQ--NNGHFTDLER 553

622 IDCPF-----LARFLCMVKKGYRDRPYHNMMAFVSFHCYLLYNKLELSNYLDEI 674

554 KGLLIACIChULDHRGSGNSYLQKFDHPLALYST--STMEQHNPSCQVTSILOEGHNIF 611

675 FALFISCHCHLDHRGTNNSPFVASKVTAALVSESGVVERHHPAQAIALNLNHCNIF 734

612 STLSSEVQVLEIRKAIITADLALYRGNKQLEBMYQTSLLMHNOSHDRYIGLMT 671

735 DHFSKQDQRMQLDRDIIILATDLNHHIRIKYDLQKAAEVC--YRRNNQHHRLILCLMT 793

672 ACDCISVYKLPVYKTLTANDIYAEFWAGDEMKLGIQIPIWMDRDKRDEVQCOLGFYN 731

794 SCDLSDQKMGKTKRIKLAELLYKEFFSGDGLKAMGNRPMEMDRKKA--YIPELQISFME 852

732 AVAIPCYTTLTQILPTEPRLKACRDLNINQEKV-----IRG 768

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Db      853 HITAPITVLTLDLPFKRAALYERVA$NREHMKVSHKFTIRG 894
|||||
RESULT 6
S30762
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004
C:Accession: S30762; S13031; S13121
R:Baehr, W.
submitted to the EMBL Data Library, June 1991
A:Reference number: S30762
A:Accession: S30762
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-856 <BA2>
A:Cross-references: UNIPROT:P23440; UNIPARC:UPI00000405A; EMBL:X60133; NID:953595; PIDN:
P23440
PDBS Letc. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha-
chain of the beta-subunit gene.
A:Reference number: S13030; MUID:91130581; PMID:1847109
A:Accession: S13031
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-559, 'G', 561-856 <BA2>
A:Cross-references: UNIPARC:UPI00001759BC; EMBL:X60133
R:Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.
Nature 347, 677-680, 1990
A:Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subunit c
A:Reference number: S13121; MUID:91015387; PMID:1977087
A:Accession: S13121
A:Molecule type: mRNA
A:Residues: 1-2, 'X', '4', 'G', '6-18, 'S', '20-48, 'DV', '51-157, 'T', '159-175, 'C', '177-231, 'R', '233-235,
A:Cross-references: UNIPARC:UPI0000161CP2; EMBL:X55968; NID:953616; PIDN:CAA39439.1; PID:
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match      16.5%; Score 693.5; DB 2; Length 856;
Best Local Similarity 25.3%; Pred. No. 1.7e-43;
Matches 226; Conservative 165; Mismatches 332; Indels 169; Gaps 31;

Cy      23 SLTDEKVAAYL$HPOVLDEPFVSESVSAETV-----EKWLK-----RKTNKAKDEP$PKR 72
|||||
2 SLSE$QV$AFDGN$TP$H$QYFGK$LSPEN$VAGAC$DGLAD$G$RLCQV$ESAL$FE 61
Db      73 V-SRYQDTNNOGVVYELNSYIEORLDT---GQDNHLLY-ELSSITIRITKAD$P$LY- 125
|||
62 LVQDQ$E$VNMERVY$FK-----ILRLCTILHADRC$LFMYRQ$NG$AEILATRL--F$VQ$P 115
Cy      126 --FLGE$CN$SLCV$F$P$MK$E$Q$P$RL$P$AG$IT$G$TT$A$Y$V$K$RTLL$V$ED$IL$G$D$E$F 183
|||||
116 D$LE$D$C-----LV$P$D$E$-----IV$P$LD$IG--IV$G$H$A$Q$TK$M$IV$Q$V$A$E$CP$H$F 160
Db      184 PRGT$E$SGTR$IQ$SVL$CL$P$TV$A$IG$DL$IG$LE$LYR$M$K$E$A$F$CL$SHOE$V$AT$M$A$V$S- 242
|||||
161 SSF$D$EL$D$VY$TK$NL$SP$IR$M$NG-KD$V$AV$M$A$V$N$LD$E$C$F$S$B$D$E$V$TK$YL$F$AT$LN 219
Cy      243 -----AI$H$O$V$C$R$GL$AK$Q$T$E$LD$F$LD$V$K$TY$F$D$NI$V$A$D$SL$E$H$M$IT$V$K$N$LV$N$AD 295
|||||
220 LKIYH$LY$H$NC$ET$R$G-----Q$V$L$M$S$N$K$Y$E$E$B$LD$IER$Q$H$K$A$FY$TV$R$A$Y$N$C$E 271
Cy      296 R$A$L$P$Q$V$D$H$K$K$E$L$Y$S$D$L$E$D$I-----G$E$K$-----E$G$K$I--F$K$T-----K$E$R$--- 333
Db      272 RYSV$GL$D$MT$K$E$K$E$F$V$W$P$V$M$E$Q$P$Y$S$G$P$RT$P$G$R$E$IV$E$Y$K$IV$D$Y$IL$H$K$E$D$IK$V$IP 331
Cy      334 -----F$S$E$K$G$IQ$A$Q$V$A$R$T$E$V$L$NI$P$D$A$Y$A$D$P$R$F--R$E$V$D$L--Y$T$G$Y$T$T$N$IL$C$M$P$V$S- 384
|||||
332 TRPAD$H$M$A$G$L$P$TY$V$A$E$S$G$F$IC$NIM$A$S$A$B$E$M$F$P$Q$G$P$LD$D$S$C$W$IV$IK$N$V$S$M$P$IV$N$K 391

```


A>Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBI:109784)
 R.Khrasov, N.V.; Fechenko, E.A.; Snelova, V.A.; Shmukler, B.E.; Terpigov, B.E.; Raki
 FEBS Lett. 327, 275-278, 1993
 A>Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu
 A:Reference number: 834590; MUID:93351644; PMID:8394243
 A:Accession: 834590
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-854 <NR>
 A:Cross-references: UNIPARC:UPI000012731; EMBL:X66142; NID:g336492; PION:CAA6932.1; PI
 R.Weber, B.; Rees, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowdel, D.; Andrew, S.; Sc
 Nucleic Acids Res. 19, 6263-6268, 1991
 A>Title: Genomic organization and complete sequence of the human gene encoding the beta-
 A:Reference number: S18715; MUID:92066478; PMID:1720239
 A:Accession: S18715
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-314, 'Q', 316-319, 'L', 321-359, 'R', 361-697, 'I', 699-854 <WEB>
 A:Cross-references: UNIPARC:UPI000016A6BE; EMBL:X62694
 A:Genetics:
 A:Gene: GDB:PDEB, PDEB
 A:Cross-references: GDB:125915; OMIM:180072
 A:Map position: 4p16.3-4p16.3
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
 C:Keywords: cGMP binding; phosphoric diester hydrolase
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
 Query Match 16.4%; Score 689.5; DB 2; Length 854;
 Best Local Similarity 24.7%; Pred. No. 3,3e-43;
 Matches 219; Conservative 165; Mismatches 343; Indels 159; Gaps 28;
 23 SLTDEKVAAYLSLHPOVDFEVSASAEVY-----EKMILKRTNKAQD-----EPSPKEVS 74
 2 SLSEQASFLDQNDPFAQYFGKSLSPENVRGCGDCCPPDCSIRDCQVEESTALIE 61
 75 RYQD-----TNMGVYELNSYIEORLDTGDNHLLYLELSIIRATKADGFALY---FL 127
 62 LVQDMQESINERVVFKYLRCLTLLQDRCLFMYRQNGVLAELATRL--PSVQPDSTL 119
 128 GECNNSLCVFPPEKMEGQRLIPAGPITQGTITSAVYAKSKRTLLVEDILDERPFGT 187
 120 EDC-----LVPEPDE-----IVFPLDIG--VVGHVQTKMNVVEDVACPHSSPA 164
 188 GLESTRIQSVLCPIYTAIGDLIGILEYRHMKEAFCLSHQEVATAMLAASV----- 242
 165 DELTYKTKNMLATPTIMG-KQVAVIYAVANKLNGEPFESBEDVFLKTLNFAITLKY 223
 243 ---AIHQVQVCGRLAKQTELDNPLDVSRTYFDNIYALDSLEHIMITYAKNLVNDRCAL 299
 224 HLYSLHNCETRG-----QVLLMSANKVPEBELDIERQPHKAFYTVRAVLNCEYASV 275
 300 FOVDHKNELYSDDLFDI--GEER-----EGKPI-FKKT-----KEIR----- 333
 276 GLLDWTKEKEFPDVSVMGSEQPYSGPRTPDGRBIVFYKVIDYILHGKEIKVLPESA 335
 334 --FSLEKGIAGVATGEVLNTPDAVADBRFNRVDLY--TGVTNNILCMPIVS-RGSV 388
 336 DHWALASGIPSYVASGFTCNTMNASADMEFKYQEGALDSDGLINVLNVSMPYVNGKEI 395
 389 IGVGVVVKISGSAASKTDENNFKMFAYECALALHCANNYHRIHSECIYRTMEKLSYH 448
 386 VGVAFYVRKQKQKPDDEQDEVLMESITQFLGWSVNMVTDVYDKNKLKNDKQADQMVLYH 455
 449 SICTSEEMQ-----GLMRNLPARICRDIELHF--DIGPE 483
 456 VACDDEIDILPTARLKEPADCEDDELGEILKEELGPTTFDIYEYHFDLCTEILD 515
 484 NMWPIPIYMIHRSCTSGFEL-----EKCRFTMSVKVYKVRVRYNNMGAAVY 533
 516 LVKCIQWY-----YELGVVRKFOIPOEVLVRFLEPISKGRIRIYNNMRGENV 565
 534 AHCMYAILQNN--NGLFTDLERKGLIACLDLHGRFSNSYLQKFDPLALAYSTSTM 591

DB 566 AQWTFLLMTGKLSYTYDLNAFNAVTAQLCHDIDHRGTNNLYOMKQNPPLAKHGSSIL 625
 592 EOHHSQVTSILQLEGHNIPTLSSESEYOELEIRKAIITDALYGNRKQLEEM--- 648
 626 EKHHEPCKFLSESTTLTYQNLNRQSHVYHMDIILATDLYIKKRAMPKQIKYDE 685
 649 ---YQTGS-----LNIHQSHRDVYGLMNTACDLSVTKMLPYTKLTANDIYAEFMAEG 700
 666 SKNYDDKXSWYEYLSLET-TRKEIYMAWMTACDLSAITKPEVQSKVALLVAEFMEQG 744
 701 D-EMKGLGIOTIPMDRDKRDEVPQGGVFNVAVAPCYTTLTQLPFPREPLKCRDL 759
 745 DLERTVLQOQPIPMWDRKKAELPPLQVGFDFVCTFPYKESRPHSEILPWFRLQNNR 804
 760 NQW-----EKVIRGETAMWISGPPAPSKST 786
 805 KEMKALADEYKAKVAKLEKEKEBERVAAKKVGTETLNGGPAPKST 850
 RESULT 9
 A47451
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A47451; S34290
 R:Suber, M.L.; Pittler, S.J.; Qin, N.; Wright, G.C.; Holcombe, V.; Lee, R.H.; Craft, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 3968-3972, 1993
 A>Title: Irish setter dogs affected with rod/cone dysplasia contain a nonsense mutation i
 A:Reference number: A47451; MUID:93248211; PMID:8387203
 A:Accession: A47451
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-856 <SUB>
 A:Cross-references: UNIPROT:P33726; UNIPARC:UPI00001728BD; GB:Z23014; NID:g312327
 A:Experimental source: Irish setter, retina
 A>Note: sequence inconsistent with the nucleotide translation
 R:Clements, P.J.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S34290
 A:Accession: S34290
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-184, 'D', 186-856 <CIB>
 A:Cross-references: UNIPARC:UPI000012730; EMBL:Z23014; NID:g312327; PION:CAA80557.1; PI
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
 C:Keywords: cGMP binding; phosphoric diester hydrolase
 F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
 Query Match 16.3%; Score 687.5; DB 1; Length 856;
 Best Local Similarity 25.2%; Pred. No. 4,7e-43;
 Matches 225; Conservative 151; Mismatches 346; Indels 171; Gaps 26;
 23 SLTDEKVAAYLSLHPOVDFEVSASAEVYKMLKRTNKAQDPSPEVSRYD---T 79
 2 SLSEQVQHPFLDQNDPFDQYFGKTLSEHVA-----GACGQGPOTDCAFSRELQY 53
 80 NMQGVYELNSYIEORLDTGDNHLLYLELSIIRATKADGFALYFLGECNNSLCVFP 139
 54 BESALPFLVODMOSVNMERVFYKILRLCTILR---ADRCSLFMYRQR----- 101
 140 PQMKEGQRLIPAGITQGTIS-----AYAKSKRTLLVEDILGD 180
 102 -GVAEIATRLRSVP--GSALEDCLVPPDESIYFPLDIGVGHVAAQTKMNVNDVYEC 157
 181 BRFPRTGLESTRIQSVLCPIYTAIGDLIGILEYRHMG-----KEAFLSHQEVAT 234
 158 PHFSPADELGYERNILATPTIMGKEVAVVIMANKLDGCFESBEDVFLKTLNFGT 217
 225 ANLAASVA-IHQVQVCGRLAKQTELDNPLDVSRTYFDNIYALDSLEHIMITYAKNLVN 293
 218 IMLKYHLSYLHNCETRG-----QVLLMSANKVPEBELDIERQPHKAFYTVRAVLN 269

QY 294 ADRCALFOVDHKKKELYSDLFDI-----GEF-----KEGKI 325
|||:::|||||:
Db 270 CDRTSGELDMTEKEKFEDVWPVLMEGAOPYSGRTPDGRIVFYKYIDYLHGKDITK 329
|||:::|||||:
QY 326 FKTKETIRPSIEKGINGQVARTGEVLNI PDAVPAPRFN-REVDL-YTGYYTRNIIICMPIV 383
|||:::|||||:
Db 330 ITPSPADHWALASGLPTLYVAESGFICINIMTADEMFTFGCGPILDDSGWVKNYLSMFI V 389
|||:::|||||:
QY 384 S-RGSYIGVVQVNWKISGSAFSKTDENNFKMAFAVCALALAHCAANNRIIRHSECIYRVTM 442
|||:::|||||:
Db 390 NKKEEIVGATVFYNRKDGKCFDEDEVLMESTQLFGWSVINTDTDYDKNKLENKDOI AQ 449
|||:::|||||:
QY 443 EKLYSTHSICTSEWQGLM---RNLPARICRODI ELHFPHDIGPEENMGPG---IFVYMIH 495
|||:::|||||:
Db 450 DMVLHYVRCDKDEIQLLPTPRERLGKPADCEDELGITL---LKEVLPDSKEDIYE FH 505
|||:::|||||:
QY 496 RS-----CGTSC-FEL-----EKLCREFMSVKKNRYRPYANMHGAVTV 533
|||:::|||||:
Db 506 FSDLECTELELVKCGIMTYELGVYRKQIPQEVLYRFLPSVSKGYRIITTHNMWHGNV 565
|||:::|||||:
QY 534 AHCMYAAILQNN--NGLFPTDERKGLLIACLCHDDLHRGFSNSYLOKHPIPLAALYSTSTM 591
|||:::|||||:
Db 566 AQMFFILLTTGKLKSYTDLAEAFAMVTAGLCHDIDHRGTNNLYQCKSONPLAKLHGSSITL 625
|||:::|||||:
QY 592 EOHHPQSOTYSILOEGHNITSTSSSEBYOULLEIKRAIITNDLALYGNKRQOLEEMQT 651
|||:::|||||:
Db 626 ERHHEFGFKLLSETLTINIYONLNRRQEHYIHMDIAIITDIALYFKCKTMFEKTIYD- 684
|||:::|||||:
QY 652 GSANIINHOSHRDR-----VTGLMTACDLCSVTXLMPTXYTLTANDIYAE 695
|||:::|||||:
Db 685 -----BSKNVEDRSKWVEYISLETTRKEIYVAAAMMTACDLSAITPFWEVSQSVALLVAAE 739
|||:::|||||:
QY 696 FNAEGD-EMKKGIQIPIPMMDRDNRDEVPQOGUFGYNAVAI PCYTTLT---QILPTEP 750
|||:::|||||:
Db 740 FMWGQDLERTVLDQQPIPMMDRNKAABL PKUGVGTIDFCVTYKEFSFHBEILLPMFDR 799
|||:::|||||:
QY 751 L-----LKACRONLNOEKVIYRGEEBTFAMTMSGGPAPASKST 786
|||:::|||||:
Db 800 LQNNRKEMKALADEYEAKLKBEEKOOOEHTTAKAGTEICNGPAPAKSST 852
|||:::|||||:

RESULT 10

A36617

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine

N:Alternate names: cGMP phosphodiesterase beta chain

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004

R:Lipkin, V.M.; Khrantsov, N.V.; Vasilevskaaya, T.A.; Atabekova, N.V.; Muradov, K.G.; Gub J. Biol. Chem. 265, 12955-12959, 1990

J>Title: Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase. Comparison with A:Reference number: A36617; MUID:90330632; PMID:2165490

A:Accession: A36617

A:Molecule type: mRNA

A:Residues: 1-853 <LRP>

A:Cross-references: UNIPROT:P23439; UNIPARC:UPI0000127C2F; GB:J05553; NID:g162824; PIDN:A:Experimental source: retina

A>Note: 40-Arg was also found

R:Lipkin, V.

submitted to the EMBL Data Library, December 1990

A:Reference number: SI9145

A:Accession: SI9145

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-853 <LRP>

A:Cross-references: UNIPARC:UPI0000127C2F, EMBL:X57146; NID:g209; PIDN:CAA40436.1; PID:SI9145

R:Lipkin, V.M.; Gubanov, V.V.; Khrantsov, N.V.; Vasilevskaaya, T.A.; Atabekova, N.V.; Mur Biorg. Khim. 16, 118-120, 1990

A>Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the beta A:Reference number: SI4011; MUID:90267525; PMID:2161230

A:Accession: SI4011

A:Molecule type: mRNA

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2,'P',4-90,'P',92-93,'H',95-202,'VN',205-469,491-853 <LI2>
A:Cross-references: UNIPAC:UPI000017598A; EMBL:X57146
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.; N
PDBS Lett. 223, 169-173, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha
A:Reference number: S00161; MUID:88030033; PMID:2822478
A:Accession: S00251
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 534-536,'R'536,'Y',598-601,'W',603-606,'QLT' <OV>
A:Cross-references: UNIPAC:UPI000017598B
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide ph
C:Keywords: acetylated amino end; blocked amino end; cGMP; cGMP binding; phosphoric diest
E/2-853/Product: 3',5'-cyclic-GMP phosphodiesterase beta chain status predicted <MAT>
F/556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>
F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 16.3%; Score 684; DB 2; Length 853;
Best Local Similarity 24.5%; Pred. No. 8.5e-43;
Matches 218; Conservative 152; Mismatches 354; Indels 164; Gaps 25;

Qy	23	SLTDEKVAKYLSPHVLDEFVSSEVSAETVEKMKLRKTKAKADEBPSPKVRSD---	T	79
Db	2	SLSEGVHFLDQNPFGADQYFGKRLSPEDVA-----NACDGECEGTSFRELQV	53	
Qy	80	NMQGVVVELSYIEGLDITGSDNHLLEYDSIIRATKADGFLYFAGECNISLVEIP	139	
Db	54	EESSALFELVQDMQENVMNERVVFKILRLCSLIH---ADRCGLFMYRQSN-----	101	
Qy	140	PGMKEGQPLIPAGP-----ITGGTTISAVVAKSRKTLVEVDLIGDERF	183	
Db	102	-GVAEIATLFLSQPQSVLEDCVPPDSEIVFLPIDIGVGHVAGTKKQVNVQVMECPHF	160	
Qy	184	PRGTGSESTRQSIVCLPIVTAIGDLIGILEYRHHGKAFCLSHQEV-----ATAN	236	
Db	161	SEFPADELTYVTNTIATPIIMG-KDVAAVIMAVNKLDGCFSTSEDEVEFLKYLNFGLTN	219	
Qy	237	LMAASYA-IHQVQVCGLAKQTELDNFDLVSKYFNINIVADSLLEHIMITYAKNLVAD	295	
Db	220	LKTYHLSYLNCESTRK-----QVLLMSANKVFEELDIEHQFHAFYTVRAVLMCD	271	
Qy	296	RCALPQVDHKKELYSDFDI-----GEE-----KEGKPIFK	327	
Db	272	RYSVGGLDMTKKEKFPDVMFLMGEAQAYSGPRTPDREILFYKVIDYILHGKEIDIKYIP	331	
Qy	328	KTKETLPSIEKGIAGQVARTGEVLINIPDAYADPPN-REVDL-YTGTYTNILCMPIVS-	384	
Db	332	SPPADHMAALSGLPYVAESGFLCINMAPDENFENQEGPLDSGWLIVKLVNLPYVAK	391	
Qy	385	RGSVIGVGVNKLISGSAFSTDENNFKMFAPCALALHCANMYRIHSHSECIYVTEK	444	
Db	392	KEEIVAGVATYNNKDGKRFDBODEVLMESLQFLQMSVLTNDITYDKMKLENRKIDAQDM	451	
Qy	445	LSYHSICTSEWQGLM---RFLNPARICRDIELFHFDIGEPENKMPG---IFVYMIHRS	497	
Db	452	VLVHVRCDREIEIQLILPTREILKEPADCEDEDELGLI---LKEVLPQAKPDIYEFHRS	507	
Qy	498	-----CGNSC-FEL-----EKLGRFMSYKKNRVRVPVHNKHAIVTVAH	535	
Db	508	DLECTEELVKKCGIOMYELFGVVRKFOIPQVLRVLFELSVSGKRYRIITYHNRRHGNVQ	567	
Qy	536	CMVAIIQNN--NGLFDTLERKGLLIACIChDLDRGFSNSYLOKFDHPLAALYSTTMEQ	593	
Db	568	TMFLTLMTGKLKSYTDLDEAFAMTYAGICHIDIRHGTNNLVQMSQONPLAKHGSSILRR	627	
Qy	594	HHFSQVTSIIQLEGHNIPTSLSSSEYBOVLEIRKAIATDIALYFGNRKOLEMYQTQS	653	
Db	628	HHLEFGKFLSEETLIYONINRRQHEHVIHIMDAIATDIALYFKKRTMFQKIVD---	684	
Qy	654	LNLHNSGHRB-----VIGLMMTCADICSVTKLMPVTGLTANDIYAEFF	697	
Db	685	---BSKNYEDKSNVEYISETTKETKELVMAAMMTKCDLSATIKPEVQSKVALLVAEEFW	741	

[illegible][illegible]

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QY 345 ARTGEVLINIPDAYADPRENR---VDLYTGTTNNILCPPIYS-RGSVIGVQMNKISG 400
DB 348 AENGETICMNLNAPADEYFTQKGPVD-ETGWYIKVLSLPVINKEDIDYGAFTYNRKQG 406
QY 401 SASFSTIDENPFQMFVFCALALHCAVMYRIHSHSECIYAVTMEKLSYHSICSEMOGLM 460
DB 407 KPFDYDEHIAETLTQFLGWSLNTDTYKMNKLENRKDIQOBMLNHTKATPDEIKSL 466
QY 461 RF-----NLPARICDIELFHFDIGPEENMMPGIPVYMIHR- 496
DB 467 KKEKLNIDVIDEDCEKQVLTLLKEDLPDPRADLYEPRFRHLPIE-----HEL 516
QY 497 -SCGTSCF-----ELEKLCRFINSVKKNYRRVYPYHMKGAATVAHGMVAILQNN 544
DB 517 ICGRLRLEFELINVEKFKVPEVLTFRMNTYRKGYAATYHNRHGFNGQTMFTLLMTG 576
QY 545 --NGLPTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTMEOHHSQTVAI 602
DB 577 RLKRYTDLERAPAMLAARFCHDIDHGTNNLYQMKSTSPLARLHSGSILRHHLEYSKTL 636
QY 603 LQEGHNIPSTLSSEYEQVLEIRKAIITDIALYFGNRKQLEEM----- 648
DB 637 LDDESANITQNLNKRQYEVYIHLFEVAIITATDIALYFKKRTMPQKIVDACENKETEELAI 696
QY 649 -YQTSGLNHNQSHRDVYIGLMTACDLSVTKLMPYTKLTANDIYAEFWABGD-EMKKL 706
DB 697 KRYT-----IDPKEEIIIMAMMTACDLSAITKPEVQSQVALLVANEFEQDLERTYVL 751
QY 707 GIQPIPMNRDRKDEVPQOGLGFYNAVALPCYTTLTQILPTEPLKACRDLNOME--- 763
DB 752 QOQPIPMNRKNDDELPKLOVGFIDFVCTFVYKESFRFHEKITPMLNGLQNNVEMKSLA 811
QY 764 -----KYI-----RGEETAMMISGPGAPSPKS 785
DB 812 DEYDEKMKVIEEMKQEBEGTTTBAVBDGGGDDDKS 849

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RESULT 13

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - mouse
 S13030
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S13030
 R/Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
 FBS Lett. 278, 107-114, 1991
 A/Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha chain of the beta-subunit gene.
 A/Reference number: S13030; MUID:91130581; PMID:1847109
 A/Accession: S13030
 A/Molecule type: DNA
 A/Residues: 1-859 <BAE>
 A/Cross-references: UNIPROT:P27664; UNIPARC:UPI000016CF96; EMBL:X60664; NID:953587; PIDN A/Cross-family: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P C/Keywords: GMP binding; phosphoric diester hydrolase
 F/558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

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Query Match 16.0% Score 674.5; DB 2; Length 859;
Best Local Similarity 25.1%; Pred. No. 4.4e-42;
Matches 211; Conservative 140; Mismatches 351; Indels 139; Gaps 19;

QY 48 VSAETVEKMLKRYTNKAD-----EPSPKEVSRYQDTNM---QGVVYE 87
DB 4 VTAEBVEKFLDSNIGFAKQYNNLHYRGKVISDLLGAKEAAVDSNHYDVNSVESSEIIFD 63
QY 88 LNSYIEQRDLTDGGNHLILYELSIITATKADGAPALYFGECCNSLCVPIIPGMKEGP 147
DB 64 LRLDVQENLQAEKCTFYVMKKLCEPLN---ADRVSLFMYRTN-----GIAELAT 110
QY 148 RL-----IPAG-----PIQGTTISAVYAKSRKTLVLVEDLIDDERFPRTGL 189
DB 111 RLRYVHMDAVLBDCLVNPDSIYVPLDMS--VGHVHASKKIANVPRTBEDDEHCDPVVN 168
QY 190 ESGRIQSVLCLPIVTAIGDLIGLILRYRMGKEAFCLSHQEVATNLANMASVA----- 243

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DB 169 LREYTKNIIASPIWNG-KDVVAITMAVKNKIDEBHFTKRDEIILKYLVNFVLIMKVFHL 227
QY 244 --HQVQCRGLAQKTEINDFLLDVSKTYFDNIYVAIDSLLEIMYAKNLVNADECALFQ 301
DB 228 SYLHNCETRRG-----QILLMSGSKYFELTDIEROFHAKLYTVAFLNCDHYSVGL 279
QY 302 VDHKKELXSLDFDI-----GEE-----KSGKPIFKTKKIR 333
DB 280 LDMTKQKFEFDVPMKGEAPAYSGPRTPDGKREINPYKVIDYILGKEDIKVIENPRADH 339
QY 334 FSEIKGIAGVARTGEVNLINIPDAYADP--RFRREVDLYTGTTNNILCPPIYS-RGSVIG 390
DB 340 WALVGLDEPPYVAQNLICINMAPADPFEPQKEPLDSSGMHMKVLSPIYTKKKEIYG 399
QY 391 VVQVWNKISGSAFSTIDENPFQMFVFCALALHCAVMYRIHSHSECIYAVTMEKLSYHSI 450
DB 400 VATFYNRKDGKFPDDMDDELMTESLTQFLGWSVLANPDYTESMNKLENRKDIPODIVCYHYK 459
QY 451 CTSEMOGLMR-----NLPARICDIELFHFDIGP---FENM 485
DB 460 CDBEIOKILKTRREYVYKKEPMECEEBELAILQRELPDAESYEINKFHSDDLPLELELV 519
QY 486 WPGIPVYMIHRSCGTSCFELKLCRFINSVKKNYRRVYPYHMKGAATVAHGMVAILQNN- 544
DB 520 KCGIQMTYELRWDXDHPHIEQALYVFMYSLSKGYRITTHMNRHGFNGQTMFSLVYTK 579
QY 545 -NGLPTDLERKGLIACLDHLDHGFNSYLOKEDHPLAALYSTMEOHHSQTVAI 603
DB 580 LKRYFTDLERALAMVTAARFCHDIDHGTNNLYQMKSQNPILAKLHSGSILRHHLEFQKTL 639
QY 604 QLEGNHIFSTLSSEYEQVLEIRKAIITDIALYFGNR-----KQLEEMVQTS 653
DB 640 RDESLNIFQNLNRROHEHAIHMDIAIITDIALYFKKRTMPQKIVDQSKTYESTQEWQ 699
QY 654 LNLHNQSHRDVYIGLMTACDLSVTKLMPYTKLTANDIYAEFWABGD-EMKKLGIQPI 712
DB 700 YMLEQTRKEIYVAMMTACDLSAITKPEVQSKVALLVAAEFWEGDLERTVLOQNP 759
QY 713 MMDRDRKDEVPQOGLGFYNAVALPCYTTLTQILPTEPLKACRDLNOMEKYIRGEET 772
DB 760 MMDRNRKADLPLKLOVGFIDFVCTFVYKESFRFHEKITPMLDGTNNRKEMKALADEYAK 819
QY 773 M 773
DB 820 M 820

```

RESULT 14

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
 S06418
 N/Alternate names: cGMP phosphodiesterase alpha chain
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C/Accession: S06418; S27007; S00161; A34611; S08516
 R/Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zak Doki. Biochem. 296, 303-307, 1987
 A/Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpi
 A/Reference number: S06418
 A/Accession: S27007
 A/Molecule type: protein
 A/Residues: 211; 22-27; 32-40; 95-98; 112-115; 180-193; 248-267; 275-282; 297-306; 312-330; 361-371; 645; 654-661; 663-667; 703-712; 734-736; 751-760; 766-771; 787-798; 811-819 <OVC>
 A/Cross-references: UNIPARC:UPI00001728A8; UNIPARC:UPI00001728A9; UNIPARC:UPI00001728AA; 8AF; UNIPARC:UPI00001728B0; UNIPARC:UPI00001728B1; UNIPARC:UPI00001728B2; UNIPARC:UPI0000 100001728B3; UNIPARC:UPI00001728B4; UNIPARC:UPI00001728B5; UNIPARC:UPI00001728B6; UNIPARC A/Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S R/Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.;

FEBS Lett. 223, 169-173, 1987
 A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alpha
 A:Reference number: S00161; MUID:88030033; PMID:2822478
 A:Accession: S00161
 A:Molecule type: mRNA
 A:Residues: 1-859 <CNP>
 A:Cross-references: UNIPARC:UPI000016C2D7; EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PI
 A:Note: part of this sequence was confirmed by protein sequencing
 A:Note: 381-Val was also found
 R:Pittler, S.U.; Behr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTunen,
 Genomics 6, 272-283, 1990
 A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
 A:Reference number: A34611; MUID:90169986; PMID:2155175
 A:Accession: A34611
 A:Molecule type: mRNA
 A:Residues: 1-193, 'V', 195-423, 'T', 425-674, 'F', 676-859 <PIT>
 A:Cross-references: UNIPARC:UPI000016C2D8; GB:M26043; NID:g162833; PIDN:AAA30443.1; PID
 A:Comment: This protein is involved in the transduction and amplification of the visual
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
 C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolyase; ret
 F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <NP
 F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
 F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match 15.8%; Score 666.5; DB 1; Length 859;
 Best Local Similarity 25.0%; Pred. No. 1,8e-41;
 Matches 210; Conservative 144; Mismatches 348; Indels 139; Gaps 20;

48 VSATVEKMLKRTKTKAK-----DESPKREV---SRVQDTNM---QGVYVE 87
 4 VTAEVEKFLDSNVSPFAQYVNLRYRAKVISDLLPREAAVDFSNVHALNSVESEILFD 63
 88 LNSVTEQRLDTGDNHLLLYELSSIIIRATKADGFALYLGECNNSLCTFIPRKGEGP 147
 64 LTRDFQDNLQA---EKCVFNVKKLCLLLQADRMSLFMYTRRN-----GIAELAT 110
 148 RLIPAG-----PITQGTTSAAVYAKSKRTLLVEDILGDERFRGTGL 189
 111 RLFNHKAVALBECVAPOSEIVFPDLMG--VGVHVALSKITLVNVPNTREDEHFCDFVDT 168
 190 ESGTRIGSVLCPIVTAIGDLIGILEYHMKGEAFCLSHQEAATANLMA5A----- 243
 169 LTBVQTKNIIASFPMNG-KDVVAIIMAVNVKVDGPHTEDEBEILLKYLFANLIMKVFHL 227
 244 --IHQVQVCRGLAKTGLNDPLLDVSKTYFDNIVAIDSLLEHIMITYAKLVNADRCALFQ 301
 228 SYLHNCESTRRG-----QILLMSGKVFEELTDIERQFHAKLYTVRAFLNCDRSVGL 279
 302 VDHKKKELYSDFDI-----GEE-----KEGKPIFKTKKEIR 333
 280 LDMTKQKFRFVWVPLMGEAPRYAPRTPDGRINPYKVIDYILHGKEDIKYIPNRPDH 339
 334 PSIEKGIAGQVARTGEVLTNPDAVDP--RFNREVDTLYGTTNNILCMPYVS-RGSVIG 390
 340 WALVAGLPTVVAQNGLICINMNAPESEDFAPQKEPLDESGMMIKVNLSPMIVNKEEILYG 399
 331 VVQVMNKSIGSAFSKTDENNFKMPFAVFCALALHCAANNYRIHSECIYVNMEXLSYHSI 450
 400 VATFNRRDKGKFPDEMDETLMESLAQFLGMSVLANPDTYELMKNLEKRDIFODMKYHNK 459
 451 CTSEEMOGIMRF-----NLPARICRDIELFHPDIP---FENN 485
 460 CDNEIQTITLKTRVYVGKPEWCEBELAEILQGBLPADKYEINKFHSDDPLREBELV 519
 520 KCGIOMYTELVKVDKPHI PQEALVRFMYSLSKGYRRIITGNHNRHGFNVQGTFFSLLVGK 579
 486 WPIGFVYMIHRSCTSCPELEKLCRFPIINSVKKNYRRVPYNNHKAATVAACHQVAILQNN- 544
 545 -NGLEFTDLERKLLALACLDHIDHGFNSYLOKQDHPPLAALYSTSMQHHPFSQVSL 603
 580 LKRYPTDEALAMVTAAPCHDIDHGTNNLYQMKSONPLAKLHGSSILERRHLEFGKTL 639
 604 QLEGNITSTLSSSEVEQVLEIRKAIITDIALVFGNRKQLEEM-----YQT-----GS 653

DB 640 RDESLNITQNLNRRQHEHAHMMMDIAITATDLATYCKKRTMFQKIVDQSKTYETGOEWTO 699
 QY 654 LNLNQHSDRDRVIGLMTATCLDCLSTKMPYTKLTANDIYAFNAEGD-ENKGGIGIOP 712
 DB 700 YMMLDQTKKEIYVAMMMTACDLISATTKPEWQSKVALLVAEPFEGQDLERTVLAQNP 759
 QY 723 MMDRDKRDEVQOGQGFNAVAIPCYTLTGQILPTEPELTKACRDNLQWEKVIHGEETA 772
 DB 760 MMDRKADELKLVQVGFIDFCTFYKKEFSRFBHEITFMLOGITNNRKEWKLADBEYETK 819
 QY 773 M 773
 DB 820 M 820

RESULT 15
 B34611
 3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - human
 C:Species: Homo sapiens (man)
 C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 21-Jan-2000
 C:Accession: B34611
 R:Pittler, S.U.; Behr, W.; Wasmuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTunen, I
 Genomics 6, 272-283, 1990
 A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodie
 A:Reference number: A34611; MUID:90169986; PMID:2155175
 A:Accession: B34611
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-859 <PIT>
 A:Cross-references: UNIPARC:UPI0001759B9; GB:M26061
 C:Genetics:
 A:Gene: GDB:PDE6A; PDEA
 A:Cross-references: GDB:120265; OMIM:180071
 A:Map position: 5q31.2-5q34
 C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
 C:Keywords: cGMP binding; phosphoric diester hydrolyase
 F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 15.8%; Score 663.5; DB 2; Length 859;
 Best Local Similarity 24.8%; Pred. No. 3e-41;
 Matches 208; Conservative 138; Mismatches 338; Indels 155; Gaps 21;

48 VSATVEKMLKRTKTKAKD-----BSPKREVSRVQDT 79
 4 VTAEVEKFLDSNVSPFAQYVNLRYRAKVISDLLGAKAAVDFSNVHSPSSMBSE- 59
 80 NMQGVYELNSYTEQLDTGDNHLLLYELSSIIIRATKADGFALYLGECNNSLCTFIP 139
 60 ----IIPDLRDFQENLQF---EKCIYNVKKLCLFLLQADRMSLFMYTRRN----- 103
 140 PQMKEGQRLIPAG-----PITQGTTSAAVYAKSKRTLLVEDILGDE 181
 104 -GIAELATRLFNHKAVALBECVAPOSEIVFPDLMG--IVGVHVALSKITLVNVPNTREDE 160
 182 RFPRTGLESRTIGSVLCPIVTAIGDLIGILEYR-----HMKG--EAFCLSHQEAAT 234
 161 HPCDVLDTKYTKNIIASFPMNG-KDVVAIIMAVNVKVDGSHFKRBEILTKLVN 219
 235 ANLMA5A-IVQVQVCRGLAKTGLNDPLLDVSKTYFDNIVAIDSLLEHIMITYAKLVN 293
 220 LIMKVYHLSYLNCESTRG-----QILLMSGKVFEELTDIERQFHAKLYTVRAFLN 271
 294 ADRCALPQVDHKNNELYSDFDI-----GEE-----KEGKPI 325
 272 CDRSVGLDMTKQKFRFVWVPLMGEAVPYSGPRTPDGRINPYKVIDYILHGKEDIKV 331
 326 FKTKKEIRFSIEKGIAGQVARTGEVLTNPDAVDP--RFNREVDTLYGTTNNILCMPYV 383
 332 IPNPPDHMAVLSGLPTVVAQNGLICINMNAPESEDFAPQKEPLDESGMMIKVNLSPMIV 391
 384 S-RGSVIGVQVMNKSIGSAFSKTDENNFKMPFAVFCALALHCAANNYRIHSECIYRVTM 442

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:49:20 ; Search time 79 Seconds
(without alignments)
7108.867 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206
Sequence: 1 MEDGSPNNASCFRRLTCEFL.....GPGAPSKSTPEKLNKVED 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4206	100.0	796	2 Q69C21_MOUSE	Q69C21 mus musculu
2	4123	98.0	794	2 Q9QYJ6_RAT	Q9QYJ6 rattus norv
3	4089.5	97.2	797	2 Q7TPG2_MOUSE	Q7TPG2 mus musculu
4	4080	97.0	773	2 Q7TPG1_MOUSE	Q7TPG1 mus musculu
5	4080	97.0	779	2 Q9WV11_MOUSE	Q9WV11 mus musculu
6	4072	96.8	790	2 Q8CA95_MOUSE	Q8CA95 mus musculu
7	4004	95.2	783	2 Q9ULM9_HUMAN	Q9ULM9 homo sapien
8	4003.5	95.2	883	2 Q6S9E8_RAT	Q6S9E8 rattus norv
9	3997	95.0	788	2 Q9QYJ5_RAT	Q9QYJ5 rattus norv
10	3997	95.0	852	2 Q6S9E9_RAT	Q6S9E9 rattus norv
11	3878	92.2	779	1 PDBI10_HUMAN	Q9Y213 homo sapien
12	3878	92.2	779	2 Q9NTV4_HUMAN	Q9NTV4 homo sapien
13	3872	92.1	779	2 Q6FHX1_HUMAN	Q6FHX1 homo sapien
14	3715	88.3	714	2 Q6S9E7_RAT	Q6S9E7 rattus norv
15	3639	86.5	714	2 Q9HCP9_HUMAN	Q9HCP9 homo sapien
16	3478.5	82.7	843	2 Q7ZW87_BRARE	Q7ZW87 brachydanio
17	3400	80.8	653	2 Q6S9E6_RAT	Q6S9E6 rattus norv
18	3313	78.8	754	2 Q4RQ45_TETNG	Q4RQ45 tetodon n
19	1033	24.6	1544	2 Q8MQM0_DROME	Q8MQM0 drosophila
20	1010	24.0	1365	2 Q9VJ79_DROME	Q9VJ79 drosophila
21	987.5	23.5	747	2 Q7Q8G2_ANOGA	Q7Q8G2 anopheles g
22	977	23.2	935	2 Q8VID6_RAT	Q8VID6 rattus norv
23	975	23.2	1018	2 Q9STM8_DROME	Q9STM8 drosophila
24	975	23.0	1131	2 Q9VFI9_DROME	Q9VFI9 drosophila
25	965.5	22.6	934	2 Q9HCR9_HUMAN	Q9HCR9 homo sapien
26	952	22.6	393	1 PDES_CAEEL	P91119 caenorhabdi
27	946	22.5	685	1 Q8VID7_RAT	Q8VID7 rattus norv
28	943.5	22.4	390	2 Q61CN3_CAEBR	Q61CN3 caenorhabdi
29	935	22.2	832	2 Q7QBP9_ANOCLA	Q7QBP9 anopheles g
30	933.5	22.2	859	2 Q5XHD0_XENILA	Q5XHD0 xenopus lae
31	929	22.1	684	2 Q9GZY7_HUMAN	Q9GZY7 homo sapien

32	924	22.0	833	1 PDE5A_RAT	O54735 rattus norv
33	918	21.8	865	1 PDE5A_BOVIN	Q28156 bos taurus
34	917	21.8	865	1 PDE5A_CANPA	Q77746 canis famli
35	913.5	21.7	865	1 PDE5A_MOUSE	Q8G903 mus musculu
36	912.5	21.7	875	1 PDE5A_HUMAN	Q76074 homo sapien
37	909	21.6	921	1 PDE2A_BOVIN	P14099 bos taurus
38	897	21.3	581	2 Q8VID8_RAT	Q8VID8 rattus norv
39	897	21.3	928	1 PDE2A_RAT	Q01062 rattus norv
40	894	21.3	916	1 PDE2A_MOUSE	Q92264 mus musculu
41	894	21.3	935	2 Q5PR72_MOUSE	Q5PR72 mus musculu
42	892.5	21.2	941	1 PDE2A_HUMAN	O00408 homo sapien
43	890.5	21.2	941	2 Q81W54_HUMAN	Q81W54 homo sapien
44	888.5	21.1	932	2 Q5J793_HUMAN	Q5J793 homo sapien
45	879.5	20.9	576	2 Q9HB46_HUMAN	Q9HB46 homo sapien

ALIGNMENTS

RESULT 1
Q69C21_MOUSE
ID Q69C21_MOUSE PRELIMINARY; PRT; 796 AA.

AC Q69C21;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Phosphodiesterase 10A.
GN Name=Pdel10a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;

OX
[1]
NP NUCLEOTIDE SEQUENCE.
RC STRAIN=B6CBA; TISSUE=Striatum of brain;
RX PubMed=14751289; DOI=10.1016/j.neuroscience.2003.11.009;
RA Hebb A.L., Robertson H.A., Denovan-Wright E.M.;
RT "Striatal phosphodiesterase mRNA and protein levels are reduced in
RT Huntington's disease transgenic mice prior to the onset of motor
RT symptoms.";
RT Neuroscience 123:967-981(2004).
RN [2]

STRAIN=B6CBA; TISSUE=Striatum of brain;
PubMed=15610167; DOI=10.1111/j.1460-9568.2004.03796.x;
RA Hu H., McGaw E.A., Hebb A.L., Gomez G.T., Denovan-Wright E.M.;
RT "Mutant huntingtin affects the rate of transcription of striatum-
RT specific isoforms of phosphodiesterase 10A.";
RT Eur. J. Neurosci. 20:3351-3363(2004).
RL EMBL: AY360383; AAR12579.1; -; mRNA.
DR CO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. .; IDA.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; Met_phos_hydro.
DR InterPro: IPR002073; PDase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDase_1; 1.
DR PRINTS: PR00387; PD1ESTERASE1.
DR SMART: SM00065; GAF; 2.
DR SMART: SM00471; HDC; 1.
DR PROSITE: PS00126; PDASE_1; 1.
SQ SEQUENCE 796 AA; 90338 MW; 4662D791B45E9EBA CRC64;

Query Match 100.0%; Score 4206; DB 2; Length 796;
Best local similarity 100.0%; Pred. No. 2, 1e-316;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRLTCEFLSTDEKVKAYISLHPQVLDERSVSVAETVETKYLKRR 60
DB 1 MEDGSPNNASCFRRLTCEFLSTDEKVKAYISLHPQVLDERSVSVAETVETKYLKRR 60
QY 61 TNKAKDESPKESRYQDTMKGWVEINSYIRQLDTGGDNHLLVYESSIRIATKAD 120

Dd	61	TNKADEBSPKEVSRDYDTNMOGVVYELNSYIEQRLDTGDNHLLLYELSSIIIRIATYAD	120
Qy	121	GFALYFLGECNNSLCVFPIPGMKEGQPLIPAGPIITOGTTISAVYAKSKRTLLVEDIIGD	180
Dd	121	GFALYFLGECNNSLCVFPIPGMKEGQPLIPAGPIITOGTTISAVYAKSKRTLLVEDIIGD	180
Qy	181	BRFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHQEVATANTLAWA	240
Dd	181	BRFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHQEVATANTLAWA	240
Qy	241	SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNIVAIDSLLEHIMITYAKNLVNAARCALF	300
Dd	241	SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNIVAIDSLLEHIMITYAKNLVNAARCALF	300
Qy	301	QVDHKNKELYSDFPIGEEKGKPIPKTKKEIRFSIBKGIAGVARTGVNLIPDAYADP	360
Dd	301	QVDHKNKELYSDFPIGEEKGKPIPKTKKEIRFSIBKGIAGVARTGVNLIPDAYADP	360
Qy	361	RPNREVDLYGTYYTTRNIIICMPIVSRGSYIGVQVWNKISGSAFSKTDENNPFQFAVFCAL	420
Dd	361	RPNREVDLYGTYYTTRNIIICMPIVSRGSYIGVQVWNKISGSAFSKTDENNPFQFAVFCAL	420
Qy	421	ALHCAWMYHRIHSECIYRVTEKLSYHSICTSEEWQGLMRPNLPARICRDIELFHPDIG	480
Dd	421	ALHCAWMYHRIHSECIYRVTEKLSYHSICTSEEWQGLMRPNLPARICRDIELFHPDIG	480
Qy	481	PPEMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQNYRVRPYHNMKHAIVAHCMYAI	540
Dd	481	PPEMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQNYRVRPYHNMKHAIVAHCMYAI	540
Qy	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV	600
Dd	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV	600
Qy	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV	600
Dd	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV	600
Qy	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS	660
Dd	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS	660
Qy	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS	660
Dd	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS	660
Qy	661	HRDVIIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD	720
Dd	661	HRDVIIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD	720
Qy	721	EVPOGOLGFYNAVAIPCYTTLTQILPTEPBLKACRDNLQWEKVIIRGEETAMWISGPG	780
Dd	721	EVPOGOLGFYNAVAIPCYTTLTQILPTEPBLKACRDNLQWEKVIIRGEETAMWISGPG	780
Qy	781	APSKSTPEKLVAKVED	796
Dd	781	APSKSTPEKLVAKVED	796

RESULT 2
Q9QYJ6_RAT PRELIMINARY; PRT; 794 AA.
AC Q9QYJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE PDE10A2 (EC 3.1.4.17).
GN Name=Pde10a; Synonyms=PDE10A;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Charchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
NCBI_taxid=10116;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=SD; TISSUE=Brain;
RX MEDLINE=20050627; PubMed=10583409;
RA Fujishige K., Kozera J., Omori K.,
RT "Striatal and testis-specific phosphodiesterase PDE10A: isolation and
RT characterization of a rat PDE10A".
PL Eur. J. Biochem. 266:1118-1127(1999).

DR	EMBL; AB027155; BAA68996.1; -; mRNA.	
DR	Ensembl; ENSRNOG0000011310; Rattus norvegicus.	
DR	RGD; 68434; Pde10a.	
DR	GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.	
DR	GO; GO:0016787; F:hydrolyase activity; IEA.	
DR	GO; GO:0007165; F:signal transduction; IEA.	
DR	InterPro; IPR003018; GAF.	
DR	InterPro; IPR003607; Met_phos_hydro.	
DR	InterPro; IPR02073; PDbase.	
DR	Pfam; PF01590; GAF; 2.	
DR	Pfam; PF00233; PDbase_1; 1.	
DR	PRINTS; PR00387; PD1ESTERASE1.	
DR	SMART; SM0065; GAF; 2.	
DR	SMART; SM00471; HDC; 1.	
DR	PROSITE; PS00126; PDASE_1; 1.	
DR	HydroLase. 794 AA; 90161 MW; A36C4678B385846E CRC64;	
DR	SEQUENCE	
Qy	Query Match	98.0%; Score 4123; DB 2; Length 794;
Dd	Best Local Similarity	98.4%; Pred. No. 5.6e-310;
Qy	Matches	783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
Qy	1	MEDPSSNASCRRLLTEGFLSPSLTDERVYKAYLSLHPQVLDPEFSVSATVEKWKRRK 60
Dd	1	MEDPSSNASCRRLLTEGFLSPSLTDERVYKAYLSLHPQVLDPEFSVSATVEKWKRRK 60
Qy	61	TNKADEBSPKEVSRDYDTNMOGVVYELNSYIEQRLDTGDNHLLLYELSSIIIRIATYAD 120
Dd	61	TNKADEBSPKEVSRDYDTNMOGVVYELNSYIEQRLDTGDNHLLLYELSSIIIRIATYAD 120
Qy	121	GFALYFLGECNNSLCVFPIPGMKEGQPLIPAGPIITOGTTISAVYAKSKRTLLVEDIIGD 180
Dd	121	GFALYFLGECNNSLCVFPIPGMKEGQPLIPAGPIITOGTTISAVYAKSKRTLLVEDIIGD 180
Qy	181	BRFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHQEVATANTLAWA 240
Dd	181	BRFRGTGLSEGTIRIQSVLCPIVTAIGDLIGILEYRMGKEARCLSHQEVATANTLAWA 240
Qy	241	SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNIVAIDSLLEHIMITYAKNLVNAARCALF 300
Dd	241	SVAIHQOVQCRGLAQOTELNDPLDVSKTYFPNIVAIDSLLEHIMITYAKNLVNAARCALF 300
Qy	301	QVDHKNKELYSDFPIGEEKGKPIPKTKKEIRFSIEKGIAGVARTGEVNLIPDAYADP 360
Dd	301	QVDHKNKELYSDFPIGEEKGKPIPKTKKEIRFSIEKGIAGVARTGEVNLIPDAYADP 360
Qy	361	RPNREVDLYGTYYTTRNIIICMPIVSRGSYIGVQVWNKISGSAFSKTDENNPFQFAVFCAL 420
Dd	361	RPNREVDLYGTYYTTRNIIICMPIVSRGSYIGVQVWNKISGSAFSKTDENNPFQFAVFCAL 420
Qy	421	ALHCAWMYHRIHSECIYRVTEKLSYHSICTSEEWQGLMRPNLPARICRDIELFHPDIG 480
Dd	421	ALHCAWMYHRIHSECIYRVTEKLSYHSICTSEEWQGLMRPNLPARICRDIELFHPDIG 480
Qy	481	PPEMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQNYRVRPYHNMKHAIVAHCMYAI 540
Dd	481	PPEMMPGIFVYMIHRSCTGSCFELBKLCRFIMSVKQNYRVRPYHNMKHAIVAHCMYAI 540
Qy	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV 600
Dd	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV 600
Qy	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV 600
Dd	541	LQNNNGFLTDLERKGLIACLDHLDHRGFSNSYLQKRDHPALALYSTSTMEQHHSQTV 600
Qy	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS 660
Dd	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS 660
Qy	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS 660
Dd	601	SILQEGHNISTSSSEYQVLEIRKAIINTDALYFGNRKQIEMVQTSIANTLNQS 660
Qy	661	HRDVIIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Dd	661	HRDVIIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMMDRDKRD 720
Qy	721	EVPOGOLGFYNAVAIPCYTTLTQILPTEPBLKACRDNLQWEKVIIRGEETAMWISGPG 780
Dd	721	EVPOGOLGFYNAVAIPCYTTLTQILPTEPBLKACRDNLQWEKVIIRGEETAMWISGPG 780

QY 781 APSKSTPKLVKVED 796
 DB 779 ATSKSTSEKPTRKVD 794

RESULT 3

QTPG2 MOUSE PRELIMINARY; PRT; 797 AA.

QY 07TPG2 MOUSE PRELIMINARY; PRT; 797 AA.
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Pde10a.
 GN Name=Pde10a Mus musculus;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Li S., Tian R., Bratwaite M., Waeltz P., Nagaraia R., Roe B.A.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC104323; AAP94049.1; -; Genomic DNA.
 DR GO; GO:0004114; F.3',5'-cyclic-nucleotide phosphodiesterase a. .; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003607; Met_phos_hydro.
 DR InterPro; IPR002073; PDbase.
 DR Pfam; PF01590; GAF; 2.
 DR Pfam; PR00233; PDbase_I; 1.
 DR PRINTS; PR00387; PD1ESTERAS1.
 DR SMART; SM00065; GAF; 2.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDbase_I; 1.
 DR PROSITE; PS0275; MW; BEB1442N95131C8A CRC64;
 SQ SEQUENCE 797 AA; 90275 MW; BEB1442N95131C8A CRC64;

Query Match 97.2%; Score 4089.5; DB 2; Length 797;

Best local Similarity 98.2%; Pred. No. 2.2e-307;

Matches 778; Conservative 2; Mismatches 5; Indels 7; Gaps 1;

QY 12 FRLTECPILSPS-----LTDEKVAAYLSLHPQVLDEFVSSEVSATVEKMKRKTKNKA 64
 DB 6 FQQAQCLCFEPSPSATTOGLTDEKVAAYLSLHPQVLDEFVSSEVSATVEKMKRKTKNKA 65
 QY 65 KQEPSEKVSRYODTMQGVVYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGFAL 124
 DB 66 KQEPSEKVSRYODTMQGVVYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGFAL 125
 QY 125 YFLGECNNSLCVTIPPMKEGQRLIPAGITIGTTISAVVAASRKLVLVEDLIGDERFP 184
 DB 126 YFLGECNNSLCVTIPPMKEGQRLIPAGITIGTTISAVVAASRKLVLVEDLIGDERFP 185
 QY 185 RRGGLSGRTIGSVLCPIYTAIGDLIGIELYRHMGEKAFCSHOEVATANTAMASVAI 244
 DB 186 RRGGLSGRTIGSVLCPIYTAIGDLIGIELYRHMGEKAFCSHOEVATANTAMASVAI 245
 QY 245 HQVQVCRGLAKQTELENDFLDVSRTYFDNIVAIDSLLEHIMIYAKNLVNDRCALFQVDH 304
 DB 246 HQVQVCRGLAKQTELENDFLDVSRTYFDNIVAIDSLLEHIMIYAKNLVNDRCALFQVDH 305
 QY 305 KKKELYSDFLDIGBEKGGKPIFKKTKIRPSIEKINGIAGVARTGEVNTIDVADPPENR 364
 DB 306 KKKELYSDFLDIGBEKGGKPIFKKTKIRPSIEKINGIAGVARTGEVNTIDVADPPENR 365
 QY 365 EVDLYGYTTRNLLCMPITVRSVYIGVQVWVKNKISSAFSKTDENNKKMFVFCALALHC 424
 DB 366 EVDLYGYTTRNLLCMPITVRSVYIGVQVWVKNKISSAFSKTDENNKKMFVFCALALHC 425
 QY 425 ANMYHRIHSECIYRVTMKLSYHSICTSEMOGLMFLNLPARICRDIELFHDIGEPEN 484

DB 426 ANMYHRIHSECIYRVTMKLSYHSICTSEMOGLMFLNLPARICRDIELFHDIGEPEN 485

QY 485 MWGIFVTMIHRSCTGSCFELEKLCRFMTSVYKYNRRPYNNMKAAVVAHOMVAILQNN 544

DB 486 MWGIFVTMIHRSCTGSCFELEKLCRFMTSVYKYNRRPYNNMKAAVVAHOMVAILQNN 545

QY 545 NGLFTDLERKGLIATCLCHDDHREGSNSYLQKPDHPALAYSTSTMEQHPQSOTVSILO 604

DB 546 NGLFTDLERKGLIATCLCHDDHREGSNSYLQKPDHPALAYSTSTMEQHPQSOTVSILO 605

QY 605 LEGHNIFFSTLSSEYEQVLEIRKAIINTDIALYFGNRKOLEMYQTGSLNINQSHDR 664

DB 606 LEGHNIFFSTLSSEYEQVLEIRKAIINTDIALYFGNRKOLEMYQTGSLNINQSHDR 665

QY 665 VIGLMTACDLCSTYKLPMTYKLTANDIYAEFMAEGDEMKLGIQPIPMMDKXDEVQ 724

DB 666 VIGLMTACDLCSTYKLPMTYKLTANDIYAEFMAEGDEMKLGIQPIPMMDKXDEVQ 725

QY 725 GQLGFYNAVALPCYTTLTQILPTEPLKACRDINOMEKVIRGETAMWISGPPAPSK 784

DB 726 GQLGFYNAVALPCYTTLTQILPTEPLKACRDINOMEKVIRGETAMWISGPPAPSK 785

QY 785 STEPKLVKVED 796

DB 786 STEPKLVKVED 797

RESULT 4

QTPG1 MOUSE PRELIMINARY; PRT; 773 AA.

QY 07TPG1; DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Pde10a (Fragment).
 GN Name=Pde10a Mus musculus;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RA Li S., Tian R., Bratwaite M., Waeltz P., Nagaraia R., Roe B.A.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC104323; AAP94050.1; -; Genomic DNA.
 DR GO; GO:0004114; F.3',5'-cyclic-nucleotide phosphodiesterase a. .; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003607; Met_phos_hydro.
 DR InterPro; IPR002073; PDbase.
 DR Pfam; PF01590; GAF; 2.
 DR Pfam; PR00233; PDbase_I; 1.
 DR PRINTS; PR00387; PD1ESTERAS1.
 DR SMART; SM00065; GAF; 2.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDbase_I; 1.
 DR NON_TER
 SQ SEQUENCE 773 AA; 87794 MW; 0C0E353B72940912 CRC64;

Query Match 97.0%; Score 4080; DB 2; Length 773;

Best local Similarity 100.0%; Pred. No. 1.2e-306;

Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LTDEKVAAYLSLHPQVLDEFVSSEVSATVEKMKRKTKNKAQDEPKVSRYODTMQGV 83
 DB 1 LTDEKVAAYLSLHPQVLDEFVSSEVSATVEKMKRKTKNKAQDEPKVSRYODTMQGV 60
 QY 84 VYELNSYIEQRDLDTGGDNHLLLYELSSIRIATKADGFALYFLGECNNSLCVTIPPMK 143

Db 61 VYELNSYIEQRLDTGGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIIPGK 120
Qy 144 EGQPLIPAGPIITOGTTISAVYAKSRKTLVIEDILGDERFPRGTGLESSTRIQSVLCPI 203
Db 121 EGQPLIPAGPIITOGTTISAVYAKSRKTLVIEDILGDERFPRGTGLESSTRIQSVLCPI 180
Qy 204 VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 263
Db 181 VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 240
Qy 264 LDVSKTYEDNIIVADLSLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 323
Db 241 LDVSKTYEDNIIVADLSLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 300
Qy 324 PIFKTKTKEIRSEIEKGIAGQVARTGEVLNIPDAYDPRFNREVDLYTGYTTNNILCMPIV 383
Db 301 PIFKTKTKEIRSEIEKGIAGQVARTGEVLNIPDAYDPRFNREVDLYTGYTTNNILCMPIV 360
Qy 384 SRGSYIGVQVQWVKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTVME 443
Db 361 SRGSYIGVQVQWVKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTVME 420
Qy 444 KLSYHSICTSEEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 503
Db 421 KLSYHSICTSEEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 480
Qy 504 ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAILQNNNGLFTDLERKGLIACLC 563
Db 481 ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAILQNNNGLFTDLERKGLIACLC 540
Qy 564 DLDHGFNSNYLQKFDHPALALYSTSTMEQHHPSQVTSILOEGHNITSTLSSSEYEOVL 623
Db 541 DLDHGFNSNYLQKFDHPALALYSTSTMEQHHPSQVTSILOEGHNITSTLSSSEYEOVL 600
Qy 624 EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDRIYIGLMTACDLCSTYKLM 683
Db 601 EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDRIYIGLMTACDLCSTYKLM 660
Qy 664 VTKLITANDIYAEFMAEGDEMKKLGIOPIPMMDRDKRDEVPQQLGFYNAVAIPCTYTLTLQ 743
Db 661 VTKLITANDIYAEFMAEGDEMKKLGIOPIPMMDRDKRDEVPQQLGFYNAVAIPCTYTLTLQ 720
Qy 744 ILPTEPILKACRDNLQMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 796
Db 721 ILPTEPILKACRDNLQMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 773
RESULT 5
Q9WV11_MOUSE PRELIMINARY; prt; 779 AA.
AC Q9WV11; 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DR 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE CAMP/cGMP phosphodiesterase.
GN Name=Pde10a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA MEDLINE=99289599; PubMed=10359840; DOI=10.1073/pnae.96.12.7071;
RX Soderling S.H., Bayuga S.J., Beavo J.A.;
RT "Isolation and characterization of a dual-substrate phosphodiesterase
RT gene family: PDE10A.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:7071-7076(1999).
DR EMBL; AF110507; AAD31544.1; -; mRNA.
DR Ensembl; ENSMUSG0000023868; Mus musculus.
DR MGI; MGI:1345143; Pde10a.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. .; IDA.

DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDBase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDBase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDG; 1.
DR PROSITE; PS00126; PDBASE_I; 1.
SQ SEQUENCE 779 AA; 88516 MW; 83691872PDDDEAB CRC64;
Query Match 97.0%; Score 4080; DB 2; Length 779;
Best Local Similarity 100.0%; Pred. No. 1.2e-306;
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 LTDEKRYKYLSPQVLDPEFVSESIAETVEKMLKRTKNKAKDESPREVSRYQDTNNQ 83
Db 7 LTDEKRYKYLSPQVLDPEFVSESIAETVEKMLKRTKNKAKDESPREVSRYQDTNNQ 66
Qy 84 VYELNSYIEQRLDTGGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIIPGK 143
Db 67 VYELNSYIEQRLDTGGDNHLLLYELSSIIIRATKADGFALYFLGECNNSLCVFIIPGK 126
Qy 144 EGQPLIPAGPIITOGTTISAVYAKSRKTLVIEDILGDERFPRGTGLESSTRIQSVLCPI 203
Db 127 EGQPLIPAGPIITOGTTISAVYAKSRKTLVIEDILGDERFPRGTGLESSTRIQSVLCPI 186
Qy 204 VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 263
Db 187 VTAIGDLIGILELTHRMGKEAFCLSHQEVATNLMASVAIHQOVCGRLAQOTELNDFL 246
Qy 264 LDVSKTYEDNIIVADLSLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 323
Db 247 LDVSKTYEDNIIVADLSLEHIMIYAKNLVNADRCALFOVDHKNKELYSDFDIGEKEGK 306
Qy 324 PIFKTKTKEIRSEIEKGIAGQVARTGEVLNIPDAYDPRFNREVDLYTGYTTNNILCMPIV 383
Db 307 PIFKTKTKEIRSEIEKGIAGQVARTGEVLNIPDAYDPRFNREVDLYTGYTTNNILCMPIV 366
Qy 384 SRGSYIGVQVQWVKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTVME 443
Db 367 SRGSYIGVQVQWVKISGSAFSTKDENNFMFAVFCALALHCANMYHRIHSECIYRTVME 426
Qy 444 KLSYHSICTSEEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 503
Db 427 KLSYHSICTSEEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTGSCF 486
Qy 504 ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAILQNNNGLFTDLERKGLIACLC 563
Db 487 ELEKLCRFIMSVKKNYRRVPYHNMKHAVTVAHCMTAILQNNNGLFTDLERKGLIACLC 546
Qy 564 DLDHGFNSNYLQKFDHPALALYSTSTMEQHHPSQVTSILOEGHNITSTLSSSEYEOVL 623
Db 547 DLDHGFNSNYLQKFDHPALALYSTSTMEQHHPSQVTSILOEGHNITSTLSSSEYEOVL 606
Qy 624 EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDRIYIGLMTACDLCSTYKLM 683
Db 607 EIIRKAIATDIALYFGNRKQLEEMVQOTGSLNLHNSHRDRIYIGLMTACDLCSTYKLM 666
Qy 664 VTKLITANDIYAEFMAEGDEMKKLGIOPIPMMDRDKRDEVPQQLGFYNAVAIPCTYTLTLQ 743
Db 667 VTKLITANDIYAEFMAEGDEMKKLGIOPIPMMDRDKRDEVPQQLGFYNAVAIPCTYTLTLQ 726
Qy 744 ILPTEPILKACRDNLQMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 796
Db 727 ILPTEPILKACRDNLQMEKVIIRGETAMWISGEPAPSKSTPEKLNKVED 779
RESULT 6
Q8CA95_MOUSE PRELIMINARY; prt; 790 AA.
AC Q8CA95;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TRENBLREL. 23, last sequence update)
 01-MAR-2004 (TRENBLREL. 26, last annotation update)
 Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A33007P15 product:phosphodiesterase 10A, full insert sequence.
 OS Name=Pde10a;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 Carninci P., Hayashizaki Y.;
 "High-efficiency full-length cDNA cloning";
 Meth. Enzymol. 303:19-44(1999).
 (2)
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Iehi Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsumura H. A., Ashburner M., Batalov S., Casavant T., Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Guestinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Maehima J., Mazzarelli J., Monbetsu P., Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L., Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S., Hayashizaki Y.;
 "Functional annotation of a full-length mouse cDNA collection.";
 Nature 409:685-690(2001).
 (3)
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 The RIKEN Consortium,
 The RIKEN Genome Exploration Research Group Phase I & II Team;
 "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 Nature 420:563-573(2002).
 (4)
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
 Genome Res. 10:1617-1630(2000).
 (5)
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 MEDLINE=20530933; PubMed=11076861; DOI=10.1101/gr.152600;
 Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kikunishi T., Taahiro H., Itoh M., Sumi M., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 "RIKEN integrated sequence analysis (RISA) system-364-format RT sequencing pipeline with 364 multicapillary sequencer";
 Genome Res. 10:1757-1771(2000).

[6]
 NUCLEOTIDE SEQUENCE.
 STRAIN=C57BL/6J; TISSUE=spinal cord;
 Adachi J., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T., Hori F., Imotani K., Iehi Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohnishi N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Yasunishi A., Hayashizaki Y.;
 "Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases."
 R. EMBL; AK039249; BAC30292.1; -; mRNA.
 DR Ensembl; ENSMUSG000000238668; Mus musculus.
 DR MGI; MGI:1345143; Pde10a.
 DR GO; GO:0004114; P.3',5'-cyclic-nucleotide phosphodiesterase a. .; IDA.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003607; Met_phos_hydro.
 DR InterPro; IPR002073; PDBase.
 DR Pfam; PF01590; GAF; 2.
 DR Pfam; PR00233; PDBase; 1.
 DR PRINTS; PR00387; PD1ESTERAS1.
 DR SMART; SM00065; GAF; 2.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASB_1; 1.
 DR PROSITE; PS00126; PDEASB_1; 1.
 DR SEQUENCE 790 AA; 89438 MW; 1AC6F11A5AD7B92 CRC64;
 Query Match 96.8%; Score 4072; DB 2; Length 790;
 Best Local Similarity 99.9%; Pred. No. 5e-306; 1; Indels 0; Gaps 0;
 Matches 772; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 24 LNDKAVKATSLHPQVLDVFEVSVAETVEKMLKRTKAKDPSPKVSRQDTNMG 83
 18 LIDKVKATSLHPQVLDVFEVSVAETVEKMLKRTKAKDPSPKVSRQDTNMG 77
 84 VYELNSYIEQRIDTGGDNHLLYELSSITRTATKADGALYFLGECNNSLCYFIPGK 143
 78 VYELNSYIEQRIDTGGDNHLLYELSSITRTATKADGALYFLGECNNSLCYFIPGK 137
 144 EGQPRILPAGPIPTGCTTGAAYAKSKTLLVEDIIGDERPPGTGSGRISQVCLPI 203
 138 EGQPRILPAGPIPTGCTTGAAYAKSKTLLVEDIIGDERPPGTGSGRISQVCLPI 197
 204 VTAIGDLIGLIELYRMGKEAFCLSHQEVATANIAMASVALIHQVQCRGLAKOTELNDF 263
 198 VTAIGDLIGLIELYRMGKEAFCLSHQEVATANIAMASVALIHQVQCRGLAKOTELNDF 257
 264 LDVSKTYFDNIVAIDSLLEHIMIYANLVNADRCALFOVDHKNKELYSDFDGEKEGK 323
 258 LDVSKTYFDNIVAIDSLLEHIMIYANLVNADRCALFOVDHKNKELYSDFDGEKEGK 317
 324 PIFKTKETKIRFSIEKGIQAQVARTGVNIPDAVADPRFREVDTYGTTRNIIICPIV 383
 318 PIFKTKETKIRFSIEKGIQAQVARTGVNIPDAVADPRFREVDTYGTTRNIIICPIV 377
 384 SRGSVIGVQWVKISGSAFSTKDNENPKMAFAVFCALALHCAAMYRIRHSECIYVTME 443
 378 SRGSVIGVQWVKISGSAFSTKDNENPKMAFAVFCALALHCAAMYRIRHSECIYVTME 437
 444 KLSYHSICTSEEWQGLMRPULPARICRDIELFPHDIGPEENWPGIFVTMIRSGTSCF 503
 438 KLSYHSICTSEEWQGLMRPULPARICRDIELFPHDIGPEENWPGIFVTMIRSGTSCF 497
 504 ELEKLCRFPMISYQKQRRPVYHNMKAAVVAHGMVAILLQNNNLFTDLERKGLIACLC 563
 498 ELEKLCRFPMISYQKQRRPVYHNMKAAVVAHGMVAILLQNNNLFTDLERKGLIACLC 557
 564 DLDRGFSNSYLOKFPHPALALYSTSTMEQHHSQVTSVILQLEGHNI FSTLSSEYEOVL 623
 558 DLDRGFSNSYLOKFPHPALALYSTSTMEQHHSQVTSVILQLEGHNI FSTLSSEYEOVL 617

Qy		624	EIRKALITATLUALYFGRNRKOLEEYVQGSILNLNHSRDRVTGLMTRACDLCSTVKLMP	683
Db		618	EIRKALITATDLATLFGRNRKOLEEYVQGSILNLNHSRDRVTGLMTRACDLCSTVKLMP	677
Qy		684	VTKLTANDIYAEFWAEGDEEMKKLGIOPIPMMDRDREVPQGOLGFYNVAVIPCTYTLTQ	743
Db		678	VTKLTANDIYAEFWAEGDEEMKKLGIOPIPMMDRDREVPQGOLGFYNVAVIPCTYTLTQ	737
Qy		744	ILPPPEPLLKACRDNLNQWEKVIIRGEETAMWISGCPAPASKSTPEKLNVKVED	796
Db		738	ILPPPEPLLKACRDNLNQWEKVIIRGEETAMWISGCPAPASKSTPEKLNVKVED	790
RESULT 7				
ID	Q9ULW9_HUMAN	PRT;	789 AA.	
AC	Q9ULW9;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DN	3,'5'-cyclic nucleotide phosphodiesterase 10A2.			
GN	Name=PDE10A2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Fetal lung;			
RX	MEDLINE=99373117; PubMed=10441464; DOI=10.1006/brcr.1999.1013;			
RA	Korea J., Fujishige K., Yuasa K., Omori K;			
RT	"Characterization and phosphorylation of PDE10A2, a novel alternative splice variant of human phosphodiesterase that hydrolyzes cAMP and cGMP."			
RL	Biochem. Biophys. Res. Commun. 261:551-557(1999).			
DR	EMBL; AB026816; BAA84467.1; -: mRNA.			
DR	GO; GO:0004114; F:3,'5'-cyclic-nucleotide phosphodiesterase a. . . ; IEA.			
DR	GO; GO:0016787; F:hydrolyase activity; IEA.			
DR	InterPro; IPR0031018; GAF.			
DR	InterPro; IPR003607; Met_phos_hydro.			
DR	InterPro; IPR002073; PDbase.			
DR	Pfam; PF01590; GAF; 2.			
DR	Pfam; PF00233; PDbase_1; 1			
DR	PRINTS; PR00387; PDLESTERASE1.			
DR	SMART; SM00065; GAF; 2.			
DR	SMART; SM00471; HDC; 1.			
DR	PROSITE; PS00126; PDbase_1; 1.			
SO	SEQUENCE 789 AA; 89385 MW; 7CC35F16735FB3C2 CRC64;			
Query Match				
	Best Local Similarity	95.2%; Score 4004; DB 2; Length 789;		
	Matches 753; Conservative 19; Mismatches 16; Indels 0; Gaps 0;			
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Db	1 MEDGPSNNASGFRRLTECFGLSPSLTDEKAKAYLSLHPVLDFEVSYSAAETVEKMLRK	60		
Qy	61 TNKAKDEBSPKEVSRYODTNMGVVYELNSYIEORLDTGGDNHLLLYELSIIRIATYAD	120		
Db	61 NTKSEDBSGAPKEVSRYODTNMGVVYELNSYIEORLDTGGDNHLLLYELSIIRIATYAD	120		
Qy	121 GFALYIFLGECSNNLSLVPIIPRMKESQPLLINAGPITTOGTTSAYAKSRKTLLVVDIIIGD	180		
Db	121 GFALYIFLGECSNNLSLVPIIPRMKESQPLLINAGPITTOGTTSAYAKSRKTLLVVDIIIGD	180		
Qy	181 ERPFPGTLESGETRIQSIVLCPIYTAIGDLGIILELYRHMGKEAFCLSHOEYAATNTLAMA	240		
Db	181 ERPFPGTLESGETRIQSIVLCPIYTAIGDLGIILELYRHMGKEAFCLSHOEYAATNTLAMA	240		
Qy	241 SVALIHQVGVCGKLAKQTELNDFLDVSKTYPDNIVAIDSLHEHTIMYAKNLVNADRCAF	300		

Db	241	SVALLHQVYCGGLKQKLTENDFLIDVSTKTYEDNIYALISLSLEHINIYAKNULVNAEDCALF	300
Qy	301	QVDHKNKELYSDDLFDIGEEKGKPIFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAVADP	360
Db	301	QVDHKNKELYSDDLFDIGEEKGKGFVKFKTKKEIRFSIEKGIAGQVARTGEVLNIPDAVADP	360
Qy	361	RFRNEVULYCGYTRNLICMPFIVNSGSVIGVAVQWVNKISGSAFSTEDENNFMQPAFCAL	420
Db	361	RFRNEVVDLYTYTTRNLICMPFIVNSGSVIGVAVQWVNKISGSAFSTEDENNFMQPAFCAL	420
Qy	421	ALHGANMHRIRHSECIYRYVMKEKLSYYSICTSEEMQGLMRFNLPAIRCIDYELFHFIDG	480
Db	421	ALHGANMHRIRHSECIYRYVMKEKLSYYSICTSEEMQGLMOTFLVRLCKEITELHFIDG	480
Qy	481	PFENMMPGIFVYMIHRSCGTSCEFELEKLCRFPMYSVKXNYRRVRYNMKHAVTVAHCMAI	540
Db	481	PFENMMPGIFVYMHRSCTSCFELEKLCRFPMYSVKXNYRRVRYNMKHAVTVAHCMAI	540
Qy	541	LQNNNGFLPTDIERKGLLIACLCHLDHNGFSNSYQKEDHPLAALYSTSTMEQHHPSCV	600
Db	541	LQNNHTFLPTDIERKGLLIACLCHLDHNGFSNSYQKEDHPLAALYSTSTMEQHHPSCV	600
Qy	601	SILQLEGHNISTSSSESEBOVLEIIRKAIATDIALYFGNRKQLEBMYQTSGLMHNOS	660
Db	601	SILQLEGHNISTSSSESEBOVLEIIRKAIATDIALYFGNRKQLEBMYQTSGLMHNOS	660
Qy	661	HRDEVITGLMTACDLCVYTKLMPVTKLTANDIYAEFMAEGDEMKGIGIPIPMDDRKXD	720
Db	661	HRDEVITGLMTACDLCVYTKLMPVTKLTANDIYAEFMAEGDEMKGIGIPIPMDDRKXD	720
Qy	721	EVPGGGLGFTYNAVAIPCTYITLTOLLPRPEPLKACRDNLNOMEKIRIBETATMTISGPDP	780
Db	721	EVPGGGLGFTYNAVAIPCYTITLTOLLPRPEPLKACRDNLNOMEKIRIBETATMTISGPDP	780
Qy	781	APSKTPE 788	
Db	781	APSKTPE 788	
Db	781	AQKAAASE 788	
RESULT 8			
Q6S9E8 RAT PRELIMINARY; PRT; 883 AA.			
AC	Q6S9E8		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	PDB10A12		
GN	Name=Pde10a;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=W;		
RX	PubMed=1452115; DOI=10.1074/jbc.M312500200;		
RA	O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V.,		
RA	De Zeeuw C.I., Sanger G., Hunt S.P., Richter-Levin G., Mallet J.,		
RA	Laroche S., Bliss T.V.P., French P.U.;		
RT	"Differential amplification of intron-containing transcripts reveals		
RT	long term potential-association of intron-regulation of specific Pde10A		
RT	phosphodiesterase splice variants."		
RT	J. Biol. Chem. 279:15841-15849 (2004).		
DR	EMBL; AY462092; AA521244.1; -; mRNA.		
DR	GO; GO:0004114; F:3, '5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.		
DR	GO; GO:0016787; F:hydrolyase activity; IEA.		
DR	GO; GO:0007165; P:signal transduction; IEA.		
DR	InterPro; IPR003018; GAF.		
DR	InterPro; IPR003607; Met_phos_hydro.		
DR	InterPro; IPR002073; PDasee.		
DR	Pfam; PF01590; GAF; 2.		

RA Fujishige K., Kotera J., Michibata H., Yuasa K., Takebayashi S.-I.,
 RA Okumura K., Omori K.;
 RA "Cloning and characterization of a novel human phosphodiesterase that
 RT hydrolyzes both cGMP and cGMP (PDE10A).";
 RT J. Biol. Chem. 274:18438-18445(1999).
 RU [2]
 RP NUCLEOTIDE SEQUENCE (ISOFORM PDE10A1), AND PARTIAL NUCLEOTIDE SEQUENCE
 RP (ISOFORM PDE10A2).
 RP TISSUE=Fetal brain;
 RX MEDLINE=9921805; PubMed=10393245; DOI=10.1016/S0378-1119(99)00171-7;
 RA Longhney K., Snyder P.B., Uher L., Rosman G.J., Ferguson K.,
 RA Florio V.A.;
 RT "Isolation and characterization of PDE10A, a novel human 3',5'-cyclic
 RT nucleotide phosphodiesterase.";
 RT Gene 234:109-117(1999).
 CC -1- FUNCTION: Plays a role in signal transduction by regulating the
 CC intracellular concentration of cyclic nucleotides. This enzyme can
 CC hydrolyze both cAMP and cGMP, having a higher affinity for cAMP.
 CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
 CC nucleoside 5'-phosphate.
 CC -1- COFACTOR: Divalent cations.
 CC -1- ENZYME REGULATION: Inhibited by dipyrindamole and moderately by
 CC IBMX. cAMP potentially inhibits hydrolysis of cGMP.
 CC -1- SUBCELLULAR LOCATION: Located mostly to soluble cellular
 CC fractions.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Isoforms differ in their N-terminal region;
 CC Name=PDE10A1;
 CC IsoId=Q91233-1; Sequence=Displayed;
 CC Name=PDE10A2;
 CC IsoId=Q91233-2; Sequence=VSP_004601;
 CC Note=Incomplete sequence;
 CC -1- TISSUE SPECIFICITY: Abundant in the putamen and caudate nucleus
 CC regions of brain and testis, moderately expressed in the thyroid
 CC gland, pituitary gland, thalamus and cerebellum.
 CC -1- DOMAIN: Composed of a C-terminal catalytic domain containing two
 CC putative divalent metal sites and an N-terminal regulatory domain
 CC which contains one putative cGMP-binding region.
 CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
 CC family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AB020593; BAA78034.1; -; mRNA.
 DR EMBL; AF127479; AAD32595.1; -; mRNA.
 DR EMBL; AF127480; AAD32596.1; -; mRNA.
 DR PDB; 1LRB; Model: A=501-757.
 DR Ensembl; ENSG00000112541; Homo sapiens.
 DR HGNC; HGNC:8772; PDE10A.
 DR GO; GO:0004114; F.3',5'-cyclic-nucleotide phosphodiesterase a. . .; TAS.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR002073; PDBase.
 DR Pfam; PF01590; GAF; 2.
 DR Pfam; PF00233; PDBase_1; 1.
 DR PRINTS; PR00387; PDIBESTERSB1.
 DR PROSITE; PS00126; PDASE_1; 1.
 DR 3D-structure; Alternative splicing; cGMP; cGMP-binding; Hydrolase;
 KM Nucleotide-binding; Polymorphism.
 FT NP BIND 339 416 cGMP (By similarity).
 FT BINDING 386 386 cGMP (By similarity).
 FT BINDING 387 387 cGMP (By similarity).
 FT BINDING 397 397 cGMP (By similarity).
 FT VARSPLIC 1 13 MRISERSQHLTG -> QGASFLMAAALLFGSDMEDGSP
 FT NNAACFRLTECFSPSPS (in isoform PDE10A2).
 FT /FTId=VSP_004601.
 FT L->P.
 FT VARIANT 303 303 /FTId=VAR_008797
 FT SEQUENCE 779 AA; 88412 MW; C5651BB524A32B7 CRC64;

Query Match 92.2%; Score 3878; DB 1; Length 779;
 Best Local Similarity 95.4%; Pred. No. 5.2e-291;
 Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;
 24 LTDEKVKAYLSLHPVDLDFVSESVSAETVEKMLRKTKNAKDDESPKVSRYQDTNNQ 83
 14 LTDEKVKAYLSLHPVDLDFVSESVSAETVEKMLRKTKNAKDDESPKVSRYQDTNNQ 73
 84 VVEELNSYIEORLDGTGDNHLLYLSLIRATATADGALYFLGECNNSLCVFIPGK 143
 74 VVEELNSYIEORLDGTGDNHLLYLSLIRATADGALYFLGECNNSLCVFIPGK 133
 144 EGQPLIAGPTTQSTTSAVYAKSKRTLVLDIDGDERFPRTGSGSTRIQSVLCPI 203
 134 EGQPLIAGPTTQSTTSAVYAKSKRTLVLDIDGDERFPRTGSGSTRIQSVLCPI 193
 204 VTAIGDLIGILELYHMGKEAFCLSHOEYATNLMAVVAIHQVQCRGLAKQTEINDEL 263
 194 VTAIGDLIGILELYHMGKEAFCLSHOEYATNLMAVVAIHQVQCRGLAKQTEINDEL 253
 264 LDVSKTYEDNIVADLSLEHIMITYAKNLVNAIDRCALFOVDHKKELISLFDIGEEK 323
 254 LDVSKTYEDNIVADLSLEHIMITYAKNLVNAIDRCALFOVDHKKELISLFDIGEEK 313
 324 PTFKTKTERRESIEKGIAQVARTGEVNI PDVYADPRNRREVDLYTGYTTNIIICMPY 383
 314 PTFKTKTERRESIEKGIAQVARTGEVNI PDVYADPRNRREVDLYTGYTTNIIICMPY 373
 384 SRGSYIGVQVQVNNKISGSAFSTKDENNFPAPVFCALALHCAVMYHRIHSECIYVTE 443
 374 SRGSYIGVQVQVNNKISGSAFSTKDENNFPAPVFCALALHCAVMYHRIHSECIYVTE 433
 444 KLSYISICTSEEMOGLMRENLPAICRDIELFHFDIGPEENMPGIFVTMIRSCGTSCE 503
 434 KLSYISICTSEEMOGLMRENLPAICRDIELFHFDIGPEENMPGIFVTMIRSCGTSCE 493
 504 ELEKLCRFIMSYKQYRRRPYNNMGAATVVAHCAVAILLONNGLFTDILRRKGLILCLCH 563
 494 ELEKLCRFIMSYKQYRRRPYNNMGAATVVAHCAVAILLONNGLFTDILRRKGLILCLCH 553
 564 DLDRGFSNSYLOKFPDPLAALYSTTMEQHHSQTSVILLEGHNI PSTLSSEBEQVYL 623
 554 DLDRGFSNSYLOKFPDPLAALYSTTMEQHHSQTSVILLEGHNI PSTLSSEBEQVYL 613
 624 EIIIRKAIITDIALYFGNKKOLEBMYQTGSLNLHNSHEDRYVIGLMTACDLCSTVKLP 683
 614 EIIIRKAIITDIALYFGNKKOLEBMYQTGSLNLHNSHEDRYVIGLMTACDLCSTVKLP 673
 684 VTKLTANDIYAEFMAAGDEMKKLGIOPIPMMDRDKRDEVPQGLGYNNVAIPCYTTLLQ 743
 674 VTKLTANDIYAEFMAAGDEMKKLGIOPIPMMDRDKRDEVPQGLGYNNVAIPCYTTLLQ 733
 744 ILPPEPLILKACRDNLNOMEKVI RGETAMWISGPPAPSKSTPE 788
 734 ILPPEPLILKACRDNLNOMEKVI RGETAMWISGPPAPSKSTPE 778
 RESULT 12
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 AC Q9NTV4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Phosphodiesterase 10A.
 GN Name=PDE10A; ORFNames=Rp3-416F21.1-001;
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NC NCBI_TaxId=9606;
 RN [1]

QY 264 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDPIGSEKCK 323
 DB 264 LDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDPIGSEKCK 313
 QY 324 PIFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCMPIV 383
 DB 324 PIFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCMPIV 373
 QY 344 PVFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCMPIV 373
 DB 344 PVFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCMPIV 373
 QY 384 SNGSVIGVQVQWVKISGSAFSTKDENNPFQPAVFCALALHLCANMYHRIHSECIYATME 443
 DB 374 SNGSVIGVQVQWVKISGSAFSTKDENNPFQPAVFCALALHLCANMYHRIHSECIYATME 433
 QY 444 KLSYHSICTSEBMOGLMRPNLPARICRDIELFPHFDIGPEENMPPGIFVYMIHSCGTCSCF 503
 DB 434 KLSYHSICTSEBMOGLMRPNLPARICRDIELFPHFDIGPEENMPPGIFVYMIHSCGTCSCF 493
 QY 504 ELEKLCRFPTMSYKKNRRVRYNNHMKAAVVAHGMVAIILQNNNGLFTDLERKGLLACLC 563
 DB 494 ELEKLCRFPTMSYKKNRRVRYNNHMKAAVVAHGMVAIILQNNNGLFTDLERKGLLACLC 553
 QY 564 DLDHGFSSNSYLOKFDHPPLAALYSTSTMEQHPHSQTVSILQLEGHNI FSTLSSEYEQVL 623
 DB 554 DLDHGFSSNSYLOKFDHPPLAALYSTSTMEQHPHSQTVSILQLEGHNI FSTLSSEYEQVL 613
 QY 624 EIIIRKAIITDIALYFNGRKOLEEMYTQGSILNHNQSHRDVIGLMTACDLCSTVKMP 683
 DB 614 EIIIRKAIITDIALYFNGRKOLEEMYTQGSILNHNQSHRDVIGLMTACDLCSTVKMP 673
 QY 684 VTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYYTLTQ 743
 DB 674 VTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYYTLTQ 733
 QY 744 ILPPTPEPLKACRDNINOMKXVIRGSETAMWISGPGAPSKSTPEK 786
 DB 734 ILPPTPEPLKACRDNINOMKXVIRGSETAMWISGPGAPSKSTPEK 778
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 AC Q6S9E7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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 GN Name=Pde10a;
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=W;
 RC PubMed=14752115; DOI=10.1074/jbc.M312500202;
 RA O'Connor V., Genin A., Davis S., Karishma K.K., Doyere V.,
 RA De Zeeuw C.I., Sanger G., Hunt S.P., Richter-Levin G., Mallet J.,
 RA Laroche S., Blais T.V.P., French P.J.;
 RT "Differential amplification of intron-containing transcripts reveals
 RT long term potential associated with regulation of specific Pde10A
 RT phosphodiesterase splice variants."
 J. Biol. Chem. 279.15841-15849(2004).
 DB EMBL; AY62093; AA521245.1; mRNA.
 DB GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
 DB GO; GO:0016787; F:hydrolyase activity; IEA.
 DB GO; GO:0007165; P:signal transduction; IEA.
 DB InterPro; IPR003018; GAF.
 DB InterPro; IPR003607; Met_pho_hydro.
 DB InterPro; IPR002073; pDasee.
 DB Pfam; PF01590; GAF; 2.
 DB Pfam; PF00233; pDasee; 1.
 DB PRINTS; PRO0387; PDIESTERASE1.

DR SMART; SM00065; GAF; 2.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDASE_1; 1.
 SQ SEQUENCE 714 AA; 81028 MW; 5AFBCD3669558F6 CRC64;
 Query Match 88.3%; Score 3715; DB 2; Length 714;
 Best Local Similarity 98.5%; Pred. No. 1.9e-278;
 Matches 705; Conservative 2; Mismatches 7; Indels 2; Gaps 1;
 QY 81 MGVVYELNSYEQRLDTGGDNHLLLYELSSIRATADGALFLYECNNSLCVFTRP 140
 DB 1 MGVVYELNSYEQRLDTGGDNHLLLYELSSIRATADGALFLYECNNSLCVFTRP 60
 QY 141 GKKEGQPLIPAGPITTOGTTISAVYAKSKRTLLVDDIADGEFPFGTGLESSTRIQSVLC 200
 DB 61 GKKEGQPLIPAGPITTOGTTISAVYAKSKRTLLVDDIADGEFPFGTGLESSTRIQSVLC 120
 QY 201 LPIVTAIGDLIGILELYRHMGEKAFCLSHQEVATNLAWASVAIHQVYCRGLAKQTEIN 260
 DB 121 LPIVTAIGDLIGILELYRHMGEKAFCLSHQEVATNLAWASVAIHQVYCRGLAKQTEIN 180
 QY 261 DFLDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDPIGSEK 320
 DB 181 DFLDVSKTYFDNIVAIDSLLEHIMIYAKNLVNAADRCALFOVDHKKELYSDFDPIGSEK 240
 QY 321 EKKPIFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCM 380
 DB 241 EKKPIFKTKTEIRFSEIEKGIAGQVARTGEVLNI PDAYADPRFRREVDLYGTGTTNNILCM 300
 QY 381 PIVRSQSVIGVQVQWVKISGSAFSTKDENNPFQPAVFCALALHLCANMYHRIHSECIYAV 440
 DB 301 PIVRSQSVIGVQVQWVKISGSAFSTKDENNPFQPAVFCALALHLCANMYHRIHSECIYAV 360
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 DB 421 SCEPELEKLCRFPTMSYKKNRRVRYNNHMKAAVVAHGMVAIILQNNNGLFTDLERKGLLAC 480
 QY 561 LCHDLDHGFSSNSYLOKFDHPPLAALYSTSTMEQHPHSQTVSILQLEGHNI FSTLSSEYE 620
 DB 481 LCHDLDHGFSSNSYLOKFDHPPLAALYSTSTMEQHPHSQTVSILQLEGHNI FSTLSSEYE 540
 QY 621 QVLEIIRKAIITDIALYFNGRKOLEEMYTQGSILNHNQSHRDVIGLMTACDLCSTVK 680
 DB 541 QVLEIIRKAIITDIALYFNGRKOLEEMYTQGSILNHNQSHRDVIGLMTACDLCSTVK 600
 QY 681 LMPVTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYYT 740
 DB 601 LMPVTKLTANDIYAEFWAGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYYT 660
 QY 741 LTPPTPEPLKACRDNINOMKXVIRGSETAMWISGPGAPSKSTPEKLVAYED 796
 DB 661 LTPPTPEPLKACRDNINOMKXVIRGSETAMWISGPGAPSKSTPEKLVAYED 714
 RESULT 15
 Q9HCP9 HUMAN PRELIMINARY; PRT; 714 AA.
 AC Q9HCP9;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE PDB10A1 (EC 3.1.4.17) (Fragment).
 GN Name=HSPD10A;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_Taxid=9606;
 RN [1]


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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20453115; PubMed=10998054;
RT Fujishige K., Kotera J., Yuasa K., Omori K.;
RT "The human phosphodiesterase PDE10A gene. Genomic organization and
RT evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 267:5943-5951(2000).
DR EMBL; AB041798; BAB16383.1; -; Genomic DNA.
DR GO; GO:0004114; P:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; P:hydrolyase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDBase.
DR Pfam; PF00233; PDBase_1; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDBASE_1; 1.
KW Hydrolyase.
FT NON_TER 1 1
SQ SEQUENCE 714 AA; 80887 MW; 0C43F60A307CCDF0 CRC64;

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DB 1 YODTMQGVVYELNSYIEQRDLDTGGDNHLLLYELSSIIRIATKADGFALYFLGECNNSLC 60
QY 136 VFIPGMEKGOPRLIPAGPIITOGTTISAVVAKSRKTLVLEDILGDERFPRGTGLSGTRI 195
DB 61 IFTPGMEKGOPRLIPAGPIITOGTTISAVVAKSRKTLVLEDILGDERFPRGTGLSGTRI 120
QY 196 QSVLCPLVTATGDLIGILELYRHNGKEAFCLSHOEVAATANLAMASVAIHQVQVCRGLAK 255
DB 121 QSVLCPLVTATGDLIGILELYRHNGKEAFCLSHOEVAATANLAMASVAIHQVQVCRGLAK 180
QY 256 QTELNDPLLDVSKTYFDNIVAIDSLLEHIMYAKNLVNDRCALFQVDHKNKELYSDFD 315
DB 181 QTELNDPLLDVSKTYFDNIVAIDSLLEHIMYAKNLVNDRCALFQVDHKNKELYSDFD 240
QY 316 IGEKEKGPIPKKTEKIRPSIEKGIAQVARTGEVNIIPDAVADPRENREVDLYGYTR 375
DB 241 IGEKEKGKPVFKTKIRPSIEKGIAQVARTGEVNIIPDAVADPRENREVDLYGYTR 300
QY 376 NILCMPIVSRGSGVIGVQVQVNIISGSAFSGTDENNFQMFVFCALALHCANNYHRIHSE 435
DB 301 NILCMPIVSRGSGVIGVQVQVNIISGSAFSGTDENNFQMFVFCALALHCANNYHRIHSE 360
QY 436 CIYRVTMKLSYHSICTSEEWQGLKRFNLPAICRDIELFHFIDIGPFENMPGIFVYMIH 495
DB 361 CIYRVTMKLSYHSICTSEEWQGLKRFNLPAICRDIELFHFIDIGPFENMPGIFVYMIH 420
QY 496 RSCGTSCELEKLCRFINSVKKNYRVPYHNKHAHTVAHCMYALIQNNHTLFTDLERKG 555
DB 421 RSCGTSCELEKLCRFINSVKKNYRVPYHNKHAHTVAHCMYALIQNNHTLFTDLERKG 480
QY 556 LLIACTCHDLDRGFSNSYLOKFPDHPALALYSTSTMEQHFSQTVSILOEGHNIFSTLS 615
DB 481 LLIACTCHDLDRGFSNSYLOKFPDHPALALYSTSTMEQHFSQTVSILOEGHNIFSTLS 540
QY 616 SSEYEQVEIIRKAIITADLALYFGNRKQLEEMVQTSINLHNSHDRVIGIMMTACDL 675
DB 541 SSEYEQVEIIRKAIITADLALYFGNRKQLEEMVQTSINLHNSHDRVIGIMMTACDL 600
QY 676 CSVTGLMPPTKLTANDIYAEFWABGDEMKGIGIPIPMMDRDKDEVPGQGLGFYNAVAI 735
DB 601 CSVTGLMPPTKLTANDIYAEFWABGDEMKGIGIPIPMMDRDKDEVPGQGLGFYNAVAI 660
QY 736 PCYTLTQILPPTBPLLACRDNLNQMEKVIIRGEETAMWISGPGAPAPSKSTPE 788
DB 736 PCYTLTQILPPTBPLLACRDNLNQMEKVIIRGEETAMWISGPGAPAPSKSTPE 788
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DB 661 PCYTLTQILPPTBPLLACRDNLNQMEKVIIRGEETAMWISGPGAPAPSKSTPE 713

Search completed: January 10, 2006, 13:55:30
Job time : 83 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 10, 2006, 13:52:10 ; Search time 27 Seconds
(without alignments)
2437.401 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206
Sequence: 1 MEDGSPNNASCFRRLTECF...GPGAPSKSTPEKLVKVED 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5 COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6 COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RR COMB.pep: *
6: /cgn2_6/prodata/1/1aa/backfilcell.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3997	95.0	803	1 US-08-951-648-4	Sequence 4, Appl
2	3997	95.0	803	2 US-09-174-437-4	Sequence 4, Appl
3	3997	95.0	803	2 US-09-686-055A-4	Sequence 4, Appl
4	3878	92.2	779	1 US-08-951-648-6	Sequence 6, Appl
5	3878	92.2	779	2 US-09-174-437-6	Sequence 6, Appl
6	3878	92.2	779	2 US-09-686-055A-6	Sequence 6, Appl
7	3878	92.2	779	2 US-09-420-190-1	Sequence 1, Appl
8	3873	92.1	766	1 US-08-951-648-2	Sequence 2, Appl
9	3873	92.1	766	2 US-09-174-437-2	Sequence 2, Appl
10	3873	92.1	766	2 US-09-686-055A-2	Sequence 2, Appl
11	1010	24.0	1284	2 US-10-296-144-5	Sequence 5, Appl
12	918	21.8	875	1 US-08-480-547A-10	Sequence 10, Appl
13	918	21.8	875	1 US-08-250-847B-10	Sequence 10, Appl
14	918	21.8	875	1 US-08-463-949A-10	Sequence 10, Appl
15	918	21.8	875	2 US-08-464-410A-10	Sequence 10, Appl
16	914	21.7	875	4 PCT-US94-0606-10	Sequence 10, Appl
17	912.5	21.7	875	1 US-08-480-547A-23	Sequence 23, Appl
18	912.5	21.7	875	1 US-08-250-847B-23	Sequence 23, Appl
19	912.5	21.7	875	1 US-08-463-949A-23	Sequence 23, Appl
20	912.5	21.7	875	2 US-08-464-410A-23	Sequence 23, Appl
21	912.5	21.7	875	2 US-09-226-741-5	Sequence 5, Appl
22	912.5	21.7	875	2 US-09-595-514-5	Sequence 5, Appl
23	912.5	21.7	875	2 US-09-949-002-310	Sequence 310, Appl
24	912.5	21.7	875	4 PCT-US94-0606-23	Sequence 23, Appl
25	909	21.6	921	1 US-07-872-644-39	Sequence 39, Appl
26	909	21.6	921	1 US-08-297-494-39	Sequence 39, Appl
27	909	21.6	921	1 US-08-297-510-39	Sequence 39, Appl

28	909	21.6	921	1 US-08-479-532-39	Sequence 39, Appl
29	909	21.6	921	1 US-08-455-526-39	Sequence 39, Appl
30	909	21.6	921	1 US-08-455-526-39	Sequence 39, Appl
31	909	21.6	921	2 US-09-139-491-39	Sequence 39, Appl
32	909	21.6	921	2 US-09-754-250-5	Sequence 5, Appl
33	909	21.6	921	2 US-09-883-825-39	Sequence 39, Appl
34	909	21.6	921	2 US-10-094-989-5	Sequence 5, Appl
35	909	21.6	921	4 PCT-US92-0322-39	Sequence 39, Appl
36	908	21.6	942	1 US-07-872-644-43	Sequence 43, Appl
37	908	21.6	942	1 US-08-297-494-43	Sequence 43, Appl
38	908	21.6	942	1 US-08-297-510-43	Sequence 43, Appl
39	908	21.6	942	1 US-08-479-532-43	Sequence 43, Appl
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42	908	21.6	942	2 US-09-139-491-43	Sequence 43, Appl
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44	908	21.6	942	2 PCT-US92-0322-43	Sequence 43, Appl
45	897.5	21.3	920	2 US-09-754-250-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-08-951-648-4
; Sequence 4, Application US/08951648
; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
; STREET: 233 South Wacker, Sears Tower Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ. ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 803 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-951-648-4

Query Match 95.0%; Score 3997; DB 1; Length 803;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;
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QY 1 MEDGSPNNASCFRRLTECF...GPGAPSKSTPEKLVKVR 60
DB 15 MEDGSPNNASCFRRLTECF...GPGAPSKSTPEKLVKVR 74
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DB 75 NKSEBESAPKEVSRVQDTNMGVVEINSYIEORLDGTGDNDLLLYELSSIRIRATKD 134

Qy	121	PPAYVFLGECNNSLCVPFI	PPGKKEQOPRLIPAGPITOGTTLSAVYAKSRKTLVSDIIG	180	
Db	135	GPALFLFLEBCNNSLCFT	PPGKKEQOPRLIPAGPITOGTTLSAVYAKSRKTLVSDIIG	194	
Qy	181	ERFPKGTGLESTRIQSVY	CLPIVTAIGDLIGILELYHHMGKAPCLSHOEVAATNLAMA	240	
Db	195	ERFPKGTGLESTRIQSVY	CLPIVTAIGDLIGILELYHHMGKAPCLSHOEVAATNLAMA	254	
Qy	241	SVAIHQVOVCRGLAQOTEL	NDPFLDVSKTYPFNIVATISLSLEHMTIYAKNLVNAIDRCALF	300	
Db	255	SVAIHQVOVCRGLAQOTEL	NDPFLDVSKTYPFNIVATISLSLEHMTIYAKNLVNAIDRCALF	314	
Qy	301	QVDHKNKELYSPLFDPIGE	KEGKPIFFKTKTEIRFSIENKIAQVARTGEVLNI	PAVADP 360	
Db	315	QVDHKNKELYSPLFDPIGE	KEGKPIFFKTKTEIRFSIENKIAQVARTGEVLNI	PAVADP 374	
Qy	361	RPNREVDLYGTGTNNIL	CMPIVSRGSYIGVVQWYNKISGSASFSTDENNFMAFVFCAL	420	
Db	375	RPNREVDLYGTGTNNIL	CMPIVSRGSYIGVVQWYNKISGSASFSTDENNFMAFVFCAL	434	
Qy	421	ALHCAWYHRIHSECTI	RYTMEKLSYNSICTSEEMQILMRPNIPARICRDI	ELFHPDIG 480	
Db	435	ALHCAWYHRIHSECTI	RYTMEKLSYNSICTSEEMQILMRPNIPARICRDI	ELFHPDIG 494	
Qy	481	PPEWMPGIFVYMIRSC	GTSCGTFEELKLCRFIMSYKAYRYRYPYNNMKAAVTVAHCAWYAI	540	
Db	495	PPEWMPGIFVYMIRSC	GTSCGTFEELKLCRFIMSYKAYRYRYPYNNMKAAVTVAHCAWYAI	554	
Qy	541	LONNGLFTDERKGLIAC	CHDIDHRGFSNSYLOKFDHPLAALYSTSTMEQHHFSQTV	600	
Db	555	LONNHTLTDERKGLIAC	CHDIDHRGFSNSYLOKFDHPLAALYSTSTMEQHHFSQTV	614	
Qy	601	SILQEGNISTSSSEYEO	LEIRKAIATDIALFPGNRKOLEMYOTGSLNLNHO	S 660	
Db	615	SILQEGNISTSSSEYEO	LEIRKAIATDIALFPGNRKOLEMYOTGSLNLNHO	S 674	
Qy	661	HRDRVIGLMTACDLC	SVYTKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDRD	KRD 720	
Db	675	HRDRVIGLMTACDLC	SVYTKLMPVTKLTANDIYAEFMAEGDEMKLGIOPIPMDDRD	KRD 734	
Qy	721	EVPOGQLGFYNAVAIP	CTYTLTOLLIPTEBPLIKACRDNLQWMEKTI	IRGEETNAMI	SGGFP 780
Db	735	EVPOGQLGFYNAVAIP	CTYTLTOLLIPTEBPLIKACRDNLQWMEKTI	IRGEETNAMI	SGGFP 794
Qy	781	APSKSTPE	788		
Db	795	AKKAAASE	802		
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US-09-174-437-4					
; Sequence 4, Application US/09174437A					
; Patent No. 6133007					
; GENERAL INFORMATION:					
; APPLICANT: Loughney, Kate					
; TITLE OF INVENTION: phosphodiesterase 8A					
; FILE REFERENCE: 27866/35047					
; CURRENT APPLICATION NUMBER: US/09/174,437A					
; CURRENT FILING DATE: 1998-10-16					
; EARLIER APPLICATION NUMBER: 08/951,648					
; EARLIER FILING DATE: 1997-10-16					
; NUMBER OF SEQ ID NOS: 48					
; SOFTWARE: PatentIn Ver. 2.0					
; SEQ ID NO 4					
; LENGTH: 803					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-09-174-437-4					
Query Match 95.0%; Score 3997; DB 2; Length 803;					
Best Local Similarity 95.4%; Pred. No. 0;					
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;					

QY	1	MEGSENNAS	CEBR	LTCEG	PLS	LTDE	KYKA	YL	SLAH	QV	LD	EF	SE	SV	SA	ET	YK	ML	KR	60																																				
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QY	61	TKNAKDEP	S	PKE	VS	RY	OD	TNN	Q	VY	LE	NS	YI	EO	R	LD	TG	D	NH	LL	YEL	SS	I	R	I	A	T	K	A	D	120																									
Db	75	NKSEDES	A	P	K	SV	SH	Y	OD	TNN	Q	VY	LE	NS	YI	EO	R	LD	TG	D	NH	LL	YEL	SS	I	R	I	A	T	K	A	D	134																							
QY	121	GPALY	LG	SC	NN	S	L	CV	P	IP	MG	KE	Q	P	L	I	AG	E	I	T	O	G	T	I	SA	V	A	S	R	K	T	L	L	VE	D	I	L	D	180																	
Db	135	GFALY	LG	SC	NN	S	L	CV	P	IP	PG	I	KE	Q	P	L	I	AG	E	I	T	O	G	T	I	SA	V	A	S	R	K	T	L	L	VE	D	I	L	D	194																
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Db	195	ERPR	GT	GES	TR	I	Q	S	V	L	C	P	I	V	A	I	D	L	G	I	E	L	Y	R	H	N	G	K	A	F	C	S	H	O	E	V	A	T	A	N	L	A	M	A	254											
QY	241	SVAIH	O	V	C	R	G	L	A	Q	T	E	L	N	D	F	L	D	V	S	K	T	Y	D	N	I	V	A	I	D	S	L	B	E	H	I	M	I	A	K	L	V	N	A	D	R	C	A	L	F	300					
Db	255	SVAIH	O	V	C	R	G	L	A	Q	T	E	L	N	D	F	L	D	V	S	K	T	Y	D	N	I	V	A	I	D	S	L	B	E	H	I	M	I	A	K	L	V	N	A	D	R	C	A	L	F	314					
QY	301	QV	DH	K	K	E	L	Y	S	L	P	I	G	E	K	G	K	P	I	F	K	T	X	I	R	S	I	E	K	G	I	A	G	O	V	A	R	T	G	E	V	L	N	I	P	D	A	Y	A	D	360					
Db	315	QV	DH	K	K	E	L	Y	S	L	P	I	G	E	K	G	K	P	I	F	K	T	X	I	R	S	I	E	K	G	I	A	G	O	V	A	R	T	G	E	V	L	N	I	P	D	A	Y	A	D	374					
QY	361	RFR	RE	D	V	L	T	G	T	T	N	I	L	C	M	P	I	V	S	R	G	S	V	I	G	V	O	M	N	K	I	S	S	A	F	S	K	T	D	E	N	N	K	N	F	A	V	F	C	A	L	420				
Db	375	RFR	RE	D	V	L	T	G	T	T	N	I	L	C	M	P	I	V	S	R	G	S	V	I	G	V	O	M	N	K	I	S	S	A	F	S	K	T	D	E	N	N	K	N	F	A	V	F	C	A	L	434				
QY	421	A	H	C	A	N	M	T	H	R	I	H	S	E	C	I	Y	R	V	M	E	K	L	S	H	S	I	C	T	S	E	E	O	G	L	R	F	N	L	P	A	R	I	C	H	D	I	E	L	F	H	P	D	I	G	480
Db	435	A	H	C	A	N	M	T	H	R	I	H	S	E	C	I	Y	R	V	M	E	K	L	S	H	S	I	C	T	S	E	E	O	G	L	R	F	N	L	P	A	R	I	C	H	D	I	E	L	F	H	P	D	I	G	494
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Qy	121	PPAYVFLGECNNSLCVPI	PPGKKEQOPRLIPAGPTIOGTTLSAVYAKSRKTLVSDIIG	180
Db	135	GPALFLFLEBCNNSLCFT	PPGKKEQOPRLIPAGPTIOGTTLSAVYAKSRKTLVSDIIG	194
Qy	181	ERFPRGTGLESTRIQSV	LCPIVTAIGDLIGILELYHHWGKEAFCLSHOEVAATNLAMA	240
Db	195	ERFPRGTGLESTRIQSV	LCPIVTAIGDLIGILELYHHWGKEAFCLSHOEVAATNLAMA	254
Qy	241	SVAIHQVOVCRGLAQOT	ELNDPFLDVSKTYPNNIYALISLLEHMTIYAKNLVNAORCALF	300
Db	255	SVAIHQVOVCRGLAQOT	ELNDPFLDVSKTYPNNIYALISLLEHMTIYAKNLVNAORCALF	314
Qy	301	QVDHKNKELYSPLFDPI	GEKEGKPIFFKTKTEIRFSIEKGIAGQVARTGEVLNI	360
Db	315	QVDHKNKELYSPLFDPI	GEKEGKPIFFKTKTEIRFSIEKGIAGQVARTGEVLNI	374
Qy	361	RPNREVDLYGTGTNNIL	CMPIVSRGSYIGVVQWYVKISGSASFSTDENNFMAFVFCAL	420
Db	375	RPNREVDLYGTGTNNIL	CMPIVSRGSYIGVVQWYVKISGSASFSTDENNFMAFVFCAL	434
Qy	421	ALHCAWYHRIHSECTI	RYTMKEKLSYISICTSEEMQILMRPNLPARICRDIELFHPDIG	480
Db	435	ALHCAWYHRIHSECTI	RYTMKEKLSYISICTSEEMQILMRPNLPARICRDIELFHPDIG	494
Qy	481	PPEWMPGIFVYMIRSC	GTSCGFEELEKLCRFPIYSYKQYRRVRYPNWYHKAATVAHCAWYAI	540
Db	495	PPEWMPGIFVYMIRSC	GTSCGFEELEKLCRFPIYSYKQYRRVRYPNWYHKAATVAHCAWYAI	554
Qy	541	LONNGLFTDERKGLIAC	CHDIDHRGFSNSYLOKFDHPLAALYSTSTMEQHHFSQTV	600
Db	555	LONNHTLTDERKGLIAC	CHDIDHRGFSNSYLOKFDHPLAALYSTSTMEQHHFSQTV	614
Qy	601	SILQEGNISTSSSEYEO	LEIRKALITADLAFGNRKOLEMYOTGSILNLHNS	660
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Qy	661	HRDRVIGLMTAFCDLCS	VTYKLTPIANDIYAEFMAEGDEMKLGIOPIPMDDRDYRD	720
Db	675	HRDRVIGLMTAFCDLCS	VTYKLTPIANDIYAEFMAEGDEMKLGIOPIPMDDRDYRD	734
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Qy	781	APSKSTPE	788	
Db	795	AKKAAASE	802	
RESULT 2				
US-09-174-437-4				
; Sequence 4, Application US/09174437A				
; Patent No. 6133007				
; GENERAL INFORMATION:				
; APPLICANT: Loughney, Kate				
; TITLE OF INVENTION: phosphodiesterase 8A				
; FILE REFERENCE: 27866/35047				
; CURRENT APPLICATION NUMBER: US/09/174,437A				
; CURRENT FILING DATE: 1998-10-16				
; EARLIER APPLICATION NUMBER: 08/951,648				
; EARLIER FILING DATE: 1997-10-16				
; NUMBER OF SEQ ID NOS: 48				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 4				
; LENGTH: 803				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-09-174-437-4				
Query Match 95.0%; Score 3997; DB 2; Length 803;				
Best Local Similarity 95.4%; Pred. No. 0;				
Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;				

QY	1	MEGSENNAS	CEBR	LTCEG	PLS	LTDE	KYKA	YL	SLAH	QV	LD	EF	SE	SV	SA	ET	YK	ML	KR	60																																				
Db	15	MEDGSENNAS	CEBR	LTCEG	PLS	LTDE	KYKA	YL	SLAH	QV	LD	EF	SE	SV	SA	ET	YK	ML	KR	74																																				
QY	61	TKNAKDEP	S	PKE	VS	RY	OD	TNN	Q	VY	LE	NS	YI	EO	R	LD	TG	D	NH	LL	YEL	SS	I	R	I	A	T	K	A	D	120																									
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Db	135	GFALY	LG	SC	NN	S	L	CV	P	IP	PG	I	KE	Q	P	L	I	AG	E	I	T	O	G	T	I	SA	V	A	S	R	K	T	L	L	VE	D	I	L	D	194																
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Db	195	ERPR	GT	GES	TR	I	Q	S	V	L	C	P	I	V	A	I	D	L	G	I	E	L	Y	R	H	N	G	K	A	F	C	S	H	O	E	V	A	T	A	N	L	A	M	A	254											
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LENGTH: 803
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-686-055A-4

Query Match 95.0%; Score 3997; DB 2; Length 803;
 Best Local Similarity 95.4%; Pred. No. 0;
 Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 1 MEDGSSNNASCFRRRLTECFSLPSTLDEKAKAYLSLHPQVLDSESVSAETVEKMLKKK 60
DB 15 MEDGSSNNASCFRRRLTECFSLPSTLDEKAKAYLSLHPQVLDSESVSAETVEKMLKKK 74
QY 61 TNKADSPKPKSVSRVQDTNMGGVYELNSYIEORLDGDNHLLLYELSSITRIATKAD 120
DB 75 NKSSEDESPKPKSVSRVQDTNMGGVYELNSYIEORLDGDNHLLLYELSSITRIATKAD 134
QY 121 GPALAFPLGECNNSLCFPIPPKKEGPRILIPAGPTTQGTTSAYVAKSRKTLVLEDIGD 180
DB 135 GPALAFPLGECNNSLCFPIPPKKEGPRILIPAGPTTQGTTSAYVAKSRKTLVLEDIGD 194
QY 181 ERFPGTGLESGRLOSVCPLIVTAIGDLIGILEYRMGKEAPCLSHQEVATANLAWA 240
DB 195 ERFPGTGLESGRLOSVCPLIVTAIGDLIGILEYRMGKEAPCLSHQEVATANLAWA 254
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DB 255 SVAIHQVQCRGLAKQTEINDFLLDVSKTYFDNIYADISLLEHIMIYAKNLVNAADRCALF 314
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DB 315 QVDHKKKELYSDFDIEGEEKGKPIFKTKKEIRFSEIKGIAGVATGTVLNIPDAVYADP 374
QY 361 RRRREVDLTGTTTRNIIICMPISRSQSVGVQVQWVKISGSAFSKTDENNFKMAFVFCAL 420
DB 375 RRRREVDLTGTTTRNIIICMPISRSQSVGVQVQWVKISGSAFSKTDENNFKMAFVFCAL 434
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DB 435 ALHCANMYRIRHSECIYRVYMEKLSYHSICTSEBQGLMFRNIPARICRDIELFFPDIG 494
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DB 495 PERNMMPGIFVYMIHRSCTGSCFELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAI 554
QY 541 LQNNNHLFTDLERKGLIACLDLDRHGSNSYLQFDPHPLAALYSTSTMEQHHSQTV 600
DB 555 LQNNNHLFTDLERKGLIACLDLDRHGSNSYLQFDPHPLAALYSTSTMEQHHSQTV 614
QY 601 SIQLEGHNIFSTLSSSEYEQVLEIRKAIATDLYFGNRKQLEBMYQTSILNHQS 660
DB 615 SIQLEGHNIFSTLSSSEYEQVLEIRKAIATDLYFGNRKQLEBMYQTSILNHQS 674
QY 661 HRDVIGLMWTACDLSVYTLMPVTKLTANDIYAEFAEGDEMKKIGIQTIPMDRDKPD 720
DB 675 HRDVIGLMWTACDLSVYTLMPVTKLTANDIYAEFAEGDEMKKIGIQTIPMDRDKPD 734
QY 721 EYVQGGQGFNNAVAIPCTYTLTQILPTEBPLAKCRDNLNOMEKVLRGESTAMWISGP 780
DB 735 EYVQGGQGFNNAVAIPCTYTLTQILPTEBPLAKCRDNLNOMEKVLRGESTAMWISGP 794
QY 781 APSKSTPE 788
DB 795 AOKRAASE 802

```

RESULT 4
 US-08-951-648-6
 Sequence 6, Application US/08951648
 Patent No. 5933465
 GENERAL INFORMATION:
 APPLICANT: Loughney, Kate
 TITLE OF INVENTION: Phosphodiesterase 8

NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker, Sears Tower Suite 6300
 CITY: Chicago
 STATE: Illinois
 COUNTRY: US
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/951,648
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Williams Jr., Joseph A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/34038
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 779 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-951-648-6

Query Match 92.2%; Score 3878; DB 1; Length 779;
 Best Local Similarity 95.4%; Pred. No. 0;
 Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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QY 24 LDEKVKAYLSLHPQVLDSESVSAETVEKMLKRTKAKADESPKPKSVSRVQDTNMGG 83
DB 14 LDEKVKAYLSLHPQVLDSESVSAETVEKMLKRTKAKADESPKPKSVSRVQDTNMGG 73
QY 84 VYELNSYIEORLDGDNHLLLYELSSITRIATKADGALYFLGECNNSLCFPIPPKMK 143
DB 74 VYELNSYIEORLDGDNHLLLYELSSITRIATKADGALYFLGECNNSLCFPIPPKMK 133
QY 144 EGQPRILIPAGPTTQGTTSAYVAKSRKTLVLEDIGDEFPPGTGLESSTRLOSVCPLP 203
DB 134 EGQPRILIPAGPTTQGTTSAYVAKSRKTLVLEDIGDEFPPGTGLESSTRLOSVCPLP 193
QY 204 VTAIGDLIGILEYRMGKEAPCLSHQEVATANLAWASVAIHQVQCRGLAKQTEINDFL 263
DB 194 VTAIGDLIGILEYRMGKEAPCLSHQEVATANLAWASVAIHQVQCRGLAKQTEINDFL 253
QY 264 LDVSKTYFDNIYADISLLEHIMIYAKNLVNAADRCALFOVDHKKKELYSDFDIEGEEKG 323
DB 254 LDVSKTYFDNIYADISLLEHIMIYAKNLVNAADRCALFOVDHKKKELYSDFDIEGEEKG 313
QY 324 PIFKTKKEIRFSEIKGIAGQVARTGTVLNIPDAVADPRRREVDLTGTTTRNIIICMPY 383
DB 314 PIFKTKKEIRFSEIKGIAGQVARTGTVLNIPDAVADPRRREVDLTGTTTRNIIICMPY 373
QY 384 SRGSVGVQVQWVKISGSAFSKTDENNFKMAFVFCALALHCANMYRIRHSECIYVYME 443
DB 374 SRGSVGVQVQWVKISGSAFSKTDENNFKMAFVFCALALHCANMYRIRHSECIYVYME 433
QY 444 KLSYHSICTSEBQGLMFRNIPARICRDIELFFPDIGPENMMPGIFVYMIHRSCTGSCF 503
DB 434 KLSYHSICTSEBQGLMFRNIPARICRDIELFFPDIGPENMMPGIFVYMIHRSCTGSCF 493
QY 504 ELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAILQNNNHLFTDLERKGLIACLC 563
DB 494 ELEKLCRFINSYKKNRRVYHNWKAIVYAHCMYAILQNNNHLFTDLERKGLIACLC 553
QY 564 LDRHGRFSNSYLQFDPHPLAALYSTSTMEQHHSQTVSILQLEGHNIFSTLSSSEYEQV 623

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Db      |||
554 DLDHGFNSYLOQRDHPALALYSTWEOHHFSQTVSILQEGHNISTSSSEYEOVL 613
Qy      624 EIRKAIITATDALYFGNRKQLEBMYQTSNLNHNQSHDRVIGLMTACDLCSTYKLP 683
Db      614 EIRKAIITATDALYFGNRKQLEBMYQTSNLNHNQSHDRVIGLMTACDLCSTYKLP 673
Qy      664 VTKLTAANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743
Db      674 VTKLTAANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 733
Qy      744 ILPTEPILKACRDNLNOMEKVIRGEETAMTISGPGAPSKSTPE 788
Db      724 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778

RESULT 5
US-09-174-437-6
; Sequence 6, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-174-437-6

Query Match      92.2%; Score 3878; DB 2; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy      24 LTDEKVKAYLSLHPVLDLDFVSESVAETVEKMKLRKTNKAKDESPKESRYODTNMG 83
Db      14 LTDEKVKAYLSLHPVLDLDFVSESVAETVEKMKLRKTNKAKDESPKESRYODTNMG 73
Qy      84 VYELNSYIEQRDLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFIIPGMK 143
Db      74 VYELNSYIEQRDLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFIIPGMK 133
Qy      144 EGQPLIPAGPITOGTTISAVYAKSRKTLVBDIIGDERFRPGTGLESTRIOSVLCPI 203
Db      134 EGQPLIPAGPITOGTTISAVYAKSRKTLVBDIIGDERFRPGTGLESTRIOSVLCPI 193
Qy      204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQOTELNDFL 263
Db      194 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQOTELNDFL 253
Qy      264 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKKGK 323
Db      254 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKKGK 313
Qy      324 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNREVDLYTGYTTNNILCMPIV 383
Db      314 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNREVDLYTGYTTNNILCMPIV 373
Qy      384 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAANYHRIHSECIYRYTME 443
Db      374 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAANYHRIHSECIYRYTME 433
Qy      444 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRSGTSCF 503
Db      434 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRSGTSCF 493
Qy      504 ELEKLCRFIMSKYKQYRVRPYHNMKHAIVVAHOMVAIIQNNNGLFTDLBRKGLLACLGCH 563
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Db      |||
494 ELEKLCRFIMSKYKQYRVRPYHNMKHAIVVAHOMVAIIQNNNGLFTDLBRKGLLACLGCH 553
Qy      564 DLDHGFNSYLOQRDHPALALYSTWEOHHFSQTVSILQEGHNISTSSSEYEOVL 623
Db      554 DLDHGFNSYLOQRDHPALALYSTWEOHHFSQTVSILQEGHNISTSSSEYEOVL 613
Qy      624 EIRKAIITATDALYFGNRKQLEBMYQTSNLNHNQSHDRVIGLMTACDLCSTYKLP 683
Db      614 EIRKAIITATDALYFGNRKQLEBMYQTSNLNHNQSHDRVIGLMTACDLCSTYKLP 673
Qy      664 VTKLTAANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743
Db      674 VTKLTAANDIYAEFMAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 733
Qy      744 ILPTEPILKACRDNLNOMEKVIRGEETAMTISGPGAPSKSTPE 788
Db      724 ILPTEPILKACRDNLNOMEKVIRGEETATWISSPSVAQKAASE 778

RESULT 6
US-09-686-055A-6
; Sequence 6, Application US/09686055A
; Patent No. 6566087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A
; CURRENT FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-686-055A-6

Query Match      92.2%; Score 3878; DB 2; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy      24 LTDEKVKAYLSLHPVLDLDFVSESVAETVEKMKLRKTNKAKDESPKESRYODTNMG 83
Db      14 LTDEKVKAYLSLHPVLDLDFVSESVAETVEKMKLRKTNKAKDESPKESRYODTNMG 73
Qy      84 VYELNSYIEQRDLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFIIPGMK 143
Db      74 VYELNSYIEQRDLDTGDNHLLYELSSIRIRATKADGFALYFLGECNNSLCVFIIPGMK 133
Qy      144 EGQPLIPAGPITOGTTISAVYAKSRKTLVBDIIGDERFRPGTGLESTRIOSVLCPI 203
Db      134 EGQPLIPAGPITOGTTISAVYAKSRKTLVBDIIGDERFRPGTGLESTRIOSVLCPI 193
Qy      204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQOTELNDFL 263
Db      194 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQOTELNDFL 253
Qy      264 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKKGK 323
Db      254 LDVSKTYFDNIVAIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDFDIGEKKGK 313
Qy      324 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNREVDLYTGYTTNNILCMPIV 383
Db      314 PIFKTKTEIRFSIEKGIAGQVARTGEVLNIPDAYADPRFNREVDLYTGYTTNNILCMPIV 373
Qy      384 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAANYHRIHSECIYRYTME 443
Db      374 SRGSYIGVQVWNKISGSAFSTKDENNFMFAVFCALALHCAANYHRIHSECIYRYTME 433
Qy      444 KLSYHSICTSEEWQGLMRFNLPARICRDIELFHPDIGFENMMPGIFVYMIRSGTSCF 503
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Db      424 KLSYHSICTSEBMQGLMFTLPLVRLCKEIELFHPDIPGPENNMPPGIFVYVWHRSGTSCF 493
Qy      504 ELEKLCRFMSYKQYRRVRYNNMKAIVVAHCAVYAILQNNNGLFTDLERKGLLIACLC 563
Db      494 ELEKLCRFMSYKQYRRVRYNNMKAIVVAHCAVYAILQNNNGLFTDLERKGLLIACLC 553
Qy      564 DLDHGFNSYLOKFDHPALALYSTSTMEQHFSQTVSILQLEGNHIFSTLSSSEYEQVL 623
Db      554 DLDHGFNSYLOKFDHPALALYSTSTMEQHFSQTVSILQLEGNHIFSTLSSSEYEQVL 613
Qy      624 EIIIRKAIATDIALYFGNKKOLEBMYQTGSLNLNQHSHRDVIGLMTACDLCSTYKLP 683
Db      614 EIIIRKAIATDIALYFGNKKOLEBMYQTGSLNLNQHSHRDVIGLMTACDLCSTYKLP 673
Qy      684 VTKLTANDIYAEFWABGDEMCKLGIQIPMDMDKDXDEVPOGOLGFYNAVALPCYTTLTQ 743
Db      674 VTKLTANDIYAEFWABGDEMCKLGIQIPMDMDKDXDEVPOGOLGFYNAVALPCYTTLTQ 733
Qy      744 ILPTEPLKACRDNLQWKEVIRGETAMWISGPGAPAPSKSTPE 788
Db      734 ILPTEPLKACRDNLQWKEVIRGETAMWISGPGAPAPSKSTPE 778

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RESULT 7
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. 6673564
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

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```

Query Match 92.2%; Score 3878; DB 2; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Qy      24 LTBKAVAYSLHPQVLDSEFVSSEVSAETVEKMLKRTNKADEPSPKESRYQDTMVG 83
Db      14 LTBKAVAYSLHPQVLDSEFVSSEVSAETVEKMLKRTNKADEPSPKESRYQDTMVG 73
Qy      84 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGPAFYFGECNNSLCVFIPGAK 143
Db      74 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGPAFYFGECNNSLCVFIPGAK 133
Qy      144 EGQPRILPAPPIYQGTITSAVNAKSKTLVVEDLGERPPRGGLSEGRIRISVLCPI 203
Db      134 EGQPRILPAPPIYQGTITSAVNAKSKTLVVEDLGERPPRGGLSEGRIRISVLCPI 193
Qy      204 VTAIGDILGILELRHNGKEAFCLSHOEVAATANLAMSVAIHQVQCRGLAKOTELNDFL 263
Db      194 VTAIGDILGILELRHNGKEAFCLSHOEVAATANLAMSVAIHQVQCRGLAKOTELNDFL 253
Qy      264 LDVSKTYFDNIVALDSLLEHIMIVAKULVNADRCALFOVDHKNKELYSDLFDIGEEK 323
Db      254 LDVSKTYFDNIVALDSLLEHIMIVAKULVNADRCALFOVDHKNKELYSDLFDIGEEK 313
Qy      324 PIFKKTIEIRISIEKGIAGVAFGEVYLNIPDAVADPRENNEVDLYGTYTRNLCPYV 383
Db      314 PIFKKTIEIRISIEKGIAGVAFGEVYLNIPDAVADPRENNEVDLYGTYTRNLCPYV 373

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Qy      384 SRGSYGVQWVWVKISGSAFSTDENNFKMPAVFCALALHCAWYHRIHSECIYRVME 443
Db      374 SRGSYGVQWVWVKISGSAFSTDENNFKMPAVFCALALHCAWYHRIHSECIYRVME 433
Qy      444 KLSYHSICTSEBMQGLMFTLPLVRLCKEIELFHPDIPGPENNMPPGIFVYVWHRSGTSCF 503
Db      434 KLSYHSICTSEBMQGLMFTLPLVRLCKEIELFHPDIPGPENNMPPGIFVYVWHRSGTSCF 493
Qy      504 ELEKLCRFMSYKQYRRVRYNNMKAIVVAHCAVYAILQNNNGLFTDLERKGLLIACLC 563
Db      494 ELEKLCRFMSYKQYRRVRYNNMKAIVVAHCAVYAILQNNNGLFTDLERKGLLIACLC 553
Qy      564 DLDHGFNSYLOKFDHPALALYSTSTMEQHFSQTVSILQLEGNHIFSTLSSSEYEQVL 623
Db      554 DLDHGFNSYLOKFDHPALALYSTSTMEQHFSQTVSILQLEGNHIFSTLSSSEYEQVL 613
Qy      624 EIIIRKAIATDIALYFGNKKOLEBMYQTGSLNLNQHSHRDVIGLMTACDLCSTYKLP 683
Db      614 EIIIRKAIATDIALYFGNKKOLEBMYQTGSLNLNQHSHRDVIGLMTACDLCSTYKLP 673
Qy      684 VTKLTANDIYAEFWABGDEMCKLGIQIPMDMDKDXDEVPOGOLGFYNAVALPCYTTLTQ 743
Db      674 VTKLTANDIYAEFWABGDEMCKLGIQIPMDMDKDXDEVPOGOLGFYNAVALPCYTTLTQ 733
Qy      744 ILPTEPLKACRDNLQWKEVIRGETAMWISGPGAPAPSKSTPE 788
Db      734 ILPTEPLKACRDNLQWKEVIRGETAMWISGPGAPAPSKSTPE 778

```

```

RESULT 8
US-08-951-648-2
; Sequence 2, Application US/08951648
; Patent No. 5932465
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker, Sears Tower Suite 6300
; CITY: Chicago
; STATE: Illinois
; COUNTRY: US
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/34038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 766 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: /note= "The amino acid at position 290 is either Pro
; OTHER INFORMATION: or Leu."
US-08-951-648-2

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Query Match 92.1%; Score 3873; DB 1; Length 766;

Best Local Similarity 95.3%; Pred. No. 0;
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 24 LTDEKKAVALSLHPQVLDLDFVSESVSAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 83
DB 1 LTDEKKAVALSLHPQVLDLDFVSESVSAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 60
QY 84 VVEELNSYIEORLDPTGDNHLLLYELSSIIIRIATKADGPAFLYFGECNNSLCVFIPGK 143
DB 61 VVEELNSYIEORLDPTGDNHLLLYELSSIIIRIATKADGPAFLYFGECNNSLCVFIPGK 120
QY 144 EGPRLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSGSTRIQSVLCPI 203
DB 121 EGPRLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSGSTRIQSVLCPI 180
QY 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 263
DB 181 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 240
QY 264 LDVSKTYFDNIYALDLSLEHIMIYAKNLVNAIDRCALFQVDHKNKELYSDFDISEKEGK 323
DB 241 LDVSKTYFDNIYALDLSLEHIMIYAKNLVNAIDRCALFQVDHKNKELYSDFDISEKEGK 300
QY 301 PFVKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNREVDLYTGYTTRNIIICMPIV 383
DB 301 PFVKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNREVDLYTGYTTRNIIICMPIV 360
QY 384 SRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCALAHCANMYHRIHSECIYRVME 443
DB 361 SRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCALAHCANMYHRIHSECIYRVME 420
QY 444 KLSYHSICTSEBMOGLMFPNIPARICRDIELFHPDIPFENMMPGIFYYMIHRSCTSCF 503
DB 421 KLSYHSICTSEBMOGLMFPNIPARICRDIELFHPDIPFENMMPGIFYYMIHRSCTSCF 480
QY 504 ELEKLCRFIMSVKKNYRVRPYHNMKAIVTAHCVYAILQNNNGLFTDLERKGLIACLC 563
DB 481 ELEKLCRFIMSVKKNYRVRPYHNMKAIVTAHCVYAILQNNNGLFTDLERKGLIACLC 540
QY 564 DLDHGFNSYLOKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYQVL 623
DB 541 DLDHGFNSYLOKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYQVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNNQSHRDVYIGLMMTACDLCSVTYKLP 683
DB 601 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNNQSHRDVYIGLMMTACDLCSVTYKLP 660
QY 684 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDKDEVPQGLGFTYNAVAIPCTYTLITQ 743
DB 661 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDKDEVPQGLGFTYNAVAIPCTYTLITQ 720
QY 744 ILPTEPLKACRDNLQMEKVIIRGEETAMWISGPGAPSKSTPE 788
DB 721 ILPTEPLKACRDNLQMEKVIIRGEETAMWISGPGAPSKSTPE 765
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RESULT 9
US-09-174-437-2
; Sequence 2, Application US/09174437A
; Patent No. 6133007
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/174,437A
; EARLIER FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 08/951,648
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (274)
; OTHER INFORMATION: The amino acid is either Pro or Leu
US-09-174-437-2

Query Match 92.1%; Score 3873; DB 2; Length 766;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

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QY 24 LTDEKKAVALSLHPQVLDLDFVSESVSAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 83
DB 1 LTDEKKAVALSLHPQVLDLDFVSESVSAETVEKMLKRTKNAKDESPKVSRYQDTNNMG 60
QY 84 VVEELNSYIEORLDPTGDNHLLLYELSSIIIRIATKADGPAFLYFGECNNSLCVFIPGK 143
DB 61 VVEELNSYIEORLDPTGDNHLLLYELSSIIIRIATKADGPAFLYFGECNNSLCVFIPGK 120
QY 144 EGPRLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSGSTRIQSVLCPI 203
DB 121 EGPRLIPAGPIQTGTTSAVYAKSRKTLVEDILGDERPFRGTGLSGSTRIQSVLCPI 180
QY 204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 263
DB 181 VTAIGDLIGILELYRHWGKEAFCLSHQEVATANTAMASVAIHQOVQCRGLAKQTELDNPL 240
QY 264 LDVSKTYFDNIYALDLSLEHIMIYAKNLVNAIDRCALFQVDHKNKELYSDFDISEKEGK 323
DB 241 LDVSKTYFDNIYALDLSLEHIMIYAKNLVNAIDRCALFQVDHKNKELYSDFDISEKEGK 300
QY 301 PFVKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNREVDLYTGYTTRNIIICMPIV 383
DB 301 PFVKTKKEIRFSIEKGIAGQVARTGEVANI PDAYADPRFNREVDLYTGYTTRNIIICMPIV 360
QY 384 SRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCALAHCANMYHRIHSECIYRVME 443
DB 361 SRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCALAHCANMYHRIHSECIYRVME 420
QY 444 KLSYHSICTSEBMOGLMFPNIPARICRDIELFHPDIPFENMMPGIFYYMIHRSCTSCF 503
DB 421 KLSYHSICTSEBMOGLMFPNIPARICRDIELFHPDIPFENMMPGIFYYMIHRSCTSCF 480
QY 504 ELEKLCRFIMSVKKNYRVRPYHNMKAIVTAHCVYAILQNNNGLFTDLERKGLIACLC 563
DB 481 ELEKLCRFIMSVKKNYRVRPYHNMKAIVTAHCVYAILQNNNGLFTDLERKGLIACLC 540
QY 564 DLDHGFNSYLOKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYQVL 623
DB 541 DLDHGFNSYLOKRDHPDLAALYSTSTMEQHHFSQTVSIIQLEGNHIFSTLSSSEYQVL 600
QY 624 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNNQSHRDVYIGLMMTACDLCSVTYKLP 683
DB 601 EIIRKAIATDIALYFGNRKQLEBMYQTSGLNNQSHRDVYIGLMMTACDLCSVTYKLP 660
QY 684 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDKDEVPQGLGFTYNAVAIPCTYTLITQ 743
DB 661 VTKLTIANDIYAEFMAEGDEMKGIGIPIPMMDRDKDEVPQGLGFTYNAVAIPCTYTLITQ 720
QY 744 ILPTEPLKACRDNLQMEKVIIRGEETAMWISGPGAPSKSTPE 788
DB 721 ILPTEPLKACRDNLQMEKVIIRGEETAMWISGPGAPSKSTPE 765
```

RESULT 10
US-09-686-055A-2
; Sequence 2, Application US/09686055A
; Patent No. 656087
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/09/686,055A

; CURRENT FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 08/951,648
 ; PRIOR FILING DATE: 1997-10-16
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 766
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; NAME/KEY: misc feature
 ; LOCATION: (290)
 ; OTHER INFORMATION: The amino acid is either Pro or Leu
 ; US-09-686-055A-2

Query Match 92.1%; Score 3873; DB 2; Length 766;
 Best Local Similarity 95.3%; Pred. No. 0;
 Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 24 LTDEKVKAYLSHPQVLDPEFVSESVSAETVEKYLKRTKAKADESPKXVSRYQDTNMOG 83
 DB 1 LTDEKVKAYLSHPQVLDPEFVSESVSAETVEKYLKRTKAKADESPKXVSRYQDTNMOG 60
 QY 84 VYIELNSYIEQRDPTGDNHLLLYEISSIIRIATKADGPAIYFLGSCNNSLCYFIRPGMK 143
 DB 61 VYIELNSYIEQRDPTGDNHLLLYEISSIIRIATKADGPAIYFLGSCNNSLCYFIRPGMK 120
 QY 144 EGGPRLIPAGPITQGTITISAVYAKSRKTLVEDILDERFPRTGSGSTRIGSVLCPI 203
 DB 121 EGGPRLIPAGPITQGTITISAVYAKSRKTLVEDILDERFPRTGSGSTRIGSVLCPI 180
 QY 204 VTAIGDLIGILELYRMGKEAFLSHQEVATANLANASVAIHQOVCRGLAKOTELNDPL 263
 DB 181 VTAIGDLIGILELYRMGKEAFLSHQEVATANLANASVAIHQOVCRGLAKOTELNDPL 240
 QY 264 LDVSKTYFPDNIYVADSLLEHIMTYAKLVNADRCALFOVDHKKELYSDFDIEGEEKG 323
 DB 241 LDVSKTYFPDNIYVADSLLEHIMTYAKLVNADRCALFOVDHKKELYSDFDIEGEEKG 300
 QY 324 PIKKTKEIRFSELEKGIAGOVARTGEVANIYDAVADPRFREVLYTGYTTRNLCMPY 383
 DB 301 PIKKTKEIRFSELEKGIAGOVARTGEVANIYDAVADPRFREVLYTGYTTRNLCMPY 360
 QY 384 SRGSGVIGVQVMVKISGSASFSTKDENNFKMFAVFCALALHCANMYHRIHSECIYRVTME 443
 DB 361 SRGSGVIGVQVMVKISGSASFSTKDENNFKMFAVFCALALHCANMYHRIHSECIYRVTME 420
 QY 444 KLSYHSICTSEEWQGLMRPNLPARICDILFHFIDIGPFENMMPGIVVMYIHSCTGSCF 503
 DB 421 KLSYHSICTSEEWQGLMRPNLPARICDILFHFIDIGPFENMMPGIVVMYIHSCTGSCF 480
 QY 504 ELEKLCRFIMSVKKNYRVRPYHNMKHAVTVAHCVATILNNGLFETDLERKGLLIACLC 563
 DB 481 ELEKLCRFIMSVKKNYRVRPYHNMKHAVTVAHCVATILNNGLFETDLERKGLLIACLC 540
 QY 564 DLDRHGSNSYLOKFDHPALALYSTSTMBQHHFSQVSIILQLEGNIFSTLSSESEYQVL 623
 DB 541 DLDRHGSNSYLOKFDHPALALYSTSTMBQHHFSQVSIILQLEGNIFSTLSSESEYQVL 600
 QY 624 EIRIKAIITDIALYFGNRRQLEEMYTQGSILNHNQSHRDVIGLMMTACDLCGVTCLMP 683
 DB 601 EIRIKAIITDIALYFGNRRQLEEMYTQGSILNHNQSHRDVIGLMMTACDLCGVTCLMP 660
 QY 684 VTKLTANDIYAEFAABDEMKKLGIOPIPMWDRKDBEVPOGOLGFYNAVAIPCYTTLTLO 743
 DB 661 VTKLTANDIYAEFAABDEMKKLGIOPIPMWDRKDBEVPOGOLGFYNAVAIPCYTTLTLO 720
 QY 744 ILPTEPLKACRDNLNQMEKVIIRGEETAMWISGPGAPSKSTPE 788
 DB 721 ILPTEPLKACRDNLNQMEKVIIRGEETAMWISGPGAPSKSTPE 765

RESULT 11
 US-10-296-144-5

; Sequence 5, Application US/10296144
 ; Patent No. 6919185
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer AG
 ; TITLE OF INVENTION: REGULATION OF HUMAN TRANSKETOLASE-LIKE ENZYME
 ; FILE REFERENCE: 110078
 ; CURRENT APPLICATION NUMBER: US/10/296,144
 ; PRIOR FILING DATE: 2002-11-22
 ; PRIOR APPLICATION NUMBER: 60/207,950
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 1284
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-10-296-144-5

Query Match 24.0%; Score 1010; DB 2; Length 1284;
 Best Local Similarity 32.7%; Pred. No. 4,88-97;
 Matches 248; Conservative 143; Mismatches 280; Indels 88; Gaps 18;

QY 70 PKEVR--YQDTNMOGVYIELNSYIEQRDPTGDNHLLLYEISSIIRIATKADGPAIYFL 127
 DB 197 PKLSRNLKQLEKELIFELVKDICNELEVRTLCIKILQNTS-----ILNADRGSLFLV 252
 QY 128 -GECNNSLCVFIRPGMKEG-QRRLIPAGP-----ITQGTISAVYAKSRKT 171
 DB 253 QGRKNG-----PDGIKKCLVSKLFDVCPRSTVEENQODEVRVWAGTIGAHVABSGEP 306
 QY 172 LIVEDILDERFPRTGSGSTRIGSVLCPIVTAIGDLIGILELYRMGKEAFLSHQ 231
 DB 307 VNIIPDYQDERPNCIDISTGYRTTALLCMPITKDSGDVIGVAVYINKNNGEFCSSIDEX 366
 QY 232 VATANLANASVAIHQOVCRGLAKOTELNDPLDVSKTYFPDNIYVADSLLEHIMTYAKLV 291
 DB 367 VSSSYLOFGDIGIRNMQLEKSGQLEIKRQVLLDLARMIFFBQSTIEHWVFRILTMOST 426
 QY 292 VNADRCALFOVDHKKELYSDF-----DIGEEKRPFKTK--EIRFSEKGIAGOV 344
 DB 427 IQCORVQIILVHEADKGSFSEVDFEANDLSBBE-----ATSRISPYESRPPINIGITGVH 482
 QY 345 APTGEVLANIPDAVADPRFREVLYTGYTTRNLCMPY-SRGSGVIGVQVMVKISGSASF 403
 DB 483 ATGETVNPNAVEDRPFASVDENSCFGRSLTLCALIKNSLDQIIGVLIQIKRNEIDF 542
 QY 404 SKTDENNFKMFAVFCALALHCANMYHRIHSECIYRVTMEKLSYHSICTSEEWQGL----- 459
 DB 543 TKQDENFVEAFALFCMGHINTHMEKATVAAKQSVTLLEVLSYHASATWDEAHRLRKQK 602
 QY 460 -----MRPNLPARICDILFHFIDIGPFEN-----MWPG 488
 DB 603 QQQQAVGLRQAPLSLPPRKQLQRLRVPASVHRLHDFKFDITHFDDDTLKACLRFLD 662
 QY 489 I-FVMYIHSCTGSCFCELEKLCRFIMSVKKNYRVRPYHNMKHAVTVAHCVATILNNGN-- 545
 DB 663 LDVEVERFH-----IDYEVLCRWLLSVKKNYRVRPYHNMKHAVTVAHCVATILNNGN-- 715
 QY 546 GLFTDLERKGLLIACLDHHRGFSNSYLOKFDHPALALYSTSTMBQHHFSQVSIILQ 605
 DB 716 KITGEIECLALIIIGCLCHDDHGTNNSPQIKASSPLAQLYSTVMEHHHFDCLMILTS 775
 QY 606 EGHNISTLSSESEYQVLEIIRKAIITDIALYFGNRRQLEEMYTQGSILNHNQSHRDR 664
 DB 776 RGNQILANSSDDYCRVIRVLEDAIISTDLAVYFKKGGPLESVSOPTSYWVABEP-FAL 834
 QY 665 VIGLMMTACDLCGVTCLMPYTKLTANDIYAEFAABEG-EKKKLGIOPIPMWDRKDBEV 723
 DB 835 LRAMSTVCDLSAITKWELEKRVADIVSFEQGMKEKQELNITPIDIMNREKEDLP 894
 QY 724 QGOLGFYNAVAIPCYTTLTLOILPTEPLKACRDNLNQ 762
 DB 895 MMQVNFIDISICLPYIEFAIISDKLEPLVAGVADNRGHW 933

```

RESULT 12
US-08-480-547A-10
/ Sequence 10, Application US/08480547A
/ Patent No. 5652131
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Corbin, Jackie D.
/ APPLICANT: Ferguson, Kenneth M.
/ APPLICANT: Francis, Sharon H.
/ APPLICANT: Kadlecsek, Ann
/ APPLICANT: Loughney, Kate
/ APPLICANT: McAllister-Lucas, Linda M.
/ APPLICANT: Sonnenburg, William K.
/ APPLICANT: Thomas, Melissa K.
/ TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
/ TITLE OF INVENTION: Phosphodiesterase Materials and Methods
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,547A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5652131and, Greca E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 32791
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-0448
/ TELEFAX: (312) 474-6300
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 875 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-480-547A-10

Query Match 21.8%; Score 918; DB 1; Length 875;
Best Local Similarity 30.2%; Pred. No. 1.4e-87;
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

QY 10 SCFRRLTEGFLSPSLTDE-----KTKAY---LSLHPQLVDE-----FVSSVSASE 51
DB 68 SC-----SCPLDPPSPRAESSVPGTPTRKISABFDRPLRPIYAKDSGTVSFLSDSKKE 122
QY 52 TVEKWLKRTNKAKDEPPKPEVSRDYDTMMQGVVVELNSYIEQRDLDTGDNHLLLYELSS 111
DB 123 QMPRLTSPRDNDGQCSR-----LLELVNDISHDVTLCKRIFLHNG 168
QY 112 IIRIATKADGALYPLGECNSLGVPIPGMEKGQPRLLIPAGPTQGT----- 160
DB 169 LI-----SADRYSLFLVCEBDSNDKFLI-----SLRP---DVAEGSTLEBASNNCIRL 213
QY 161 -----ISAVASRSKRTLLVEDLIDGRFPRGTGSGTRIGSVLCPIYTAIGDLIGILE 215
DB 214 EWNKGIQGVNAAFGEPLNKDAIEDPRFAEVDQITGYTOSILCPINKHREEVAVGAQ 273
QY 216 LY--RHMGKAFCLSHQEVATNLAMASVAIHQVQVCRGIAQTEINDELFDVSKTYFPDN 273

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DB 274 AINKSGNGGTETFEKDEKDFAYLAFCGIVLHMQLYETSLLENKRNQVLLDLASLIFEE 333
QY 274 IVALDSLEHIMITAKONLVNADRCALFOYDHKNKELYSDLPDIGEKKGKPIPKTKTEIR 333
DB 334 QQSLSEVILKKTAAITISPMQVKCTTFIVDEDCSDSFSSVTHMECELEKESDITLRERD 393
QY 334 FS-IEKGIAGQVARTGEVLANIPDAYADPRF--NREVDLYGTYTRNLLCMPYVS--RGS 387
DB 394 ANRIWYMYAQVYKNTMEPLNIPDYSKDRFPMTENMGNINQOCIRSLCTPIKNGKXK 453
QY 398 VIGVQVQVNTKISGS-----AFSKTDENNFKMPAYFCALALCANNYHRIHSECIYRTM 442
DB 454 VIGVQVQVNTKISGS-----AFSKTDENNFKMPAYFCALALCANNYHRIHSECIYRTM 442
QY 443 EKLSTYHSICTSEEMQGLRNFILPARI-----CRDIELFHPDIPGPNMWPPIFYVMI 494
DB 514 EULSTYHSAABEETRELO--SLAAVVPDQAOTLKTDTDSFSDFELSDLETALCTIRMTD 571
QY 495 HRSCTSCFELEKLCRFYMSYKQVYR--VPYHNMKHAATVAHCYVALIQQN--NGLFTDL 551
DB 572 LNVQNPQMKHEVLCKWILSVKQYRKVAHYHNRHAFNTAQCMFPAALAKAKIQKRLTDL 631
QY 552 ERKGLILACLCHDLDRGFSNSYLOKFDPIALALYSTIMEQHHSQTVSILQEGHNI 611
DB 632 BILALLIALSHDIDHRGVNSYIORSSEHPLAOLYCHSIMEHHHFDQCLMILNSPQOIL 691
QY 612 STLSSEVEQVLEIRKAIITADLALYFGNRKQLEEMVQTSGLNHNQSHRDRVIGLMMT 671
DB 692 SGLSTEEYKTKTKIKOAILATDIALYKRGSEFELMKQNFNEDHQKELFIAMLT 751
QY 672 ACDLCSYTKLPVTLTANDIYAEFWAGD--EMKKLGIOPIPMDDRKDEVPQQLAGFY 730
DB 752 ACDLSAIRKPPPIQRIALVATEFPDGDREKELNIEPADLNNREKKNIPMSQVQFI 811
QY 731 NAVAIPCTYTLTQILPPEPPLIKACRDLNMQEKVIRGEFTAMISG 777
DB 812 DAICQLYEALTHVSEDCFPILDGCRKNRQKQALAEQKXTL-ING 857

RESULT 13
US-08-250-847B-10
/ Sequence 10, Application US/08250847B
/ Patent No. 5702936
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Corbin, Jackie D.
/ APPLICANT: Ferguson, Kenneth M.
/ APPLICANT: Francis, Sharon H.
/ APPLICANT: Kadlecsek, Ann
/ APPLICANT: Loughney, Kate
/ APPLICANT: McAllister-Lucas, Linda M.
/ APPLICANT: Sonnenburg, William K.
/ APPLICANT: Thomas, Melissa K.
/ TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
/ TITLE OF INVENTION: Phosphodiesterase Materials and Methods
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/250,847B
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5702936and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-250-847B-10

Query Match      21.8%; Score 918; DB 1; Length 875;
Best Local Similarity 30.2%; Pred. No. 1.4e-87;
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

QY 10 SCFRRLTECFPLSLTDE-----KXKAY---LSLHPQVLDE-----FVSEVSAR 51
DB 68 SC-----SCPLQSPRAESSVPPTPRKISASEFDRPLRPVVKDSEGTVSFLSDSKKE 122
QY 52 TVEKMLKRTNKAKDESPKREVSRYODTNMGVVYELNSYIEORLDTGDNHLLLYELSS 111
DB 123 QMPLTSPRFNDNDEGDCSR-----LLELVNDISSHLVDTALCHKIFLHIHG 168
QY 112 IIRIATKADGFALYFEGCNSNLGVPIPGMKEGOPRLIPAGPIGQTT----- 160
DB 169 LI-----SADRYSLFLVCEBSSNDKFLI-----SRLF---DVAEGSTLEASNNCIRL 213
QY 161 -----ISAVYASRKTLVEDILGDERFRPGTLEGSTRIGSLPIYALIGDLIGILE 215
DB 214 ENMKGVGHVAAGPEPLNTKDAYEDPRFAEVDQITGYKQSLCMTKKNHREEVGVAAQ 273
QY 216 LV--RHMGEAFCLSHOEVAITANLMAVASVALHQVQCRGLAKOTELNDPLLDVSKTYFDN 273
DB 274 AINKSGNGSTFEKREKBPALYLCGYLVLAHQLYETSLKKNQVLLDLASLILFE 333
QY 274 IYVADSLLEHIMIVAKLVNADRCALFOVDHKNKLYSDLFIDGEKEGPIFEKTEIR 333
DB 334 QQSLLEVILKKIATITISPMQVQCTIFIVDEDCSSPVSFVHMECEBELKESDPLTRERD 393
QY 334 PS-IEKGIAQVARTGEVNLIPRAYADPRP---NREVDLYTGTTNIIICMPIVS--RGS 387
DB 394 ANRINVTYQYVKNWPEPLNIPVSKDKRPPWTNENKGINQOCIRSLCTPIKNGK 453
QY 388 VIGVGVNVNKSISG-----AFSKTDENNFMFAVFCALALHCANMYRIRHSECIYRV 442
DB 454 VIGVGVNVNMEETGTGKVAFAFNNDDEQLEAFVIFCGLGQNTOMTBAVRAAKQVTL 513
QY 443 EKLSYHSICTSEEMOGIMRPNLPARI-----CRDIELFHPDIGPFENMWGFIYVMI 494
DB 514 EYLSYHSAABEETRELQ--SLAAVVPQAQTLKITDFFSDEFLSLDELALCTIRAF 571
QY 495 HNSCGTSCPELELCRFIMSVKKNYR--VPIYHMKAAVTVYAHCMYALQNN--NGLEF 551
DB 572 LNVQFQMGHGEVLCWKILSVKKNYRKNVAYHNMRAHFNTPAOCMFALKKGKIQKRL 631
QY 552 ERKGLLIACCHLDHNGFNSYLOKFDHPALALYSTTMEOHNFSGTVASIILOEGH 611
DB 632 EYIALIALLSHDHRGVNNSYIQSEHPLAQLYCHSIMEHHFPOCLMILNSPQOIL 691
QY 612 STLSSEYEVLEIIRKAIATDIALYFGNKKOLEEMYQTSGLNHLNQSHRDYVGLMT 671
DB 692 SGLSIEBYKTKLTIKQAILATDIALYIKRGEFFELIMKNQFALPDPHOKELFLAM 751
QY 672 ACULGSTYKMPYTKLTANDIYAFMAEGD-EMKGLGIQPIPMMDRKRQBPVCGOLGY 730
DB 752 ACULSALTKEWPIQORIALVELVATEFPDQGRERKELNIBPADLNKREKKNKIPSMOV 811

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QY 731 NAVAIPCTYTLTQILPPTPEPLKACRDNLNOMEKVIIRGETAMWISG 777
DB 812 DAICQLYEAHLTVSEDCFPLLDGRKNRQKQWALAEQOEKTL-ING 857

RESULT 14
US-08-463-949A-10
Sequence 10, Application US/08463949A
Patent No. 5955583
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Corbin, Jackie D.
APPLICANT: Bergeson, Kenneth M.
APPLICANT: Francis, Sharon H.
APPLICANT: Kadlecsek, Ann
APPLICANT: Loughney, Kate
APPLICANT: McAllister-Lucas, Linda M.
APPLICANT: Sonnenburg, William K.
APPLICANT: Thomas, Melissa K.
TITLE OF INVENTION: Cyclic GMP-Binding, Cyclic GMP-Specific
TITLE OF INVENTION: Phosphodiesterase Materials and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,949A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,051
FILING DATE: 27-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5955583and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32706
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-949A-10

Query Match      21.8%; Score 918; DB 1; Length 875;
Best Local Similarity 30.2%; Pred. No. 1.4e-87;
Matches 250; Conservative 140; Mismatches 341; Indels 96; Gaps 20;

QY 10 SCFRRLTECFPLSLTDE-----KXKAY---LSLHPQVLDE-----FVSEVSAR 51
DB 68 SC-----SCPLQSPRAESSVPPTPRKISASEFDRPLRPVVKDSEGTVSFLSDSKKE 122
QY 52 TVEKMLKRTNKAKDESPKREVSRYODTNMGVVYELNSYIEORLDTGDNHLLLYELSS 111
DB 123 QMPLTSPRFNDNDEGDCSR-----LLELVNDISSHLVDTALCHKIFLHIHG 168
QY 112 IIRIATKADGFALYFEGCNSNLGVPIPGMKEGOPRLIPAGPIGQTT----- 160
DB 169 LI-----SADRYSLFLVCEBSSNDKFLI-----SRLF---DVAEGSTLEASNNCIRL 213

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[illegible]

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/464,410A
? FILING DATE: June 5, 1995
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: No. 6037119and, Greta E.
? REGISTRATION NUMBER: 35,302
? REFERENCE/DOCKET NUMBER: 27866/35705
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (312) 474-6300
? TELEFAX: (312) 474-0448
? TELEX: 25-3856
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 875 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS-08-464-410A-10

```

Query Match	21.8%;	Score 918;	DB 2;	Length 875;
Best Local Similarity	30.2%;	Pred. No. 1.4e-87;		
Matches 250;	Conservative 140;	Mismatches 341;	Indels 96;	Gaps 20;
Qy	10	SCFRRLTECFSPSLTDE-----KVAAY--LSLHPQVLDE-----FVSEVSAAE	51	
Db	68	SC-----SCFLQPSPPRAESSVPGTPRTKISASEPDRPLRIVIKDSQGVAFSLDSCKE	122	
Qy	52	TYEKTLKRTKNKAKDESPKESRYQDTNMQGVYELNSYIEQRLDPDGGDHLHLLYELSS	111	
Db	123	QMPLTSPRFNDDEDCSR-----LLELVKDISHLDPVALCHKFLIHNG	168	
Qy	112	IIRLATQADGAFALFYLGECNNNSLCVFIIPGMEKGQPLIPAGPIYQGT-----	160	
Db	169	LI-----SADRYSLFLVCEBDSNDKFLI-----SLPFI---DVABESTLEBANNCRL	213	
Qy	161	-----ISAVYAKSRKTLVLEDIDIGDERPRPGTGESGTRIQSVLCIPYVALDGLIGILE	215	
Db	214	EMNKGIQGHVAAGEPLINIDAYEDPRFNAEVLQDITGYKQISLICMPYIKHNREEVGAQA	273	
Qy	216	LY--RHWKEAFCLSHQEVATNANLMAVAIHQVQCRGLAKQTELDPLIDVSKTYFDN	273	
Db	274	AINKSGNGSTFEKEKEDPAAALYAFGCIYVLHNAQLYETSLLENKRNQVLLDLASLIFEE	333	
Qy	274	IYALIDSLLEHIMYAKLVNADRCALQOVHKNKELSDLEFDIGEEKRGKPIFKKTEIR	333	
Db	334	QQSLEVLTKKIALATITISPMVOYQKTLITIVBDCSDSSVFHMECEBIEKSSDPTLTERD	393	
Qy	334	FS--LEKGIAGQVARTGEVLNIPDAVADPRF---NREVDLYGTYYTNILCMPYVS--RGS	387	
Db	394	ANRINMYAQVYKNTEPLNIPDVSCKDKRPMTNEMNGINQOCIRSLCTPRINGKKNK	453	
Qy	388	VIGVYQWNTKISGS-----APSKTDENNFKMAFVFCALALHCANNYRIHSECTIKRYTM	442	
Db	454	VIGVQQLVNMDEETGKYKAFNRNDEQFLERFAVFCISIGIONTOMYEAVERAMAKOWYTL	513	
Qy	443	EKLSYHSCISEEMQGLMRPNLPRI-----CRDIELFHPDIGEPENMPCGIFYMY	494	
Db	514	EVLSYHNAASAAEBERELIQ--SLAAVAPSAQYTLKITDPSFSDLESLDTLCTIRNFTD	571	
Qy	495	HRSCTGSCFELEKCRPFIMSVKKQNYR--VEYHNMKHAAVTAHCHYATILQNN--NGLFPTDL	551	
Db	572	LNLVQNMGMHEVLCKWILSVKKNYRKNVAIYHNMRHAFNTAQCMCFALYKQKQKRLTDL	631	
Qy	552	ERKGLLIACLCHDLDRGFNSNYLQKFDPLALALYSTSTYBQHNFSQTVSILQEGHNIF	611	
Db	632	EIALTLIALSHDLDRGVNNSYIQRSEHPLAQYCHSIMEHNHFDQCLMINSRGNOL	691	
Qy	612	STLSSSEYQVLEIRKALITATPLALYFGNRKQLEMYQVGSINLHNSHRDRYIGLMT	671	
Db	692	SGSISEEYKTKTKIKKAILATDALYIKRGEFFELIMKNQFLBPDHOKELFLAMLT	751	

QY 672 ACDCSVTKLWPTKLTANDIYAEFWAEGD-EMKKLGIGPIPMMDRDKDEVPOGQLGFY 730
DB 752 ACDSLAIKFWPIQORIAELVATEFPDQDRERKEINIEPADLMNREKKNKIPSMQVGFPI 811
QY 731 NAVAIPTTTLTQILPTEPBLKACRDNLNOMEKVIRGEETAMWISG 777
DB 812 DAICLOLYEALTHVSEDCFPLLDGCCKNNQKWOALAEQQEKTLL-ING 857

Search completed: January 10, 2006, 13:56:39
Job time : 30 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:55:36 ; Search time 116 Seconds
(without alignments)
2867.174 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206
Sequence: 1 MEDGSPNNASCFRRRLTECF.....GPCPAPSKSTPEKLVKVED 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4206	100.0	796	3	US-09-321-801-15 Sequence 15, Appl
2	4206	100.0	796	4	US-10-618-252-15 Sequence 15, Appl
3	4123	98.0	794	6	US-11-045-860-1 Sequence 1, Appl1
4	4080	97.0	779	6	US-11-045-860-3 Sequence 3, Appl1
5	3997	95.0	803	4	US-10-440-998-4 Sequence 4, Appl1
6	3993	94.9	789	3	US-09-321-801-2 Sequence 2, Appl1
7	3993	94.9	789	4	US-10-618-252-2 Sequence 2, Appl1
8	3951.5	93.9	773	4	US-10-202-107-2 Sequence 2, Appl1
9	3951.5	93.9	773	5	US-10-887-276-2 Sequence 2, Appl1
10	3878	92.2	779	3	US-09-420-190-1 Sequence 1, Appl1
11	3878	92.2	779	4	US-10-458-839-1 Sequence 1, Appl1
12	3878	92.2	779	4	US-10-440-998-6 Sequence 6, Appl1
13	3873	92.1	766	4	US-10-440-998-2 Sequence 2, Appl1
14	3867	91.9	791	3	US-09-321-801-4 Sequence 4, Appl1
15	3867	91.9	791	4	US-10-618-252-4 Sequence 4, Appl1
16	1795	42.7	362	6	US-11-045-860-2 Sequence 2, Appl1
17	1726	41.0	329	5	US-10-771-833-26 Sequence 26, Appl
18	1726	41.0	329	5	US-10-886-949-26 Sequence 26, Appl
19	1543	36.7	300	3	US-09-321-801-13 Sequence 13, Appl
20	1543	36.7	300	3	US-09-321-801-13 Sequence 13, Appl
21	1010	24.0	1284	4	US-10-618-252-13 Sequence 13, Appl
22	1010	24.0	1284	4	US-10-256-144-5 Sequence 5, Appl1
23	1010	24.0	1284	6	US-11-097-443-42339 Sequence 5, Appl1
24	967.5	23.0	934	4	US-10-168-402-39 Sequence 39, Appl
25	965.5	23.0	934	3	US-09-891-216-12 Sequence 12, Appl
26	965.5	23.0	934	3	US-09-891-216-15 Sequence 15, Appl
27	965.5	23.0	934	4	US-10-168-402-2 Sequence 2, Appl1

28	931.5	22.1	684	4	US-10-168-402-6 Sequence 6, Appl1
29	929	22.1	684	3	US-09-891-216-14 Sequence 14, Appl
30	929	22.1	684	4	US-10-168-402-4 Sequence 4, Appl1
31	929	22.1	684	4	US-10-746-197-1 Sequence 1, Appl1
32	924	22.0	833	3	US-09-891-216-3 Sequence 3, Appl1
33	918	21.8	875	4	US-10-115-515-10 Sequence 10, Appl
34	918	21.8	875	5	US-10-353-575A-10 Sequence 10, Appl
35	912.5	21.7	874	4	US-10-427-223-3 Sequence 3, Appl1
36	912.5	21.7	874	5	US-10-837-081-3 Sequence 3, Appl1
37	912.5	21.7	875	4	US-10-115-515-23 Sequence 23, Appl
38	912.5	21.7	875	4	US-10-094-168B-5 Sequence 5, Appl1
39	912.5	21.7	875	5	US-10-771-833-1 Sequence 1, Appl1
40	912.5	21.7	875	5	US-10-886-949-1 Sequence 1, Appl1
41	912.5	21.7	875	5	US-10-353-575A-23 Sequence 23, Appl
42	909	21.6	921	3	US-09-883-825-39 Sequence 39, Appl
43	909	21.6	921	4	US-10-094-989-5 Sequence 5, Appl1
44	909	21.6	921	4	US-10-697-894-39 Sequence 39, Appl
45	908	21.6	942	3	US-09-883-825-43 Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-09-321-801-15
Sequence 15, Application US/09321801
Patent No. US20020115176A1
GENERAL INFORMATION:
APPLICANT: Lanfear, Jeremy
APPLICANT: Robas, Nicola M.
TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
FILE REFERENCE: PC9477A
CURRENT APPLICATION NUMBER: US/09/321,801
EARLIER FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: 9826777.6
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 9823882.7
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 9811500.9
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: 9908247.1
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 9910801.1
EARLIER FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 796
TYPE: PRT
ORGANISM: Mouse
US-09-321-801-15

Query Match 100.0%; Score 4206; DB 3; Length 796;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEDGSPNNASCFRRRLTECFSLTDEKVAAYLSHPQVLEDFVSSVSATVEKMLKRR	60
DB	1	MEDGSPNNASCFRRRLTECFSLTDEKVAAYLSHPQVLEDFVSSVSATVEKMLKRR	60
QY	61	TNNAKDEPSKESRQDTTMQGVYELNSYTORLDTGGDNLLLYESSIRIRTKAD	120
DB	61	TNNAKDEPSKESRQDTTMQGVYELNSYTORLDTGGDNLLLYESSIRIRTKAD	120
QY	121	GFALYFEGCNSLQVFIIPGMEKQPRLLIPAGPITQGTITISAVYAKSRKTLVBDLIGD	180
DB	121	GFALYFEGCNSLQVFIIPGMEKQPRLLIPAGPITQGTITISAVYAKSRKTLVBDLIGD	180
QY	181	ERRPRGTGSGRIGSVLCPIVTAIGDILIGILEYRHMKEAFCLSHQEVATANTAWA	240
DB	181	ERRPRGTGSGRIGSVLCPIVTAIGDILIGILEYRHMKEAFCLSHQEVATANTAWA	240
QY	241	SVAIHQVQVRGLAKQTELDPLVDVSKYTFDNIIVAIIDSLHEIMITYAKRLVNAARCALF	300


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Db      241 SVAIHQVQCRGLAQOTELANDFLDVSKTYYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Qy      301 QVDHKNKELYSDFDIGEKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIPDAYADP 360
Db      301 QVDHKNKELYSDFDIGEKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIPDAYADP 360
Qy      361 RFRREVDTLTYGTTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Db      361 RFRREVDTLTYGTTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVWMEKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVWMEKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PERNMMPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Db      481 PERNMMPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Qy      541 LQNNNGLFPTDLERKGLIACLDHHRGFSNSYLQKFDHPALALYSTIMEOHHSQTV 600
Db      541 LQNNNGLFPTDLERKGLIACLDHHRGFSNSYLQKFDHPALALYSTIMEOHHSQTV 600
Qy      601 SILQLEGNHIFSTLSSSEYEOVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Db      601 SILQLEGNHIFSTLSSSEYEOVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
Qy      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDRDRD 720
Db      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDRDRD 720
Qy      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPRLKACRDNLQWMEKYIRGETAMWISGPGP 780
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Db      781 APSKSTPEKLVKVED 796

RESULT 2
US-10-618-252-15
; Sequence 15, Application US/10618252
; Publication No. US20040018542A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robas, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477B
; CURRENT APPLICATION NUMBER: US/10/618,252
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: 9826777.6
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 9823882.7
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 9811500.9
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 9908247.1
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 9910801.1
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Mouse
US-10-618-252-15

Query Match      100.0%; Score 4206; DB 4; Length 796;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 796; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 TNKADBPSPKXVSRYQDTNNQGVVYELNSYIEORLDTGCGNNHLLYELSSIRATPAD 120
Qy      121 GPALYFLGECNNNSLCVFIIPGMKKGOPRLIPAGPTQGTSTISAVASRKTLVLEDLIGD 180
Db      121 GPALYFLGECNNNSLCVFIIPGMKKGOPRLIPAGPTQGTSTISAVASRKTLVLEDLIGD 180
Qy      181 BRFPRTGLBESGTRIQSYLCLPIVTAIGDLIGILELYHMKKEAFCLSHOBVATANLMA 240
Db      181 BRFPRTGLBESGTRIQSYLCLPIVTAIGDLIGILELYHMKKEAFCLSHOBVATANLMA 240
Qy      241 SVAIHQVQCRGLAQOTELANDFLDVSKTYYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Db      241 SVAIHQVQCRGLAQOTELANDFLDVSKTYYPDNIVAIDSLLEHIMIYAKNLVNAORCALF 300
Qy      301 QVDHKNKELYSDFDIGEKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIPDAYADP 360
Db      301 QVDHKNKELYSDFDIGEKEGKPIFKTKETIRFSIEKGIAGQVARTGVANIPDAYADP 360
Qy      361 RFRREVDTLTYGTTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Db      361 RFRREVDTLTYGTTTNNILCMPIVSRGSYIGVQVWVKISGSAFSKTDENNFKMAVFCAL 420
Qy      421 ALHCANMYHRIHSECIYRVWMEKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Db      421 ALHCANMYHRIHSECIYRVWMEKLSYHSICTSEBWQGLMRPNLPARICRDIELFHPDIG 480
Qy      481 PERNMMPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Db      481 PERNMMPGIFVYMIHRSCTSCFELEKLCRFIMSVKKNYRVPYHNMKAATVAHCMYAI 540
Qy      541 LQNNNGLFPTDLERKGLIACLDHHRGFSNSYLQKFDHPALALYSTIMEOHHSQTV 600
Db      541 LQNNNGLFPTDLERKGLIACLDHHRGFSNSYLQKFDHPALALYSTIMEOHHSQTV 600
Qy      601 SILQLEGNHIFSTLSSSEYEOVLEIRKAIATDLALYFGNRKOLEMYQTGSLNLHNS 660
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Qy      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDRDRD 720
Db      661 HDRVIGLMTACDLCSTVKLMPVTKLTANDIYAEFMAEGDEMKLGIQPIPMDRDRD 720
Qy      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPRLKACRDNLQWMEKYIRGETAMWISGPGP 780
Db      721 EVPOGOLGFYNAVAIPCTYTLTQILPTEPRLKACRDNLQWMEKYIRGETAMWISGPGP 780
Qy      781 APSKSTPEKLVKVED 796
Db      781 APSKSTPEKLVKVED 796

RESULT 3
US-11-045-860-1
; Sequence 1, Application US/11045860
; Publication No. US20050202550A1
; GENERAL INFORMATION:
; APPLICANT: Pandit, Jaywardan
; APPLICANT: Pandit, Jaywardan
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5'-CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
; FILE REFERENCE: PC25194A
; CURRENT APPLICATION NUMBER: US/11/045,860
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/552,761
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3

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SEQ ID NO 1
LENGTH: 794
TYPE: PRP
ORGANISM: Rattus norvegicus
US-11-045-860-1

Query Match 98.0%; Score 4123; DB 6; Length 794;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 783; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

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DB 61 TTKAKDEBPKEVSRYQDTNMQGVYELNSYIEORLDGTGDNHLLYELSSIRIATKAD 120
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DB 121 GPALYFLGSCNNSLCVFIPPGMKEGOPRLIPAGPTTGTTSAYAKSKRTLLVEDILGD 180
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DB 181 EEPFRGTGLESGRISVCLPTVTAIGDLIGLILYRHMGEAFCLSHOEVAATNLAWA 240
QY 241 SVAIHQVQCRGLAKQTEINDFLDVSCTYFDNIVAIDSLHEHIMIYAKNLVNADECALF 300
DB 241 SVAIHQVQCRGLAKQTEINDFLDVSCTYFDNIVAIDSLHEHIMIYAKNLVNADECALF 300
QY 301 QVDHKKELYSDFDIEGEEKGKPIRKTKEIRFSIEKGIAGQAVATGEVLNI PDAYADP 360
DB 301 QVDHKKELYSDFDIEGEEKGKPIRKTKEIRFSIEKGIAGQAVATGEVLNI PDAYADP 360
QY 361 RFRREVDLTGYTTRNIIICMPYIRSGSVIGVQVQWVKISGSAFSTKDENNFKMAFVFCAL 420
DB 361 RFRREVDLTGYTTRNIIICMPYIRSGSVIGVQVQWVKISGSAFSTKDENNFKMAFVFCAL 420
QY 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEBQGLMRFNLPARICRDIELFPHDIG 480
DB 421 ALHCANMYHRIHSECIYRVTEKLSYHSICTSEBQGLMRFNLPARICRDIELFPHDIG 480
QY 481 PFENMMPGIFVYMIHRSCTGSCFLEKLCRFIMS VKKNYRRVYHNMKAATVAHCVTAI 540
DB 481 PFENMMPGIFVYMIHRSCTGSCFLEKLCRFIMS VKKNYRRVYHNMKAATVAHCVTAI 540
QY 541 LQNNNGLFPTDLERKGLIACLDHHRGSNSYLQKFDHPLAALYSTMEQHHSQTV 600
DB 541 LQNNNGLFPTDLERKGLIACLDHHRGSNSYLQKFDHPLAALYSTMEQHHSQTV 600
QY 601 SIQLGEGHIFSTLSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSILNHNOS 660
DB 601 SIQLGEGHIFSTLSSEYEQVLEIRKAIITADLALYFGNRKQLEBMYQTSILNHNOS 660
QY 661 HRDRIYGLAMTACDLSVTKLMPVTKLTANDIYAEFMAEGDEMKLGIOPI PMMDRDKRD 720
DB 661 HRDRIYGLAMTACDLSVTKLMPVTKLTANDIYAEFMAEGDEMKLGIOPI PMMDRDKRD 720
QY 721 EYVQGGQGFNNAVAIPCYTTLTGQILPTEPRLVACPDNLNOMKEVIRGEETAMWISGPG 780
DB 721 EYVQGGQGFNNAVAIPCYTTLTGQILPTEPRLVACPDNLNOMKEVIRGEETAMWISGPG 780
QY 781 APSKSTPEKLANVVED 796
DB 779 ATSKSTSEKTRKYVD 794

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RESULT 4

US-11-045-860-3

Sequence 3, Application US/11045860

Publication No. US20050202550A1

GENERAL INFORMATION:

APPLICANT: Pfizer, Inc.

APPLICANT: Pandit, Jayvardan
TITLE OF INVENTION: CRYSTAL STRUCTURE OF 3', 5' -CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
FILE REFERENCE: PC25194A
CURRENT APPLICATION NUMBER: US/11/045,860
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 60/552,761
PRIOR FILING DATE: 2004-03-12
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.3

SEQ ID NO 3

LENGTH: 779

TYPE: PRP

ORGANISM: Mus musculus

US-11-045-860-3

Query Match 97.0%; Score 4080; DB 6; Length 779;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 24 LTDEKAYLSLHPQVLDEFVSEVSATVEKMLKRTTKAKDEBPKEVSRYQDTNMQ 83
DB 7 LTDEKAYLSLHPQVLDEFVSEVSATVEKMLKRTTKAKDEBPKEVSRYQDTNMQ 66
QY 84 VYELNSYIEORLDGTGDNHLLYELSSIRIATKADGPALYFLGSCNNSLCVFIPGK 143
DB 67 VYELNSYIEORLDGTGDNHLLYELSSIRIATKADGPALYFLGSCNNSLCVFIPGK 126
QY 144 EGOPRLIPAGPTTGTTSAYAKSKRTLLVEDILDEBFPGTGLSGSTRISQVCLPI 203
DB 127 EGOPRLIPAGPTTGTTSAYAKSKRTLLVEDILDEBFPGTGLSGSTRISQVCLPI 186
QY 204 VTAIGDLIGLILYRHMGEAFCLSHOEVAATNLAWASVAIHQVQCRGLAKQTEINDFL 263
DB 187 VTAIGDLIGLILYRHMGEAFCLSHOEVAATNLAWASVAIHQVQCRGLAKQTEINDFL 246
QY 264 LDVSKTYFDNIVAIDSLHEHIMIYAKNLVNADECALFOVDHKKELYSDFDIEGEEKG 323
DB 247 LDVSKTYFDNIVAIDSLHEHIMIYAKNLVNADECALFOVDHKKELYSDFDIEGEEKG 306
QY 324 PIFKTKKEIRFSIEKGIAGQAVATGEVLNI PDAYADPRENREVDLTGYTTRNIIICMPY 383
DB 307 PIFKTKKEIRFSIEKGIAGQAVATGEVLNI PDAYADPRENREVDLTGYTTRNIIICMPY 366
QY 384 SRGSVIGVQVQWVKISGSAFSTKDENNFKMAFVFCALALHCANMYHRIHSECIYVTE 443
DB 367 SRGSVIGVQVQWVKISGSAFSTKDENNFKMAFVFCALALHCANMYHRIHSECIYVTE 426
QY 444 KLSYHSICTSEBQGLMRFNLPARICRDIELFPHDIGPFENMMPGIFVYMIHRSCTGSCF 503
DB 427 KLSYHSICTSEBQGLMRFNLPARICRDIELFPHDIGPFENMMPGIFVYMIHRSCTGSCF 486
QY 504 ELEKLCRFIMS VKKNYRRVYHNMKAATVAHCVTAI LQNNNGLFPTDLERKGLIACLDH 563
DB 487 ELEKLCRFIMS VKKNYRRVYHNMKAATVAHCVTAI LQNNNGLFPTDLERKGLIACLDH 546
QY 564 DLDHRGSNSYLQKFDHPLAALYSTMEQHHSQTVLSIQLGEGHIFSTLSSEYEQVLE 623
DB 547 DLDHRGSNSYLQKFDHPLAALYSTMEQHHSQTVLSIQLGEGHIFSTLSSEYEQVLE 606
QY 624 EIRKAIITADLALYFGNRKQLEBMYQTSILNHNOSHDRVIGLMMTACDLSVTKLMP 683
DB 607 EIRKAIITADLALYFGNRKQLEBMYQTSILNHNOSHDRVIGLMMTACDLSVTKLMP 666
QY 684 VTKLTANDIYAEFMAEGDEMKLGIOPI PMMDRDKDEVPQGGQGFNNAVAIPCYTTLTG 743
DB 667 VTKLTANDIYAEFMAEGDEMKLGIOPI PMMDRDKDEVPQGGQGFNNAVAIPCYTTLTG 726
QY 744 ILPTEPRLVACPDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLANVVED 796
DB 727 ILPTEPRLVACPDNLNOMKEVIRGEETAMWISGPGAPSKSTPEKLANVVED 779

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RESULT 5
 US-10-440-998-4
 ; Sequence 4, Application US/10440998
 ; Publication No. US20030215919A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Loughney, Kate
 ; TITLE OF INVENTION: Phosphodiesterase 8A
 ; FILE REFERENCE: 27866/35047
 ; CURRENT APPLICATION NUMBER: US/10/440,998
 ; CURRENT FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: US/09/686,055
 ; PRIOR FILING DATE: 2000-10-11
 ; PRIOR APPLICATION NUMBER: 08/951,648
 ; PRIOR FILING DATE: 1997-10-16
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 803
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-440-998-4

Query Match 95.0%; Score 3997; DB 4; Length 803;
 Best Local Similarity 95.4%; Pred. No. 0;
 Matches 752; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESATVEKMLRK 60
 DB 15 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESATVEKMLRK 74
 QY 61 TNKADBPSPKESVRYODTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
 DB 75 NKSSEDESAPKESVRYODTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 134
 QY 121 GPALYFLGECNNSLCFTPPGMEKGPRLIPAGPTTGGTTTSAVYAKSKTLLVEDILGD 180
 DB 135 GPALYFLGECNNSLCFTPPGMEKGPRLIPAGPTTGGTTTSAVYAKSKTLLVEDILGD 194
 QY 181 BRPFGTGESGTRIQSVLCPIVTAIGDLIGLIELYRMGKEAFCLSHQEVATANLAMA 240
 DB 195 BRPFGTGESGTRIQSVLCPIVTAIGDLIGLIELYRMGKEAFCLSHQEVATANLAMA 254
 QY 241 SVAIHQOVCGRLAQOTELNDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300
 DB 255 SVAIHQOVCGRLAQOTELNDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 314
 QY 301 QVDHKNKELYSDDLPIGEEKGKPIFKTKTIRFSIEKIGAGVARTGEVLPDAVADP 360
 DB 315 QVDHKNKELYSDDLPIGEEKGKPIFKTKTIRFSIEKIGAGVARTGEVLPDAVADP 374
 QY 361 RNRREVDLYTGTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCAL 420
 DB 375 RNRREVDLYTGTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCAL 434
 QY 421 ALHCANMYRIRHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARLCRDIELFHPDIG 480
 DB 435 ALHCANMYRIRHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARLCRDIELFHPDIG 494
 QY 481 PRNNMPPGIFVTYMHRSCTSCFELEKLCRFITMSYKQNTRRVPTNNMKAAVTVAHQMTAI 540
 DB 495 PRNNMPPGIFVTYMHRSCTSCFELEKLCRFITMSYKQNTRRVPTNNMKAAVTVAHQMTAI 554
 QY 541 LONNNGLPFLDERKGLIACLDHIDHGFNSYLOKPDHPLAALYSTSTMOQHHSQTV 600
 DB 555 LONNNGLPFLDERKGLIACLDHIDHGFNSYLOKPDHPLAALYSTSTMOQHHSQTV 614
 QY 601 SILQEGHNIFSTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEMYQTGSLNLHNS 660
 DB 615 SILQEGHNIFSTLSSSEYEQVLEIRKAIITADLALYFGNRKQLEMYQTGSLNLHNS 674
 QY 661 HRDRVIGLMTACDLCSVTKLMPVTKLITANDIYAEFMAEGDEMKULGIOTIPIMDRDKXD 720
 DB 675 HRDRVIGLMTACDLCSVTKLMPVTKLITANDIYAEFMAEGDEMKULGIOTIPIMDRDKXD 734

QY 721 EVPOGGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINQMEKYIRGEETAMNISCGBP 780
 DB 735 EVPOGGLGFYNAVAIPCYTTLTQILPTEPPLKACRDNINQMEKYIRGEETAMNISCGBP 794
 QY 781 APSKSTPE 788
 DB 795 AOKAASE 802

RESULT 6
 US-09-321-801-2
 ; Sequence 2, Application US/09321801
 ; Patent No. US20020115176A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanfear, Jeremy
 ; APPLICANT: Robas, Nicola M.
 ; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
 ; FILE REFERENCE: PC9477A
 ; CURRENT APPLICATION NUMBER: US/09/321,801
 ; CURRENT FILING DATE: 1999-05-27
 ; EARLIER APPLICATION NUMBER: 9826777.6
 ; EARLIER FILING DATE: 1998-12-04
 ; EARLIER APPLICATION NUMBER: 9823882.7
 ; EARLIER FILING DATE: 1998-10-30
 ; EARLIER APPLICATION NUMBER: 9811500.9
 ; EARLIER FILING DATE: 1998-05-28
 ; EARLIER APPLICATION NUMBER: 9908247.1
 ; EARLIER FILING DATE: 1998-04-09
 ; EARLIER APPLICATION NUMBER: 9910801.1
 ; EARLIER FILING DATE: 1999-05-10
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 789
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-321-801-2

Query Match 94.9%; Score 3993; DB 3; Length 789;
 Best Local Similarity 95.3%; Pred. No. 0;
 Matches 751; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESATVEKMLRK 60
 DB 1 MEDGSPNNASCFRRRLTECFSPSLTDEKVKAYLSLHPQVLDEFVSSESATVEKMLRK 60
 QY 61 TNKADBPSPKESVRYODTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
 DB 61 NKSSEDESAPKESVRYODTNMGGVYELNSYIEORLDTGDNHLLLYELSSIIIRIATKAD 120
 QY 121 GPALYFLGECNNSLCFTPPGMEKGPRLIPAGPTTGGTTTSAVYAKSKTLLVEDILGD 180
 DB 121 GPALYFLGECNNSLCFTPPGMEKGPRLIPAGPTTGGTTTSAVYAKSKTLLVEDILGD 180
 QY 181 BRPFGTGESGTRIQSVLCPIVTAIGDLIGLIELYRMGKEAFCLSHQEVATANLAMA 240
 DB 181 BRPFGTGESGTRIQSVLCPIVTAIGDLIGLIELYRMGKEAFCLSHQEVATANLAMA 240
 QY 241 SVAIHQOVCGRLAQOTELNDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300
 DB 241 SVAIHQOVCGRLAQOTELNDFLDVSKTYPDNIVAIDSLLEHIMIYAKNLVNAADRCLF 300
 QY 301 QVDHKNKELYSDDLPIGEEKGKPIFKTKTIRFSIEKIGAGVARTGEVLPDAVADP 360
 DB 301 QVDHKNKELYSDDLPIGEEKGKPIFKTKTIRFSIEKIGAGVARTGEVLPDAVADP 360
 QY 361 RNRREVDLYTGTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCAL 420
 DB 361 RNRREVDLYTGTTRNIIICMPIVSRGSVIGVQVWNKISGSAFSTKDENNFMFAVFCAL 420
 QY 421 ALHCANMYRIRHSECIYRVTEKLSYHSICTSEEWGLMRFNLPARLCRDIELFHPDIG 480

Db 421 ALHCANMTHRIHSHSCIRYVMEKLSYHSICTSEEMOGLMOFTLPEVRUCKEIELEPHFDIG 480
QY 481 PPENNMPGIFVYMHRSOGTSCFELEKLCRFIMSVKKNYRRVYPYNNMKHAAVVAHGMVAI 540
Db 481 PPENNMPGIFVYMHRSOGTSCFELEKLCRFIMSVKKNYRRVYPYNNMKHAAVVAHGMVAI 540
QY 541 LONNNGLFTDLERKGLLIACLDHDFHGFNSYLOKFDHPLAALYSTSTMEQHHSQTV 600
Db 541 LONNHTLFTDLERKGLLIACLDHDFHGFNSYLOKFDHPLAALYSTSTMEQHHSQTV 600
QY 601 SILOEGHNIFSTLSSSEYEOVLEIRKAIITDIALYFGNKKOLEMYQTSGLNLHNS 660
Db 601 SILOEGHNIFSTLSSSEYEOVLEIRKAIITDIALYFGNKKOLEMYQTSGLNLHNS 660
QY 661 HRDRIYGLMTACDLCSTVKLPMPVTKLTANDIYAEFMAEGDEMKLGIOPIMDRDKD 720
Db 661 HRDRIYGLMTACDLCSTVKLPMPVTKLTANDIYAEFMAEGDEMKLGIOPIMDRDKD 720
QY 721 EYPOGOLGFYNAVAIPCYTTTLTQIILPTEPLKACRDNINQWEKVIKGETAMTISGPGP 780
Db 721 EYPOGOLGFYNAVAIPCYTTTLTQIILPTEPLKACRDNINQWEKVIKGETAMTISGPGP 780
QY 781 APSKSTPE 788
Db 781 AOKKAASE 788
RESULT 7
US-10-618-252-2
; Sequence 2, Application US/10618252
; Publication No. US20040018542A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robae, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477B
; CURRENT APPLICATION NUMBER: US/10/618,252
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: 9826777.6
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 9823882.7
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 9811500.9
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 9908247.1
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: 9910801.1
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Human
US-10-618-252-2
Query Match 94.9%; Score 3993; DB 4; Length 789;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 751; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
QY 1 MEDGSPNNASCPRRLTECFSPSLTDEKVAAYLSLHPQVLDEFVSSESVAETVEKMLKRX 60
Db 1 MEDGSPNNASCPRRLTECFSPSLTDEKVAAYLSLHPQVLDEFVSSESVAETVEKMLKRX 60
QY 61 TNKAKDESPKESVRYQDTMKGVVYELNSYIEQRDLDTGDNHLLLYELSSIIIRIATKAD 120
Db 61 TNKAKDESPKESVRYQDTMKGVVYELNSYIEQRDLDTGDNHLLLYELSSIIIRIATKAD 120
QY 121 GFLALYTGECNNLSICVPIPGMKEGORPLIPAGITQGTISAVVASRKTLLVEDILGD 180
Db 121 GFLALYTGECNNLSICVPIPGMKEGORPLIPAGITQGTISAVVASRKTLLVEDILGD 180
QY 181 ERPRGTGLESRTIQSVLCPIVTAIGDLIGILELYRMHNGKAFCLSHQBVAATANLAWA 240

Db 181 ERPRGTGLESRTIQSVLCPIVTAIGDLIGILELYRMHNGKAFCLSHQBVAATANLAWA 240
QY 241 SVAIHQVQVCGGLAKQOTELNDFLDVSTYFEDNVAIDSLLEHIMIYAKNI VNAARCALF 300
Db 241 SVAIHQVQVCGGLAKQOTELNDFLDVSTYFEDNVAIDSLLEHIMIYAKNI VNAARCALF 300
QY 301 QVDHKNKELISDLPDIGEKEGKPIFKTKTEIRFSEIKGIAQVARTGEVANI PDAVADP 360
Db 301 QVDHKNKELISDLPDIGEKEGKPIFKTKTEIRFSEIKGIAQVARTGEVANI PDAVADP 360
QY 361 RFRREVDTLYGTITNIIICMPIVSRGSYIGVQVWNKISGSAFSTDDENNFRMPAVFCAL 420
Db 361 RFRREVDTLYGTITNIIICMPIVSRGSYIGVQVWNKISGSAFSTDDENNFRMPAVFCAL 420
QY 421 ALHCANMTHRIHSHSCIRYVMEKLSYHSICTSEEMOGLMFPNIPARICROIELEPHFDIG 480
Db 421 ALHCANMTHRIHSHSCIRYVMEKLSYHSICTSEEMOGLMFPNIPARICROIELEPHFDIG 480
QY 481 PPENNMPGIFVYMHRSOGTSCFELEKLCRFIMSVKKNYRRVYPYNNMKHAAVVAHGMVAI 540
Db 481 PPENNMPGIFVYMHRSOGTSCFELEKLCRFIMSVKKNYRRVYPYNNMKHAAVVAHGMVAI 540
QY 541 LONNNGLFTDLERKGLLIACLDHDFHGFNSYLOKFDHPLAALYSTSTMEQHHSQTV 600
Db 541 LONNHTLFTDLERKGLLIACLDHDFHGFNSYLOKFDHPLAALYSTSTMEQHHSQTV 600
QY 601 SILOEGHNIFSTLSSSEYEOVLEIRKAIITDIALYFGNKKOLEMYQTSGLNLHNS 660
Db 601 SILOEGHNIFSTLSSSEYEOVLEIRKAIITDIALYFGNKKOLEMYQTSGLNLHNS 660
QY 661 HRDRIYGLMTACDLCSTVKLPMPVTKLTANDIYAEFMAEGDEMKLGIOPIMDRDKD 720
Db 661 HRDRIYGLMTACDLCSTVKLPMPVTKLTANDIYAEFMAEGDEMKLGIOPIMDRDKD 720
QY 721 EYPOGOLGFYNAVAIPCYTTTLTQIILPTEPLKACRDNINQWEKVIKGETAMTISGPGP 780
Db 721 EYPOGOLGFYNAVAIPCYTTTLTQIILPTEPLKACRDNINQWEKVIKGETAMTISGPGP 780
QY 781 APSKSTPE 788
Db 781 AOKKAASE 788
RESULT 8
US-10-202-107-2
; Sequence 2, Application US/10202107
; Publication No. US20030096323A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: James, Larry C.
; APPLICANT: Lebel, Lorraine A.
; APPLICANT: Menitzi, Frank S.
; APPLICANT: Strick, Christine A.
; TITLE OF INVENTION: PD810 CELL-BASED ASSAY AND SEQUENCES
; FILE REFERENCE: PC23111ANIS
; CURRENT APPLICATION NUMBER: US/10/202,107
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/308,978
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-202-107-2
Query Match 93.9%; Score 3951.5; DB 4; Length 773;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 757; Conservative 3; Mismatches 8; Indels 5; Gaps 4;
QY 24 LTDEKVAAYLSLHPQVLDEFVSSESVAETVEKMLKKTITKAKDBSPKESVRYQDTMKG 83

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DB      4  LTDEKVAKATSLHPQVLDFEVSSESVAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQ 62
QY      84  VVYEINSLYIEQRLDPTGDNHLLLYELSSIIIRIATADGFALYFLGECNNSLCVFPIPGMK 143
DB      63  VVYEINSLYIEQRLDPTGDNHLLLYELSSIIIRIATADGFALYFLGECNNSLCVFPIPGMK 122
QY      144 EGQPLIPAGPITQGTITSAVYAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 203
DB      123 EGQPLIPAGPITQGTITSAVYAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 182
QY      204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQTEINDFL 263
DB      183 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQTEINDFL 242
QY      264 LDVSKTYFDNIYAIDSLLEHIMIYAKNLVNAORCALFOVDHKNKELYSDLFDIGEKEGK 323
DB      243 LDVSKTYFDNIYAIDSLLEHIMIYAKNLVNAORCALFOVDHKNKELYSDLFDIGEKEGK 302
QY      324 PIFKKTKEIRFSIEKGIAGVARTGEVLNIPDAVADPRFNRREVLDYTGTTNNILCMPIV 383
DB      303 PIFKKTKEIRFSIEKGIAGVARTGEVLNIPDAVADPRFNRREVLDYTGTTNNILCMPIV 362
QY      384 SRGSYIGVQVWVKISGSAFSKTDENNFKMPAVFCALALHCANMYHRIHSECIYRTWE 443
DB      422 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 503
QY      444 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 503
DB      422 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 481
QY      504 ELEKLCRFIMSKYKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 563
DB      482 ELEKLCRFIMSKYKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 541
QY      564 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSIIQLEGHNIPTSLSSSEYQVL 623
DB      542 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSIIQLEGHNIPTSLSSSEYQVL 600
QY      624 EIIRKAIITADLALYFGNRKQLEBMYQTSGLNLHNSHRDVIYGLMNTACDLCSVTYKLM 683
DB      601 EIIRKAIITADLALYFGNRKQLEBMYQTSGLNLHNSHRDVIYGLMNTACDLCSVTYKLM 660
QY      684 VTKLTIANDIYAFMAEGDEMKGIGIPIPMMDRDRKDEVPOQGLGFYNAVAIPCTYTLTQ 743
DB      661 VTKLTIANDIYAFMAEGDEMKGIGIPIPMMDRDRKDEVPOQGLGFYNAVAIPCTYTLTQ 720
QY      744 ILPTEPLLKACRDNLQWEKVIYRGEETAMWISGPGAPSKSTPEKLANVKYED 796
DB      721 ILPTEPLLKACRDNLQWEKVIYRGEETAMWIS--GPAITSKSTSEKPTRKXVD 771

RESULT 9
US-10-887-276-2
; Sequence 2, Application US/10887276
; Publication No. US20050026236A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: James, Larry C.
; APPLICANT: Leibel, Lorraine A.
; APPLICANT: Menliti, Frank S.
; APPLICANT: Strick, Christine A.
; TITLE OF INVENTION: PD510 CELL-BASED ASSAY AND SEQUENCES
; FILE REFERENCE: PC23111ANIS
; CURRENT APPLICATION NUMBER: US/10/887,276
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: US/10/202,107
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/308,978
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

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; LENGTH: 773
; TYPE: prt
; ORGANISM: Rattus sp.
US-10-887-276-2

Query Match      93.9%; Score 3951.5; DB 5; Length 773;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 757; Conservative 3; Mismatches 8; Indels 5; Gaps 4;

QY      24  LTDEKVAKATSLHPQVLDFEVSSESVAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQ 83
DB      4  LTDEKVAKATSLHPQVLDFEVSSESVAETVEKMKLRKKNKADEBSPKEV-RYQDTNNQ 62
QY      84  VVYEINSLYIEQRLDPTGDNHLLLYELSSIIIRIATADGFALYFLGECNNSLCVFPIPGMK 143
DB      63  VVYEINSLYIEQRLDPTGDNHLLLYELSSIIIRIATADGFALYFLGECNNSLCVFPIPGMK 122
QY      144 EGQPLIPAGPITQGTITSAVYAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 203
DB      123 EGQPLIPAGPITQGTITSAVYAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 182
QY      204 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQTEINDFL 263
DB      183 VTAIGDLIGILELYRHWGKEAFCLSHQEVATNLANMASVAIHQOVCGRLAQTEINDFL 242
QY      264 LDVSKTYFDNIYAIDSLLEHIMIYAKNLVNAORCALFOVDHKNKELYSDLFDIGEKEGK 323
DB      243 LDVSKTYFDNIYAIDSLLEHIMIYAKNLVNAORCALFOVDHKNKELYSDLFDIGEKEGK 302
QY      324 PIFKKTKEIRFSIEKGIAGVARTGEVLNIPDAVADPRFNRREVLDYTGTTNNILCMPIV 383
DB      303 PIFKKTKEIRFSIEKGIAGVARTGEVLNIPDAVADPRFNRREVLDYTGTTNNILCMPIV 362
QY      384 SRGSYIGVQVWVKISGSAFSKTDENNFKMPAVFCALALHCANMYHRIHSECIYRTWE 443
DB      422 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 503
QY      444 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 503
DB      422 KLSYHSICTSEBMOGLMHPNLPARICRDIELFHPDIGFENMMPGIFYYMIHRSCTSCF 481
QY      504 ELEKLCRFIMSKYKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 563
DB      482 ELEKLCRFIMSKYKQYRVRPYHNMKAAYTVAHCMYAILQNNNGLFPTDLERKGLIACLC 541
QY      564 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSIIQLEGHNIPTSLSSSEYQVL 623
DB      542 DLDHGFNSYLOKRDHPLAALYSTSTMEQHHFSQTVSIIQLEGHNIPTSLSSSEYQVL 600
QY      624 EIIRKAIITADLALYFGNRKQLEBMYQTSGLNLHNSHRDVIYGLMNTACDLCSVTYKLM 683
DB      601 EIIRKAIITADLALYFGNRKQLEBMYQTSGLNLHNSHRDVIYGLMNTACDLCSVTYKLM 660
QY      684 VTKLTIANDIYAFMAEGDEMKGIGIPIPMMDRDRKDEVPOQGLGFYNAVAIPCTYTLTQ 743
DB      661 VTKLTIANDIYAFMAEGDEMKGIGIPIPMMDRDRKDEVPOQGLGFYNAVAIPCTYTLTQ 720
QY      744 ILPTEPLLKACRDNLQWEKVIYRGEETAMWISGPGAPSKSTPEKLANVKYED 796
DB      721 ILPTEPLLKACRDNLQWEKVIYRGEETAMWIS--GPAITSKSTSEKPTRKXVD 771

RESULT 10
US-09-420-190-1
; Sequence 1, Application US/09420190
; Patent No. US20020081633A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; TITLE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71

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; CURRENT APPLICATION NUMBER: US/09/420,190
; CURRENT FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FaSTSeq for Windows Version 3.0
; SEQ ID NO: 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-420-190-1

Query Match      92.2%; Score 3878; DB 3; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 24 LTDEKVKAYLSLHPQVLDFEVSSESAETVEKMLKRTNKAKDEBSPKESVRYODTNMG 83
DB 14 LTDEKVKAYLSLHPQVLDFEVSSESAETVEKMLKRNKKSDEBSPKESVRYODTNMG 73
QY 84 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVPIPGMK 143
DB 74 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCIETPGIK 133
QY 144 EGQPLIPAGPIITGGTTSAVYAKSKRTLLVEDILGDERPPRGTSLESTRISQVLCPI 203
DB 134 EGQPLIPAGPIITGGTTSAVYAKSKRTLLVEDILGDERPPRGTSLESTRISQVLCPI 193
QY 204 VTAIGDLIGILELYRMGKEAFCLSHOEVAATNLAMASVALIHQOVCRGLAQTEINDEL 263
DB 194 VTAIGDLIGILELYRMGKEAFCLSHOEVAATNLAMASVALIHQOVCRGLAQTEINDEL 253
QY 264 LDVSKTYFPDNIYALDSLEHIMIYAKNLVNAIDRCALFOVDHKNKELYSDFDIEGEEKG 323
DB 254 LDVSKTYFPDNIYALDSLEHIMIYAKNLVNAIDRCALFOVDHKNKELYSDFDIEGEEKG 313
QY 324 PI FPKTKELRFSEKGIAGQVARTGEVLNI PDAYADPRNREVDLYGTGTTNII LCMPIV 383
DB 314 PVFKTKELRFSEKGIAGQVARTGEVLNI PDAYADPRNREVDLYGTGTTNII LCMPIV 373
QY 384 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALH CANMYRIRHSECIYVTWE 443
DB 374 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALH CANMYRIRHSECIYVTWE 433
QY 444 KLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIGPEENMPGIFVYMIHRSCTSGCF 503
DB 434 KLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIGPEENMPGIFVYMIHRSCTSGCF 493
QY 504 ELEKLCRFPTMSYKKNRYRYPYNNMKALVYAHCMYAILLONNNGLPFDLBRKGLLIACLG 563
DB 494 ELEKLCRFPTMSYKKNRYRYPYNNMKALVYAHCMYAILLONNNGLPFDLBRKGLLIACLG 553
QY 564 DLDHRGFSNSYLQKFPDPLAALYSTSTMEQHHSQTVSIIQLEGHNI FSTLSSSEYQVL 623
DB 554 DLDHRGFSNSYLQKFPDPLAALYSTSTMEQHHSQTVSIIQLEGHNI FSTLSSSEYQVL 613
QY 624 EIRKAIITADLALYFNGRKQLEBMYQTGSLINLHNSHRDRIYGLMWTACDLCSTVKLMP 683
DB 614 EIRKAIITADLALYFNGRKQLEBMYQTGSLINLHNSHRDRIYGLMWTACDLCSTVKLMP 673
QY 684 VTKLTANDIYAEFWAGDEKKLGIQPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743
DB 674 VTKLTANDIYAEFWAGDEKKLGIQPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 723
QY 744 ILPTEPLKACRDNLNOMEKVI RGETAMWISGPAPASKSTPE 788
DB 734 ILPTEPLKACRDNLNOMEKVI RGETAMWISGPAPASKSTPE 778

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; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: Methods for Using 22045, A Human Cyclic
; FILE OF INVENTION: Nucleotide Phosphodiesterase
; FILE REFERENCE: 5800-71
; CURRENT APPLICATION NUMBER: US/10/458,839
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 1999-10-18
; SOFTWARE: FaSTSeq for Windows Version 3.0
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO: 1
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-458-839-1

Query Match      92.2%; Score 3878; DB 4; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 24 LTDEKVKAYLSLHPQVLDFEVSSESAETVEKMLKRTNKAKDEBSPKESVRYODTNMG 83
DB 14 LTDEKVKAYLSLHPQVLDFEVSSESAETVEKMLKRNKKSDEBSPKESVRYODTNMG 73
QY 84 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCVPIPGMK 143
DB 74 VVEELNSYIEQRDLDTGDNHLLLYELSSIRIATKADGALYFLGECNNSLCIETPGIK 133
QY 144 EGQPLIPAGPIITGGTTSAVYAKSKRTLLVEDILGDERPPRGTSLESTRISQVLCPI 203
DB 134 EGQPLIPAGPIITGGTTSAVYAKSKRTLLVEDILGDERPPRGTSLESTRISQVLCPI 193
QY 204 VTAIGDLIGILELYRMGKEAFCLSHOEVAATNLAMASVALIHQOVCRGLAQTEINDEL 263
DB 194 VTAIGDLIGILELYRMGKEAFCLSHOEVAATNLAMASVALIHQOVCRGLAQTEINDEL 253
QY 264 LDVSKTYFPDNIYALDSLEHIMIYAKNLVNAIDRCALFOVDHKNKELYSDFDIEGEEKG 323
DB 254 LDVSKTYFPDNIYALDSLEHIMIYAKNLVNAIDRCALFOVDHKNKELYSDFDIEGEEKG 313
QY 324 PI FPKTKELRFSEKGIAGQVARTGEVLNI PDAYADPRNREVDLYGTGTTNII LCMPIV 383
DB 314 PVFKTKELRFSEKGIAGQVARTGEVLNI PDAYADPRNREVDLYGTGTTNII LCMPIV 373
QY 384 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALH CANMYRIRHSECIYVTWE 443
DB 374 SRGSVIGVQVMNKISGSAFSKTDENNFMFAVFCALALH CANMYRIRHSECIYVTWE 433
QY 444 KLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIGPEENMPGIFVYMIHRSCTSGCF 503
DB 434 KLSYHSICTSEBMOGLMRFNLPARICRDIELFHPDIGPEENMPGIFVYMIHRSCTSGCF 493
QY 504 ELEKLCRFPTMSYKKNRYRYPYNNMKALVYAHCMYAILLONNNGLPFDLBRKGLLIACLG 563
DB 494 ELEKLCRFPTMSYKKNRYRYPYNNMKALVYAHCMYAILLONNNGLPFDLBRKGLLIACLG 553
QY 564 DLDHRGFSNSYLQKFPDPLAALYSTSTMEQHHSQTVSIIQLEGHNI FSTLSSSEYQVL 623
DB 554 DLDHRGFSNSYLQKFPDPLAALYSTSTMEQHHSQTVSIIQLEGHNI FSTLSSSEYQVL 613
QY 624 EIRKAIITADLALYFNGRKQLEBMYQTGSLINLHNSHRDRIYGLMWTACDLCSTVKLMP 683
DB 614 EIRKAIITADLALYFNGRKQLEBMYQTGSLINLHNSHRDRIYGLMWTACDLCSTVKLMP 673
QY 684 VTKLTANDIYAEFWAGDEKKLGIQPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 743
DB 674 VTKLTANDIYAEFWAGDEKKLGIQPIPMMDRDKDEVPOGOLGFYNAVAIPCYTTLTQ 723
QY 744 ILPTEPLKACRDNLNOMEKVI RGETAMWISGPAPASKSTPE 788
DB 734 ILPTEPLKACRDNLNOMEKVI RGETAMWISGPAPASKSTPE 778

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RESULT 11
US-10-458-839-1
; Sequence 1, Application US/10458839
; Publication No. US20030215898A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana

```

```
RESULT 12
US-10-440-998-6
; Sequence 6, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-998-6

Query Match          92.2%; Score 3878; DB 4; Length 779;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 730; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

24 LTDEKVAYLHHPQVLDFVSESVSAETVEKWLKRTNKAKDEPSPEKVSRYQDTNNQG 83
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14 LTDEKVAKAYLSHPQVLDFVSESVSAETVEKWLKRNKKSDEBSAPKESRYQDTNNQG 73
|||||
84 VVYELNSYIEORLDTGDNHLLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGKM 143
|||||
74 VVYELNSYIEORLDTGDNQQLLYELSSITIKIATADGFALYFLGECNNSLCIFIPGK 133
|||||
144 EGQPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 203
|||||
134 EGKPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 193
|||||
204 VTAIGDLIGILELYRHMGKEAFCLSHQEVATANLAMASVALHVOVCGRLAKQTELNDPL 263
|||||
194 VTAIGDLIGILELYRHMGKEAFCLSHQEVATANLAMASVALHVOVCGRLAKQTELNDPL 253
|||||
264 LDVSKTYFDNIVALIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDDLPIGEEKG 323
|||||
264 LDVSKTYFDNIVALIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDDLPIGEEKG 313
|||||
324 PIFKTKIEIRFSIEKGIAGVARTGEVLANIPDAVADPRFNRVDLYTGYTTNNILCMPIV 383
|||||
314 PVFKTKIEIRFSIEKGIAGVARTGEVLANIPDAVADPRFNRVDLYTGYTTNNILCMPIV 373
|||||
384 SRGSYIGVVQVWNKISGSAFSTDENNFKMPAVFCALALHCANNMYHRIHSECIYRVYME 443
|||||
374 SRGSYIGVVQVWNKISGSAFSTDENNFKMPAVFCALALHCANNMYHRIHSECIYRVYME 433
|||||
444 KLSYHSICTSEEMQGLMFPNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQGSTGCF 503
|||||
434 KLSYHSICTSEEMQGLMFPNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQGSTGCF 493
|||||
504 ELEKLCRFIMSVKKNYRRVRYNNMKGAVTVAHCMYALIONNNGLFTDLERKGLIACLC 563
|||||
494 ELEKLCRFIMSVKKNYRRVRYNNMKGAVTVAHCMYALIONNNGLFTDLERKGLIACLC 553
|||||
564 DLDHGFNSNYLQKFDHPLAALYSTSTWEOHNFSGTVSILQLEGNHIFSTLSSSEYQVL 623
|||||
554 DLDHGFNSNYLQKFDHPLAALYSTSTWEOHNFSGTVSILQLEGNHIFSTLSSSEYQVL 613
|||||
624 EIRKAAIATDALYKGRKOLEMYOQGSLLHNSHSDRYIGLMMTRACDLCSTYKLM 683
|||||
614 EIRKAAIATDALYKGRKOLEMYOQGSLLHNSHSDRYIGLMMTRACDLCSTYKLM 673
|||||
684 VTKLTIANDIYAEFNAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLLQ 743
|||||
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DB 674 VTKLTIANDIYAEFNAEGDEMKKLGIOPIPMMDRDKDEVPOGOLGFYNAVALPCYTTLLQ 733
QY 744 ILTPTEPLIKACRDNLNOMEKVIKGEETAMWISGPGAPSKSTDE 788
DB 734 ILTPTEPLIKACRDNLNOMEKVIKGEETATWISSPSVAQKAAASE 778

RESULT 13
US-10-440-998-2
; Sequence 2, Application US/10440998
; Publication No. US20030215919A1
; GENERAL INFORMATION:
; APPLICANT: Loughney, Kate
; TITLE OF INVENTION: Phosphodiesterase 8A
; FILE REFERENCE: 27866/35047
; CURRENT APPLICATION NUMBER: US/10/440,998
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/686,055
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 08/951,648
; PRIOR FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc. feature
; LOCATION: (290)
; OTHER INFORMATION: The amino acid is either Pro or Leu
US-10-440-998-2

Query Match          92.1%; Score 3873; DB 4; Length 766;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 729; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

24 LTDEKVAYLHHPQVLDFVSESVSAETVEKWLKRTNKAKDEPSPEKVSRYQDTNNQG 83
|||||
1 LTDEKVAKAYLSHPQVLDFVSESVSAETVEKWLKRNKKSDEBSAPKESRYQDTNNQG 60
|||||
84 VVYELNSYIEORLDTGDNHLLLYELSSIRIATKADGFALYFLGECNNSLCVFIIPGKM 143
|||||
61 VVYELNSYIEORLDTGDNQQLLYELSSITIKIATKADGFALYFLGECNNSLCIFIPGK 120
|||||
144 EGQPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 203
|||||
121 EGKPLIPAGPIITGGTISAVVAKSRKTLVEDIIGDERPFRGTGLESSTRIQSVLCPI 180
|||||
204 VTAIGDLIGILELYRHMGKEAFCLSHQEVATANLAMASVALHVOVCGRLAKQTELNDPL 263
|||||
181 VTAIGDLIGILELYRHMGKEAFCLSHQEVATANLAMASVALHVOVCGRLAKQTELNDPL 240
|||||
264 LDVSKTYFDNIVALIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDDLPIGEEKG 323
|||||
241 LDVSKTYFDNIVALIDSLLEHIMITYAKNLVNADRCALFOVDHKNKELYSDDLPIGEEKG 300
|||||
324 PIFKTKIEIRFSIEKGIAGVARTGEVLANIPDAVADPRFNRVDLYTGYTTNNILCMPIV 383
|||||
301 PVFKTKIEIRFSIEKGIAGVARTGEVLANIPDAVADPRFNRVDLYTGYTTNNILCMPIV 360
|||||
384 SRGSYIGVVQVWNKISGSAFSTDENNFKMPAVFCALALHCANNMYHRIHSECIYRVYME 443
|||||
361 SRGSYIGVVQVWNKISGSAFSTDENNFKMPAVFCALALHCANNMYHRIHSECIYRVYME 420
|||||
444 KLSYHSICTSEEMQGLMFPNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQGSTGCF 503
|||||
421 KLSYHSICTSEEMQGLMFPNLPARI CRDIELFHPDIGFENMMPGIFVYMHRSQGSTGCF 480
|||||
504 ELEKLCRFIMSVKKNYRRVRYNNMKGAVTVAHCMYALIONNNGLFTDLERKGLIACLC 563
|||||
481 ELEKLCRFIMSVKKNYRRVRYNNMKGAVTVAHCMYALIONNNGLFTDLERKGLIACLC 540
|||||
564 DLDHGFNSNYLQKFDHPLAALYSTSTWEOHNFSGTVSILQLEGNHIFSTLSSSEYQVL 623
|||||
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Db |D|H|R|G|F|S|N|S|Y|Q|K|D|H|P|L|A|L|Y|S|T|S|T|W|E|Q|H|F|S|Q|T|V|S|I|L|Q|E|G|N|I|F|S|T|S|S|E|Y|Q|L| 600
Qy |E|I|R|R|A|I|A|T|D|A|L|Y|F|G|N|R|K|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 683
Db |E|I|R|R|A|I|A|T|D|A|L|Y|F|G|N|R|K|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 660
Qy |V|T|K|L|T|A|N|D|I|A|E|F|W|A|B|G|D|E|M|K|G|I|O|P|I|P|M|D|R|D|K|D|E|V|P|Q|G|L|G|F|Y|N|A|I|P|C|Y|T|T|L|T|Q| 743
Db |V|T|K|L|T|A|N|D|I|A|E|F|W|A|B|G|D|E|M|K|G|I|O|P|I|P|M|D|R|D|K|D|E|V|P|Q|G|L|G|F|Y|N|A|I|P|C|Y|T|T|L|T|Q| 720
Qy |I|L|P|T|E|P|L|K|A|C|R|D|N|L|S|O|W|E|K|V|I|R|G|B|E|T|A|T|W|I|S|P|S|V|A|Q|K|A|A|S|E| 765
Db |I|L|P|T|E|P|L|K|A|C|R|D|N|L|S|O|W|E|K|V|I|R|G|B|E|T|A|T|W|I|S|P|S|V|A|Q|K|A|A|S|E| 765

RESULT 14
US-09-321-801-4
; Sequence 4, Application US/09321801
; Patent No. US20020115176A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robae, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477A
; CURRENT APPLICATION NUMBER: US/09/321,801
; EARLIER FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Human
US-09-321-801-4

Query Match 91.9%; Score 3867; DB 3; Length 791;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 728; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
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Qy |S|R|G|S|V|G|V|O|W|N|K|I|S|G|S|A|F|S|K|T|D|E|N|F|K|M|F|A|V|C|A|L|A|H|C|A|N|T|H|R|I|R|H|S|C|I|Y|R|V|T|W|E| 443
Db |S|R|G|S|V|G|V|O|W|N|K|I|S|G|S|A|F|S|K|T|D|E|N|F|K|M|F|A|V|C|A|L|A|H|C|A|N|T|H|R|I|R|H|S|C|I|Y|R|V|T|W|E| 445
Qy |K|L|S|Y|S|I|C|T|S|E|B|E|O|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 503
Db |K|L|S|Y|S|I|C|T|S|E|B|E|O|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 505
Qy |E|L|E|K|L|C|R|P|I|S|Y|K|Q|R|Y|R|V|P|Y|N|H|A|V|T|V|A|H|C|W|A|I|I|O|N|N|G|L|E|T|D|L|E|R|K|G|L|L|A|C|H| 563
Db |E|L|E|K|L|C|R|P|I|S|Y|K|Q|R|Y|R|V|P|Y|N|H|A|V|T|V|A|H|C|W|A|I|I|O|N|N|G|L|E|T|D|L|E|R|K|G|L|L|A|C|H| 565
Qy |D|L|D|H|R|G|F|S|N|S|Y|Q|K|D|H|P|L|A|L|Y|S|T|S|T|W|E|Q|H|F|S|Q|T|V|S|I|L|Q|E|G|N|I|F|S|T|S|S|E|Y|Q|L| 623
Db |D|L|D|H|R|G|F|S|N|S|Y|Q|K|D|H|P|L|A|L|Y|S|T|S|T|W|E|Q|H|F|S|Q|T|V|S|I|L|Q|E|G|N|I|F|S|T|S|S|E|Y|Q|L| 625
Qy |E|I|R|R|A|I|A|T|D|A|L|Y|F|G|N|R|K|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 683
Db |E|I|R|R|A|I|A|T|D|A|L|Y|F|G|N|R|K|Q|L|E|E|Y|Q|T|S|L|N|I|N|Q|S|H|R|D|R|V|I|G|L|M|T|A|C|D|L|C|S|Y|T|K|L|P| 685
Qy |V|T|K|L|T|A|N|D|I|A|E|F|W|A|B|G|D|E|M|K|G|I|O|P|I|P|M|D|R|D|K|D|E|V|P|Q|G|L|G|F|Y|N|A|I|P|C|Y|T|T|L|T|Q| 743
Db |V|T|K|L|T|A|N|D|I|A|E|F|W|A|B|G|D|E|M|K|G|I|O|P|I|P|M|D|R|D|K|D|E|V|P|Q|G|L|G|F|Y|N|A|I|P|C|Y|T|T|L|T|Q| 745
Qy |I|L|P|T|E|P|L|K|A|C|R|D|N|L|S|O|W|E|K|V|I|R|G|B|E|T|A|T|W|I|S|P|S|V|A|Q|K|A|A|S|E| 788
Db |I|L|P|T|E|P|L|K|A|C|R|D|N|L|S|O|W|E|K|V|I|R|G|B|E|T|A|T|W|I|S|P|S|V|A|Q|K|A|A|S|E| 790
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RESULT 15
US-10-618-252-4
; Sequence 4, Application US/10618252
; Publication No. US20040018542A1
; GENERAL INFORMATION:
; APPLICANT: Lanfear, Jeremy
; APPLICANT: Robae, Nicola M.
; TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
; FILE REFERENCE: PC9477B
; CURRENT APPLICATION NUMBER: US/10/618,252
; EARLIER FILING DATE: 2003-07-11
; EARLIER APPLICATION NUMBER: 9826777.6
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 9823882.7
; EARLIER FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 9811500.9
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: 9908247.1
; EARLIER FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: 9910801.1
; PRIOR FILING DATE: 1999-05-10
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Human
US-10-618-252-4

Query Match 91.9%; Score 3867; DB 4; Length 791;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 728; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
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QY 204 VTAIGDLIGILELYRMGKEAFCLSHQVATANLAMASVAIHQVYCRGLAKOTELNDPL 263
DB 206 VTAIGDLIGILELYRMGKEAFCLSHQVATANLAMASVAIHQVYCRGLAKOTELNDPL 265
QY 264 LDVSKTYFPDNIYVAIDSLLEHIMIYAKNLVADRACALFOVDHKNKELYSDFDIGEEKGK 323
DB 266 LDVSKTYFPDNIYVAIDSLLEHIMIYAKNLVADRACALFOVDHKNKELYSDFDIGEEKGK 325
QY 324 PIFKKTKEIRFSIEKGIAGQVARTGEVLNI PDAYADPRFNREVDLYTGYTTNNILCMPIV 383
DB 326 PVFKKTKEIRFSIEKGIAGQVARTGEVLNI PDAYADPRFNREVDLYTGYTTNNILCMPIV 385
QY 384 SRGSYIGVVQWVKISGSAFSTKDENNFCMPAFVFCALALHCANMTHRIHSECIYRVTME 443
DB 386 SRGSYIGVVQWVKISGSAFSTKDENNFCMPAFVFCALALHCANMTHRIHSECIYRVTME 445
QY 444 KLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTSCF 503
DB 446 KLSYHSICTSEMOGLMRPNLPARICRDIELFHPDIGPENMPGIFVYMIHRSCTSCF 505
QY 504 ELEKLCRFPMYSVKYVRVRYNNMKHAAVTVAHCMYAILQNNNGLFTDLERKGLLIACLCH 563
DB 506 ELEKLCRFPMYSVKYVRVRYNNMKHAAVTVAHCMYAILQNNNGLFTDLERKGLLIACLCH 565
QY 564 DLDHRGFSNSYLOKPDHPLAALYSTSTMEOHPSQTVSILQLEGHNIESTLSSEYEQVL 623
DB 566 DLDHRGFSNSYLOKPDHPLAALYSTSTMEOHPSQTVSILQLEGHNIESTLSSEYEQVL 625
QY 624 EIIRKAIITDIALYFGNRKQLEMYQTSNLNLNQHSHRDRIYGLMNTACDLCSYTKLMP 683
DB 626 EIIRKAIITDIALYFGNRKQLEMYQTSNLNLNQHSHRDRIYGLMNTACDLCSYTKLMP 685
QY 684 VTKLTANDIYAEFMAEGDEMCKLGIQPIPMMDRDKRDEVPOGOLGFYNAVAIPCYTTLTQ 743
DB 686 VTKLTANDIYAEFMAEGDEMCKLGIQPIPMMDRDKRDEVPOGOLGFYNAVAIPCYTTLTQ 745
QY 744 ILPTEPILKACRDNLNQEKVIRGETAMWISGPGAPSKSTPE 788
DB 746 ILPTEPILKACRDNLNQEKVIRGETAMWISGPGAPSKSTPE 790

Search completed: January 10, 2006, 14:06:37
Job time : 119 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 10, 2006, 13:56:07 ; Search time 28 Seconds
(without alignments)
241.462 Million cell updates/sec

Title: US-10-618-252-15

Perfect score: 4206
Sequence: 1 MEDGSPNNASCFRRUTCEFL.....GGPAPSKSTPKLVNVED 796

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/pcodata/1/pubppaa/US09_NEW_PUB.pep:*
2: /cgn2_6/pcodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/pcodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/pcodata/1/pubppaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/pcodata/1/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/pcodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/pcodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/pcodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.5	7.5	507	7 US-11-091-018-10	Sequence 10, App1
2	315.5	7.5	585	7 US-11-091-018-9	Sequence 9, App1
3	315.5	7.5	673	7 US-11-091-018-6	Sequence 6, App1
4	315.5	7.5	687	7 US-11-091-018-8	Sequence 8, App1
5	315.5	7.5	745	7 US-11-091-018-4	Sequence 4, App1
6	315.5	7.5	748	6 US-10-492-835-12	Sequence 12, App1
7	315.5	7.5	748	6 US-10-492-835-28	Sequence 28, App1
8	315.5	7.5	809	7 US-11-091-018-2	Sequence 2, App1
9	308.5	7.3	747	6 US-10-492-835-15	Sequence 15, App1
10	307.5	7.3	747	6 US-10-492-835-8	Sequence 8, App1
11	307.5	7.3	747	6 US-10-492-835-27	Sequence 27, App1
12	107	2.5	1216	6 US-10-873-528-12	Sequence 12, App1
13	106	2.5	1451	7 US-11-046-346-1	Sequence 1, App1
14	92.5	2.2	1045	7 US-11-113-424-54	Sequence 54, App1
15	92.5	2.2	1094	6 US-10-821-234-1097	Sequence 1097, App1
16	92.5	2.2	2376	7 US-11-096-051-4	Sequence 4, App1
17	92.5	2.2	2715	7 US-11-096-051-2	Sequence 2, App1
18	92.5	2.2	2721	7 US-11-096-051-10	Sequence 10, App1
19	92.5	2.2	2725	7 US-11-096-051-8	Sequence 8, App1
20	89.5	2.1	1531	7 US-11-087-227-24	Sequence 24, App1
21	89.5	2.1	1531	7 US-11-186-284-211	Sequence 211, App1
22	89	2.1	1092	6 US-10-821-234-999	Sequence 999, App1
23	88.5	2.1	2715	7 US-11-113-424-51	Sequence 51, App1
24	88	2.1	1467	6 US-10-507-956-1	Sequence 1, App1
25	87.5	2.1	1075	7 US-11-174-150-34	Sequence 34, App1

26	87.5	2.1	1114	7 US-11-174-150-35	Sequence 35, App1
27	87	2.1	189	6 US-10-995-561-806	Sequence 806, App
28	86.5	2.1	498	6 US-10-467-657-5006	Sequence 5006, App
29	86	2.0	277	6 US-10-454-437-214	Sequence 214, App
30	85	2.0	805	6 US-10-927-641-77	Sequence 77, App
31	84	2.0	664	6 US-10-485-517-308	Sequence 308, App
32	84	2.0	767	7 US-11-043-693-2	Sequence 2, App1
33	84	2.0	1306	6 US-10-995-561-905	Sequence 905, App
34	84	2.0	1356	6 US-10-995-561-904	Sequence 904, App
35	84	2.0	1356	6 US-10-995-561-906	Sequence 906, App
36	84	2.0	2710	7 US-11-051-453-41	Sequence 41, App1
37	83.5	2.0	2890	7 US-11-115-639-31	Sequence 31, App1
38	83.5	2.0	2890	7 US-11-115-639-32	Sequence 32, App1
39	83.5	2.0	2890	7 US-11-115-639-33	Sequence 33, App1
40	83	2.0	615	7 US-11-172-145-6	Sequence 6, App1
41	82.5	2.0	360	7 US-11-043-542-12	Sequence 12, App1
42	82.5	2.0	367	7 US-11-043-542-10	Sequence 10, App1
43	82.5	2.0	372	7 US-11-043-542-8	Sequence 8, App1
44	82.5	2.0	373	7 US-11-043-542-14	Sequence 14, App1
45	82.5	2.0	385	7 US-11-043-542-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-11-091-018-10
; Sequence 10, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gretearsdotit, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; TITLE OF INVENTION: METHODS OF TREATMENT
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/611,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-10

Query Match 7.5%; Score 315.5; DB 7; Length 507;
Best Local Similarity 25.4%; Pred. No. 8.1e-21;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;
QY 442 MEKLSYHSICTSEWQGLMKFNLPAR---ICRDIELFHFIDIGPFENMGFIVYMIRHS 497
DB 65 VKTLMHSSSLTN---SSIPRFVKTQEDVLAKELE---DV---NKW-GLHVFRIAEI 112
QY 498 CG-----TSCFELKLCRIMSVKKNYRR-VPRYMKKHAIVTAHCM 537
DB 113 SGRRPLVIVIMHTIFQERDLKTFKIPVDLTITVMTLEDYHADVAVHNHIVADVQST 172
QY 538 YATLQNN--NGLPTDERKGLLACLDHDFRGSNSYLQKFDHPLAALYS--TSTMEQH 594
DB 173 HVLSTPALEAVFTDLIELAIFASAIHDVDHGVNSQFLINTNSLALMYNDSVLENH 232

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QY 595 HPSQVTSILOEGHNIPTLSSEYEQVLEIRKAIITDIALYGNRKOLEMYQT--- 651
DB 233 HIAVGFKLQENNCIFQNLTKKQOSLRKQVIDLATDMSKHNNLLADLKTWVETKKV 292
QY 652 ---GSLINHNOSHRDVRIGLMTACDLSVTKLMPVTKLTIANDIYAEFMAEGDEMKKLG 708
DB 293 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTRIMEEFPQGDREBERGM 352
QY 709 QIPIMDDKDEVPQOGLGFYNNAVAICPTTTLTQIL-PPTPEPLKACRDNLNOMEK 767
DB 353 EISPMCDKGNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADQDILDTLEDNRNEMWQSTIP 411
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 412 -----QSPSPAP--DDPEE 423

RESULT 2
US-11-091-018-9
/ Sequence 9, Application US/11091018
/ Publication No. US20050287551A1
/ GENERAL INFORMATION:
/ APPLICANT: Greteardottir, Solveig
/ APPLICANT: Thorleifsson, Gudmar
/ APPLICANT: Gulcher, Jeffrey R.
/ TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
/ TITLE OF INVENTION: METHODS OF TREATMENT
/ FILE REFERENCE: 2345.2010-016
/ CURRENT APPLICATION NUMBER: US/11/091,018
/ PRIOR FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: PCT/US03/29906
/ PRIOR FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: 10/255,120
/ PRIOR FILING DATE: 2002-09-25
/ PRIOR APPLICATION NUMBER: 10/419,723
/ PRIOR FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: 10/650,120
/ PRIOR FILING DATE: 2003-08-27
/ PRIOR APPLICATION NUMBER: 10/067,514
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 09/811,352
/ PRIOR FILING DATE: 2001-03-19
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: FaSTSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 585
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-091-018-9

Query Match 7.5%; Score 315.5; DB 7; Length 585;
Best Local Similarity 25.4%; Pred. No. 1e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWQGLMRFLPAR---ICRDIELFHPDIGPEENMMPGIFVYMIHRS 497
DB 143 VKKLHSSSLTN---SSIPRFQVKTQEDVLAKELE---DV---NKM-GLHVRIML 190
QY 498 CG-----TSCFELEKCRFISVKKNYR-VYNNMKHAAVTVAHCM 537
DB 191 SGNRPFLVIMHTIFQERDLTKFKIPVDLTLYLMTLEBDHYADVAYNNHIAADVOST 250
QY 538 YAILQNN--NGLFTDLERKGLLIACLDLHGRFSNSYLOKFDHPLAALYS-TSTMEOH 594
DB 251 HYLSTPALAEVFTDLELIAAFASAIHDVDHVGVSNGFLINTNSBLALMYNDSVLENH 310
QY 595 HPSQVTSILOEGHNIPTLSSEYEQVLEIRKAIITDIALYGNRKOLEMYQT--- 651
DB 311 HIAVGFKLQENNCIFQNLTKKQOSLRKQVIDLATDMSKHNNLLADLKTWVETKKV 370
QY 652 ---GSLINHNOSHRDVRIGLMTACDLSVTKLMPVTKLTIANDIYAEFMAEGDEMKKLG 708

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DB 371 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTRIMEEFPQGDREBERGM 430
QY 709 QIPIMDDKDEVPQOGLGFYNNAVAICPTTTLTQIL-PPTPEPLKACRDNLNOMEK 767
DB 431 EISPMCDKGNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADQDILDTLEDNRNEMWQSTIP 489
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 490 -----QSPSPAP--DDPEE 501

RESULT 3
US-11-091-018-6
/ Sequence 6, Application US/11091018
/ Publication No. US20050287551A1
/ GENERAL INFORMATION:
/ APPLICANT: Greteardottir, Solveig
/ APPLICANT: Thorleifsson, Gudmar
/ APPLICANT: Gulcher, Jeffrey R.
/ TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
/ TITLE OF INVENTION: METHODS OF TREATMENT
/ FILE REFERENCE: 2345.2010-016
/ CURRENT APPLICATION NUMBER: US/11/091,018
/ PRIOR FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: PCT/US03/29906
/ PRIOR FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: 10/255,120
/ PRIOR FILING DATE: 2002-09-25
/ PRIOR APPLICATION NUMBER: 10/419,723
/ PRIOR FILING DATE: 2003-04-18
/ PRIOR APPLICATION NUMBER: 10/650,120
/ PRIOR FILING DATE: 2003-08-27
/ PRIOR APPLICATION NUMBER: 10/067,514
/ PRIOR FILING DATE: 2002-02-04
/ PRIOR APPLICATION NUMBER: 09/811,352
/ PRIOR FILING DATE: 2001-03-19
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: FaSTSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 673
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-091-018-6

Query Match 7.5%; Score 315.5; DB 7; Length 673;
Best Local Similarity 25.4%; Pred. No. 1.3e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWQGLMRFLPAR---ICRDIELFHPDIGPEENMMPGIFVYMIHRS 497
DB 231 VKKLHSSSLTN---SSIPRFQVKTQEDVLAKELE---DV---NKM-GLHVRIML 278
QY 498 CG-----TSCFELEKCRFISVKKNYR-VYNNMKHAAVTVAHCM 537
DB 279 SGNRPFLVIMHTIFQERDLTKFKIPVDLTLYLMTLEBDHYADVAYNNHIAADVOST 338
QY 538 YAILQNN--NGLFTDLERKGLLIACLDLHGRFSNSYLOKFDHPLAALYS-TSTMEOH 594
DB 339 HYLSTPALAEVFTDLELIAAFASAIHDVDHVGVSNGFLINTNSBLALMYNDSVLENH 398
QY 595 HPSQVTSILOEGHNIPTLSSEYEQVLEIRKAIITDIALYGNRKOLEMYQT--- 651
DB 399 HIAVGFKLQENNCIFQNLTKKQOSLRKQVIDLATDMSKHNNLLADLKTWVETKKV 458
QY 652 ---GSLINHNOSHRDVRIGLMTACDLSVTKLMPVTKLTIANDIYAEFMAEGDEMKKLG 708
DB 459 TSSGVLILDNYSDRIQVLQNNVHCADLSNPTKPLQLYRQWTRIMEEFPQGDREBERGM 518
QY 709 QIPIMDDKDEVPQOGLGFYNNAVAICPTTTLTQIL-PPTPEPLKACRDNLNOMEK 767
DB 519 EISPMCDKGNA-SVEKSGVGFIDYIVHPLMETWADLVHPDADQDILDTLEDNRNEMWQSTIP 577
QY 768 GEETAMWISGPGAPASKSTPEK 789

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; CURRENT FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 12
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-12

Query Match      7.5%; Score 315.5; DB 6; Length 748;
Best Local Similarity 25.4%; Pred. No. 1.5e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWOGMRNLPAR---ICRDIELFPHDIGPENNMPGIFVYMIHRS 497
DB 306 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVFRIAEI 353
QY 498 CG-----TSCFELEKLCRFINSVKKNYR--VPYNNMKAATVAHGM 537
DB 354 SGNRPITYIMHTIFQERDLTKTFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 413
QY 538 YAILQNN--NGLEPTLERKGLLIACLDHLDHGRFSNSYLQKFDHPPLAALYS-TSTMEOH 594
DB 414 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTNSBLAMVNDSSVLENH 473
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEMYQT--- 651
DB 594 EISPCDKHNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDRNEWYQSTIP 652
QY 498 CG-----TSCFELEKLCRFINSVKKNYR--VPYNNMKAATVAHGM 537
DB 354 SGNRPITYIMHTIFQERDLTKTFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 413
QY 538 YAILQNN--NGLEPTLERKGLLIACLDHLDHGRFSNSYLQKFDHPPLAALYS-TSTMEOH 594
DB 414 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTNSBLAMVNDSSVLENH 473
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEMYQT--- 651
DB 594 EISPCDKHNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDRNEWYQSTIP 652
QY 709 QPIPMMDKDEBVOGQGFYNAVAIPCYTTLTQIL-PTPEPLKACRDINQMEKYR 767
DB 594 EISPCDKHNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDRNEWYQSTIP 652
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 653 -----QSPSPAP--DDPEE 664

RESULT 7
US-10-492-835-28
; Sequence 28, Application US/10492835
; Publication No. US2005028960A2
; GENERAL INFORMATION:
; APPLICANT: MEMORY PHARMACEUTICALS CORPORATION
; TITLE OF INVENTION: CYCLIC AMP PHOSPHODIESTERASE 4D7 ISOFORMS AND METHODS
; FILE REFERENCE: MEMORY 4 WO
; CURRENT APPLICATION NUMBER: US/10/492,835
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 28
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-492-835-28

Query Match      7.5%; Score 315.5; DB 6; Length 748;
Best Local Similarity 25.4%; Pred. No. 1.5e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWOGMRNLPAR---ICRDIELFPHDIGPENNMPGIFVYMIHRS 497
DB 306 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVFRIAEI 353
QY 498 CG-----TSCFELEKLCRFINSVKKNYR--VPYNNMKAATVAHGM 537
DB 354 SGNRPITYIMHTIFQERDLTKTFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 413

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QY 538 YAILQNN--NGLEPTLERKGLLIACLDHLDHGRFSNSYLQKFDHPPLAALYS-TSTMEOH 594
DB 414 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTNSBLAMVNDSSVLENH 473
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEMYQT--- 651
DB 474 HLAVGFKLQRENCIDIFONTLKQROSLRKRVIVIVLATDMSKMNLLADLKTWETKCV 533
QY 652 ---GSLNHNSHDRVIGLMMTACDLCSTYKLPVTKLTANDIYAEFMAEGDEMKLGI 708
DB 534 TSSGVLLLDNYSDRLOVQNNVHCADLSNPTKPLQLYRQWTRIMEEFPQGDREBERGM 593
QY 709 QPIPMMDKDEBVOGQGFYNAVAIPCYTTLTQIL-PTPEPLKACRDINQMEKYR 767
DB 594 EISPCDKHNA-SVEKSGVGFIDYIVHPLMETWADLVHPDAQDILDLEDRNEWYQSTIP 652
QY 768 GEETAMWISGPGAPASKSTPEK 789
DB 653 -----QSPSPAP--DDPEE 664

RESULT 8
US-11-091-018-2
; Sequence 2, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Gierardotfir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Guichef, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010.016
; CURRENT APPLICATION NUMBER: US/11/091.018
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-091-018-2

Query Match      7.5%; Score 315.5; DB 7; Length 809;
Best Local Similarity 25.4%; Pred. No. 1.7e-20;
Matches 97; Conservative 75; Mismatches 153; Indels 57; Gaps 14;

QY 442 MEKLSYHSICTSEEWOGMRNLPAR---ICRDIELFPHDIGPENNMPGIFVYMIHRS 497
DB 367 VKLHMSSSLTN---SSIPRGVKTQEDVLAKELE---DV---NKM-GLHVFRIAEI 414
QY 498 CG-----TSCFELEKLCRFINSVKKNYR--VPYNNMKAATVAHGM 537
DB 415 SGNRPITYIMHTIFQERDLTKTFKIPVDLTITYLMTLEDHYNADVAHYNNHAAADVOST 474
QY 538 YAILQNN--NGLEPTLERKGLLIACLDHLDHGRFSNSYLQKFDHPPLAALYS-TSTMEOH 594
DB 475 HVLSTPALAEAVFTDLIELAIIPASAIHDVDHPGVSNQFLINTNSBLAMVNDSSVLENH 534
QY 595 HPSQTVSLQLEGNHIFSTLSSEYBOVLEIRKAIITDIALYFGNKKOLEMYQT--- 651
DB 535 HLAVGFKLQRENCIDIFONTLKQROSLRKRVIVIVLATDMSKMNLLADLKTWETKCV 594

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Db      354  SGNRLPLVIMHTIFQERDLTKTFKLPVDLTITLMTLEBDYHADVAHYNNIHAADVQST 413
Qy      538  YAILONN--NGAFTDLERKGLIACCHDLDRGFNSVLOKFDHLLALYS--TSMEOH 594
Db      414  HVLSTPALAEAVFTDLEIILAAIPASAIHVDPHGVSNQFLINTNSLAMYDSSVLENH 473
Qy      595  HFSQTVSILQLEGHNFSTLSSSEYEQVLEIRKAIATDLALYFGNRKQLEMYQT--- 651
Db      474  HIAVGFKLQENECDFOLUTKKQKQSLKMAIDIVLATDMGKHMLLADLKTMYETKYV 533
Qy      652  ---GSLINHGSHRDRVIGLMTACDLCGVTKLMPVTKLTANDIYAEFAEDEMKGUGI 708
Db      534  TSSGVLTLDNYSRDLQVLQNMVHCADLSNPTKPLQLYRQWTRIMEEFPQCDREERGM 593
Qy      709  QPIPMMDRKREBVPQGGGFYNAVAIPCYTTLTQL--PTEPBLKACDNLNOMEKVIR 767
Db      594  EISPMCDKRNA--SVEKSYQGFIDYIVHPLMETWADLVHPDADLIDTLEDNEMYQSTIP 652
Qy      768  GETAMWISGPGAP 782
Db      653  -----QSPSPAP 659

RESULT 12
US-10-873-528-12
; Sequence 12, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129MO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-12

Query Match      2.5%; Score 107; DB 6; Length 1216;
Best Local Similarity 18.9%; Pred. No. 0.33;
Matches 166; Conservative 119; Mismatches 273; Indels 320; Gaps 46;

Qy      46  ESVAETVEKMLKRTNKAKD-----PSPK-----VSRYODTN 80
Db      366  QSFMSDFEAYARQKQENAFEFADISHYTIILENFQVRSYQERFHEVAVDEYODTN 425
Qy      81  MGVVYELNSYIEORLDTGSDNHLLEYLSIIRIATKADGAFALYFGECSNLCVPIFP 140
Db      426  -----HIQER-----MLEILS-----NGNRRPMVGDIKQSIYRF-- 454
Qy      141  GMEKGGPRLIPAGPIITGTTISAVAKSKRTLVEDILDERPPRTGLESSTRLOSVC 200
Db      455  --RQADPOIF-----NEKFOR-----YAQNQE--- 475
Qy      201  LPIVTAIGDLIGILEYRIMGKAPCLSHQEVATANTLAWASVAIHQVYCRGLAQTEIN 260
Db      476  -----GRLLIKENFR-----SSSEVLST-----NDVF 499
Qy      261  DELLD--VSKYFDNIIVALIDSLEHIMTYA--KNLVNADRCALFOVDHKNKELYDLPDI 316
Db      500  ERLMDQVEGEIINYDN-----KHQLVFANTKLTLPNPNKAAF-----LTYDKDDT 543

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Qy      317  GEEKGKPIFKTKYIRPSI-----EKGI-----GOVARTGEVINTIDPAVADP 360
Db      544  GEEBSQVETLGTGEMRLVIEKILKHOEKGVAFREIALLTSSSRNDQILLALSEYGP 603
Qy      361  -----RFRREVDLYGTYTRNILCPYVRSQSVGVOMNKSIGSAPSKTDENNFK 412
Db      604  VKTQGEQNNTYQSLSEVQVMTDLRLVHNPLQDYALV-----ALMKSPPFGDEDELA 655
Qy      413  MPAVCAALAHCAAMMYHIRSE-----CIYRVTEKL--SYHSICTSEMOGLMR-- 461
Db      666  RLSTQKADKQHEINLEYELVNAQKASQKGLHTLALAEKUKOFNDILAS--WRLYAKTH 713
Qy      462  --FNLPARICRDIIEFHD--IGPENMMPGIFVYMIRHSCSTSGFE--LEKRCRFMSV 515
Db      714  SLVDLWKIYND--RFYDYDYGALPN--GPANQANLYALALADQPEKSNFGLSIFIMI 770
Qy      516  KKNTRRVEYHNWKI--AVTYAHCMYAILQNNNGLFEDLERKL--LIACLCHDLD-- 566
Db      771  DQVLEA-----QHDLASVAAVAPPKDAV-----ELMTIHKSGGLEFPYVFIANDQDPNK 819
Qy      567  -----HRGPNSTYLKFPDHPPLAALYSTSMEOHHSQTV--SILQLEGHNIPST 613
Db      820  QDSMSEVILSRONGGVKTIKME-----TGAVED--HYPKTIKLSIPSLTRQONEE 870
Qy      614  LSSSEYEQVLEIRKAIATDLALYF--GNRKQLE--MYQGSIN--LHNSHR 662
Db      871  LQLASYSQRMRLVYAMTRAKKLYLVGKSGREKLESKEYPAAKNGKLNSTRLOANRFQ 930
Qy      663  DRVIGLMMTACDLCGVTKLMPVTKLTAND--IYAEFAE-----GDEMKGLGIQPI 711
Db      931  D-----WLMASIKVFTFKDKLNFYSYRFGEDQLTREAIQLELETSPLODS 974
Qy      712  PMDRDKREBVPQ-----OLGFYN-----AVAIPCYTTLQILPTEPBLKACDNLN 761
Db      975  SQADRQSDITKEALDEMKVEYVNTLHRAIIEIPSVQTSPIKQFIETPVM----- 1026
Qy      762  WEKYIRGEETAMWISGPGA-----PSKSTPEKL 790
Db      1027  -----MEGYE-----IAGQGSYVKKISPLPDPSTREKV 1056

RESULT 13
US-11-046-346-1
; Sequence 1, Application US/11046346
; Publication No. US20050255502A1
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Institute
; APPLICANT: D'Andrea, Alan D
; TITLE OF INVENTION: Method for Determination and Quantification of Radiation or Genotc
; FILE REFERENCE: 7032/2082
; CURRENT APPLICATION NUMBER: US/11/046,346
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 60/540380
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-046-346-1

Query Match      2.5%; Score 106; DB 7; Length 1451;
Best Local Similarity 18.0%; Pred. No. 0.53;
Matches 159; Conservative 131; Mismatches 266; Indels 326; Gaps 44;

Qy      21  SPSLTDEKVAUYLSLHPQVDEPFVSASVETVEKMLKRTNKAKDPSPKSVRYODTN 80
Db      592  SPSLTQF--RANLS-----DEQCTQVTS-----LLQVLHSC--SQDSQVQASALYTD-- 633
Qy      81  MGVVYELNSYIEORLDTGSDNHLLEYLSIIRIATKADGAFALYFGE--CNNSLCVFI 138

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